

	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460.1 ubinu	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
5	449909	AA004681	Hs.59432	ESTs	3.5
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
10	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
15	423645	AI215632	Hs.147487	ESTs	3.4
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.4
	434966	AA657494		gb:nt66f04.s1 NCL_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902: Homo sapiens progesterone induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
20	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheti	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056: Plasma membrane calcium	3.4
25	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AI655662	Hs.197698	ESTs	3.4
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
30	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.4
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	3.4
35	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
40	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
45	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23543	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
50	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
55	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
60	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp584C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
65	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
70	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
	436654	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
75	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263: HSPC213.	3.3
80	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (fr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78855 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.3
	432363	AA534489		gb:mf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV555234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hibr1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
30	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AI077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zpp99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypothi	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	S-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chal	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypothi	3.2
80	452295	BE379936	Hs.28866	programmed cell death 10	3.2
	437517	AB927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2



	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
	433852	AI378329	Hs.126629	ESTs	3.2
5	439735	AI635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
	415715	F30364	Hs.302204	ESTs	3.2
10	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
	408784	AW971350	Hs.63386	ESTs	3.2
15	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.2
	405558			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
20	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13348	3.2
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
25	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
30	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
	438666	AW014493	Hs.126727	ESTs	3.1
35	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypothi	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
	443331	AI052026	Hs.149995	ESTs	3.1
60	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
	438979	AW976218	Hs.32565	ESTs	3.1
70	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
75	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440099	AL080058	Hs.6909	DKFZP584G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
5	400664			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
15	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:428026, mRNA,	3.0
20	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
	439703	AF086539	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443967	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	415954	AA171850	Hs.42251	ESTs	3.0
50	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
60	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
65	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:z97g10.r1 NCL_CGAP_GC81 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

TABLE 60B

Key: Unique Eos probeset identifier number

CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
5	411479	1247077_1 AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
10	411667	1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	414372	143909_1 AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	414680	147525_1 AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
15	415989	156454_1 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416288	1585983_1 H51299 H44619 H46391 R86024 H51892 T72744
	416882	162718_1 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
20	416913	163001_1 AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	417379	167238_1 AA196390 AA507837 AA196468
	418304	173658_2 AA215702 AA368006 AA215703 BE066555 BE006876
	418647	177521_1 AA226198 AA226513 AA383773
25	418866	179788_1 T65754 AA229857 AA229658
	419536	185688_1 AA603305 AA244095 AA244183
	419544	185760_2 AI909154 AA526337 AA244193 AI909153
	423412	228001_1 AF109300 AI299378 AI202654
	423800	232161_1 AA331156 AA331157 AA331155
	426226	262918_1 AA769045 AA372590 AW963633
	426413	266650_1 AA377823 AW954494 AI022688
	426503	268283_1 AA380153 AA380233 AW963529
	426775	271683_1 AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
30	426991	27415_1 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
	428342	290035_2 AI739168 AA426249 AI199536 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
35	429163	300543_1 AA884766 AW974271 AA592975 AA447312
	429220	301384_1 AW207206 AW341473 AA448195 AI951341
	429258	301917_1 AA448765 C04967 C03045 AA658293
	430935	325772_1 AW072916 AI184913 AA489196 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
	430968	326269_1 AW972830 AA527647 AA489820 AA570362
	431429	33313_1 AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA056148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T35956 BE618035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308 AA187561 AA311680
40	432093	341283_1 H28383 AW972670 H28359 AA525808
	432125	341776_1 AW972667 AA526539 AI057032 AW167842
	432189	342819_1 AA527941 AI810608 AI620190 AA635266
	432340	345248_1 AA534222 AA632632 T81234
45	432363	345469_1 AA534489 AW970240 AW970323
	432600	350959_1 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	432810	354375_1 AA863400 AI991439 AW016017 AW014704 AI367512 H17550 AA744752 R46187 AW471324 AI126670 AA826033 AI276287 AI094253 AI286003 AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI359156 AA555542
50	434579	38916_1 T55958 T57205 AF147346
	434966	396504_1 AA657494 AI582663 AI581639
	435023	398093_1 AI692552 AI393343 AI800510 AI377711 F24263 AA661876
	437866	44433_2 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
55	438147	45074_1 AW250553 L07876 Z36843 R30693 AI190097 AW965317
	439092	468554_1 AA830149 AW978407 M85983 AW503637
	439518	47334_1 W76326 AF086341 W72300
	439904	479942_1 AW892676 AA853877 D44747
60	440840	50357_2 AW629566 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877
	441102	509604_1 AA973905 AI299888 AA917019 H63235 T90771
	442562	54500_2 BE379584 R34211 BE544768 AW973709 AI653056 AI653173 AI266043 AI656750 H74180 AI492830 AI376080 AI472184 D59940 AW170056 AI082443 AW021142 AI167921 AI348677 AI278577 AW130886 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA554902 D62102 AI0007
65	443161	561305_1 AI038316 AI344631 AI261653
	445808	65133_1 AV655234 AW966332 AA340239
	447082	707248_1 T85314 AI360684 T85628 T91254
	448212	755099_1 AI475858 AW969013
70	449625	8113_1 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 O59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816888 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
75	450582	83933_1 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	452260	9074_1 AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228 BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI659875 AW272338 AI423136 AI089270 AI160904 AA664354 BE1
80	452598	92338_2 AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AI138076 BE180510 AI926721 AI399955 AA749139 AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI816834 N25206 AA828301 AI084565 AI302816 AA026905 AA77255
	452815	93255_1 AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
	453802	981589_1 AL134757 AW079131
	455100	1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034

457728 393853\_1 AW974811 AA651634 AA650072

## 5 TABLE 60C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham 1. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NI\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

45	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of prostate tumor to normal adult body tissue			
	R2:	Ratio of prostate tumor to normal prostate tissue			
50					
	Pkey	ExAccn	UnigenelD	Unigene Title	R1 R2
55	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2 42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.2 26.5
	420729	AW964897	Hs.290825	ESTs	3.7 15.8
	401197			ENSP00000229263*.HSPC213.	3.0 12.6
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4 12.4
	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3 12.3
60	443271	BE568568	Hs.195704	ESTs	11.6 11.6
	434078	AW680709	Hs.283683	chromosome 8 open reading frame 4	2.1 11.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4 9.4
	417315	AI080042	Hs.180450	ribosomal protein S24	2.3 9.0
	416182	NM_004354	Hs.79069	cyclin G2	8.4 8.4
65	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2 8.4
	434217	AW014795	Hs.23349	ESTs	8.3 8.3
	425782	U68468	Hs.159525	cell growth regulatory with EF-hand doma	8.3 8.3
	442501	AA315267	Hs.23128	ESTs	2.0 8.3
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1 8.1
70	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.1 8.0
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0 7.9
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5 7.5
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4 7.4
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4 7.3
75	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2 7.2
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0 7.0
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0 6.6
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3 6.3
	411373	BE326276	Hs.8861	ESTs	3.2 6.3
80	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7 6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	2.3 6.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	6.1 6.1
	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	2.6 6.0

5	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.3	5.9
	431548	AJ834273	Hs.9711	novel protein	15.7	5.8
10	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.65744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
15	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
	451684	AF216751	Hs.26813	CDA14	3.9	5.4
20	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
25	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
30	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
	439024	R96696	Hs.35598	ESTs	5.4	4.8
35	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (tr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464		gb:tt8804.x1 NCI_CGAP_Pr28 Homo sapiens	9.1	4.7
40	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476:gil12737279[ref]XP_012163.1]	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSDH region gene 1	2.1	4.6
45	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155955	ESTs	2.2	4.6
	427078	AI676062	Hs.111902	ESTs	4.8	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
50	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
55	428826	AL048842	Hs.194019	attractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	418701	AA814948	Hs.95343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbH19W	2.2	4.2
60	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
	443622	AI911527	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
65	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433887	AW204232	Hs.279522	ESTs	4.1	4.1
70	436556	AI364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443646	AI085198	Hs.164226	ESTs	4.1	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
75	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KIX 18)	3.9	3.9
	444755	AA431791	Hs.113823	CtpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
80	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

5	422975	AA347720	Hs.122659	KIAA0264 protein	2.2	3.8
	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
10	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	AI263307	Hs.239884	H2B histone family, member L	9.2	3.8
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	3.7	3.7
15	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	AI571940	Hs.7549	ESTs	3.6	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
	451009	AA013140	Hs.115707	ESTs	4.1	3.6
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	AI357412	Hs.157601	ESTs	7.7	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
25	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332086	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieli	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KIX 4, clone HF.1	2.2	3.5
30	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	AI918950	Hs.123642	EphA3	16.5	3.5
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
35	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288909	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.1	3.4
	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
40	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5867	RNA binding motif protein 7	3.3	3.3
	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
45	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
50	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
55	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
	444489	AI151010	Hs.157774	ESTs	3.2	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
60	453078	AF053551	Hs.31584	metaxin 2	2.1	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
	434804	AA649530	Hs.348148	gbms44f05.s1 NCL_CGAP_Alv1 Homo sapiens	2.1	3.1
	445840	AI277811	Hs.146291	ESTs	3.1	3.1
65	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW962912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
70	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245582	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400286	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
	420154	AI093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
75	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
	433285	AW975944	Hs.237396	ESTs	7.7	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
80	445921	AW015211	Hs.146181	ESTs	4.3	3.0
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	A1628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	A1582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debris	2.9	2.9
	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	2.9	2.9
5	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	A1287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	A093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451796	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (f	2.9	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
15	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calcisarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIF, polype	2.8	2.8
	433865	N29862	Hs.44104	ESTs	2.8	2.8
20	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95087	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654660	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE622685	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
35	422667	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
40	442633	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
55	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A45010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW556008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191060	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
	431474	AL133990	Hs.190642	ESTs	9.3	2.5
70	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656: Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82265	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49354 59 protein	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA448765		gb:zx10e09.r1 Soares_talal_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
15	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
20	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
40	419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
	443194	AI954958	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfor1)	4.1	2.3
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405885			C2002829:gi4507689 ref NP_003298.1  tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478::SECRETORANIN III.	2.2	2.2
	418281	U09550	Hs.1154	ovoiductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	tol-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2



	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
5	438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
	424036	AA770688		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
10	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008:gi7303957 gb AAAF59000.1  (AE00	3.1	2.1
	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
15	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
20	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
	452959	AI933416	Hs.189574	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
25	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
30	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
35	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
45	436278	BE396290	Hs.5097	synaplogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	Integral membrane protein 2B	2.3	2.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
50	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
	413627	BE182082	Hs.246973	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
55	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
	409219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
60	434128	W83170	Hs.284164	protein x 0004	2.7	2.0
	434503	T96231	Hs.17762	ESTs	2.0	2.0
	443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
65	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
70	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
75	437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
80	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 618

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150955 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189605 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749884 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 WD4957 W63676 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
15	424036	23460_1	AA770688 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290558 C15404
	426413	266650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA448765 CD4967 CD3045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095553 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
20	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV655234 AW956332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T813
	450580	83929_1	N40087 H12925 AA480779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt\_position: Indicates nucleotide positions of predicted exons.

40

Pkey	Ref	Strand	Nt_position
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402802	3287156	Minus	53242-53432
403047	3540153	Minus	59793-59968
404641	9796810	Minus	32247-32362
405685	4508129	Minus	37956-38097
406068	9114084	Plus	382-543

45

50

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

65 R1: Ratio of prostate tumor to normal prostate tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	15.8
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
75	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	12.6
	401197			ENSP00000229263~HSPC213.	12.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
80	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE568568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
20	425174	D87450	Hs.154978	KIAA0261 protein	8.6
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
25	434217	AW014795	Hs.23349	ESTs	8.3
	417353	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (StII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-link	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426759	AI590401	Hs.21213	ESTs	6.8
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AJ796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75365	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
65	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-ref avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AI745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9

	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	5.9
	431548	AI834273	Hs.9711	novel protein	5.8
5	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	siatyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
15	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
20	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AFD13168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
25	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheli	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
30	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449507	AA004825	Hs.103281	ESTs	5.4
35	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
40	403851			C5002154*gi17299015 gb AA54217.1  (AE0	5.3
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
45	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (tr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
50	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
55	414212	AA136569	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
60	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435708	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
65	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
70	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	AI470523	Hs.135336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
75	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheli	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
80	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (tr	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	slap II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AI692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AI685464		gb:tl88f04.x1 NCI_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C15000476*:gll12737279[refl]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425807	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AI676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46967	HSPCO34 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443956	Hs.31595	ESTs	4.4
40	443250	AI041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:zkl85d12.r1 Soares_pregnant_uterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
45	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
	430259	BE550182	Hs.127826	RafGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
	436446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438656	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
55	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_008732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-in	4.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressorHDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b5?	4.2
	439518	W76326		gb:zld60d04.r1 Soares_fetal_heart_NbHH19W	4.2
	450651	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AI421645	Hs.139851	caveolin 2	4.2
	414291	AI289619	Hs.13040	G protein-coupled receptor 85	4.2
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AI911527	Hs.11805	ESTs	4.1

	436576	AI458213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567669	Hs.40342	putative nuclear protein	4.1
	445468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
15	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
20	436556	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	VW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
	439394	AA149250	Hs.56105	ESTs	3.9
45	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-tyrosine/alpha-aminoadipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypothe	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422975	AA347720	Hs.122569	KIAA0264 protein	3.8
	403100			C2001027:g[17296271]gb AA051562.1  (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0510	3.8
	432363	AA534489		gb n76911.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861896	Hs.304505	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-lik	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350:gil6578126lgblAAAF17706.1 AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopolei	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KIX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446416	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb:yg12c04.r1 Soares infant brain 1NIB H	3.5
	435613	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb:yy59d111.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
75	401744			Target Exon	3.4
	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

5	432741	AI72358	Hs.185118	ESTs, Moderately similar to A37413 catbl	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
	428466	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
10	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
15	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
	431689	AA305688	Hs.267695	UDP-GalbetaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
20	403389			C3001393*gi13327090 dbj BAA31613.1  (AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
25	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
	417295	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
30	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955695	Hs.90960	ESTs	3.3
35	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALL5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
40	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA: cDNA DKFZp564D1164 (f	3.3
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family Inhibitor	3.3
45	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	Integrin, alpha 1	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
50	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
55	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
60	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
65	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
70	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
75	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
80	448944	AB014605	Hs.22599	atrophy-1 Interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2



	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
15	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177654	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
	445840	AI277811	Hs.146291	ESTs	3.1
20	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434i1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
25	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
	403423			Target Exon	3.1
30	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1
35	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypothe	3.1
	422481	AL050163	Hs.117339	DNA-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
40	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothe	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A45010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R06054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
80	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015583	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (I	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI674468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148
414680	147525_1	AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282786 AA137264 AW236107 AW769
415528	1539409_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
416128	157163_1	AA708749 AA644620 AA652769 AA242975 AA151074 T19890
416882	162718_1	R17236 R52580 F11642
422673	219674_1	AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
426448	267323_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
430935	325772_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
430968	326269_1	NS9027 AA314694 NS3937 R08100
431304	331286_1	R06054 AA378789 AW956453
431676	336411_1	AW072916 AI184913 AA489195 AW466994 AW469044 NS9350 AI819542 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
432125	341776_1	AW972630 AA527647 AA489820 AA570362
432363	345469_1	BE157283 BE157287 AA502438
437158	43392_5	AI685464 AW971336 AA513587 AA525142
437866	44433_2	AW972667 AA526539 AI057032 AW167842
439047	468139_1	AA534489 AW970240 AW970323
439518	47334_1	AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
450506	836_1	AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
450580	83929_1	AA156781 AW293839 U52054 AA024953 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
452260	9074_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
453024	944876_28	AW979177 AA846994 AA829672
454573	1292917_1	W76326 AF086341 W72300
456719	222707_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AI150883 AW8
		AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903358 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984801 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE602530 Z25032 AA805324 AA449241 AI651825 AI264853
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8119067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39824-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

5

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75<sup>th</sup> percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

10

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

15

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of normal prostate tissue to prostate tumor tissue

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Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	A1738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	A1791314		gb:aa46g12y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	A1459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	A1280308	Hs.274361	amiloride-sensitive cation channel 2, na	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936:g[3746443]gb AAC63969.1  (AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	A1523646	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1N1B H	4.6
441040	AW449782	Hs.178903	ESTs	4.6
442764	A1762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	A1535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	A1801500	Hs.128457	ESTs	4.4
436781	A1914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*:Homo sapiens runt-related tra	4.3
442931	A1024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457138	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	A1580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AI218950	Hs.125461	hypothetical protein FLJ11539	4.1
5	425094	AJ955956	Hs.21417	ESTs	4.1
	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AJ028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
15	449233	BE048401	Hs.196511	ESTs	3.9
	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AJ821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
20	409679	BE250521		ras homolog gene family, member A	3.8
	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:mp86b01.s1 NCL_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
25	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
	443313	AJ796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gil6679124[ref]NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
30	408229	AW176091		gb:QVO-BT0107-250899-007-b08 BT0107 Homo	3.7
	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*gil12654691[gb]AAH01185.1[AAH0	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
35	436524	AA922236	Hs.221037	ESTs	3.7
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
40	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
45	442097	AW015799	Hs.128474	ESTs	3.6
	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
50	400749			NM_003105*:Homo sapiens sortilin-related	3.6
	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63f08.r1 NCL_CGAP_GCB1 Homo sapiens	3.5
55	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
	429043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AJ371978	Hs.128326	ESTs	3.4
60	445045	AI652676	Hs.147256	ESTs	3.4
	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KIAA1578 protein (Fragm	3.4
	445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
65	444286	AI625304	Hs.190312	ESTs	3.4
	442027	AI652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gil2695979[emb]CAA70854.1] (Y0	3.4
70	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
75	418672	L44284	Hs.12915	ESTs	3.3
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
80	458539	AI733837	Hs.145661	ESTs	3.3
	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

5	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
10	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
15	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	filin-cap (telithonin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
	451686	AA059246	Hs.110293	ESTs	3.1
20	423637	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
25	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Bm52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
30	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
35	419386	AA236867		ESTs, Weakly similar to I38022 hypothei	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658*:HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
40	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
45	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
50	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_UI4 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI635539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
55	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
60	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypothei	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
65	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipooxygenase 3	2.9
70	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
75	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fs, clone L	2.9
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCL_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:zi199b10.s1 Soares_testis_NHT Homo sap	2.8
80	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypothei	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fs, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

	426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656			Target Exon	2.8
	407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	Hs.117341	ESTs	2.8
	433565	AA599763	Hs.112520	ESTs	2.8
	451004	AA044967		gb:z53409.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770			NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	Hs.189788	ESTs	2.8
	454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060	Hs.34382	ESTs	2.8
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	Hs.208919	ESTs	2.7
15	406337			C14000021:gl 7242973 dbj BAA92547.1  (AB	2.7
	401884			Target Exon	2.7
	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	Hs.201201	ESTs	2.7
	450044	R66444	Hs.51891	ESTs	2.7
20	403630			C3001708*:gl 4758028 ref NP_004360.1  co	2.7
	445514	AJ241280	Hs.148906	ESTs	2.7
	446362	AW612481	Hs.104105	ESTs	2.7
	432492	AW275110	Hs.271106	ESTs	2.7
	430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330	Hs.118796	annexin A6	2.7
	413155	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041	Hs.199291	numb (Drosophila) homolog-like	2.7
	446523	NM_003063	Hs.334629	sarcolipin	2.7
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hbrf1)	2.7
	405678			CX001454:gl 8393794 ref NP_058681.1  myo	2.7
	432789	D26361	Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	Hs.284284	zinc finger 1111	2.7
	415984	R19046	Hs.5010	gb:yg21f11.r1 Soares infant brain 1N1B H	2.7
	402844			C1000118*:gl 9951913 ref NP_062832.1  pr	2.7
	456666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	Hs.244621	ribosomal protein S14	2.7
40	404979			Target Exon	2.7
	412318	AW936911	Hs.326729	hypothetical protein MGC11082	2.7
	424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ110689 fis, clone NT	2.7
	412542	AW961516	Hs.95097	ESTs	2.7
	441975	AW173248	Hs.344285	EST	2.7
45	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205	Hs.305890	BCL2-like 1	2.7
	439204	AF087987	Hs.42695	EST	2.7
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	2.7
50	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
	443359	AJ792583	Hs.135354	ESTs	2.7
	447336	AW139383	Hs.245437	ESTs	2.7
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
	436030	R02287	Hs.121052	ESTs	2.7
55	449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AJ345995	Hs.127383	ESTs	2.6
	415054	AJ733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	Hs.293896	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	Hs.256879	ESTs	2.6
60	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083		wee1 (S. pombe) homolog	2.6
	426629	AJ203933	Hs.97142	ESTs	2.6
	415831	H15145	Hs.30509	ESTs	2.6
	412281	AJ810054	Hs.14119	ESTs	2.6
65	434898	AW500458	Hs.28956	KIAA0460 protein	2.6
	422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061		gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AJ215667	Hs.175044	ESTs	2.6
	438548	AA813125	Hs.146335	ESTs	2.6
70	450399	AW511049	Hs.202007	ESTs	2.6
	420833	R47948	Hs.188732	ESTs	2.6
	453903	AW299606	Hs.232777	ESTs	2.6
	443650	AJ698330	Hs.151444	ESTs	2.6
	427419	NM_000200	Hs.177888	histatin 3	2.6
75	423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	Hs.40730	ESTs	2.6
	441358	AW173212	Hs.129041	ESTs	2.6
	402706			Target Exon	2.6
	436054	AJ076262	Hs.119813	ESTs	2.6
80	402749			Target Exon	2.6
	442472	AW806859		gb:MRO-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AJ734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872		gb:zo57d07.s1 NCL_CGAP_Lu5 Homo sapiens	2.6
	405564			Target Exon	2.6

	405003		Target Exon	2.6	
	459584	AI910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.6
	445060	AA830811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902:gil403440[gb]AAA73168.1 (M817	2.6
	416628	W03955		gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypothe	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA225522		gb:nc25c06.r1 NCI_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	Hs.90744	ESTs	2.6
	455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AI220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb:cm67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	Hs.170058	ESTs	2.6
20	441063	AA913819	Hs.188025	ESTs	2.6
	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	AI125263	Hs.170410	ESTs	2.5
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AI693930	Hs.148816	ESTs	2.5
	413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	Hs.6658	ESTs	2.5
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb:yf79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibitor	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	455401	W28146		gb:43f11 Human retina cDNA randomly prim	2.5
45	404678			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
	429906	AL080137	Hs.193743	ESTs	2.5
50	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
	438353	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

55	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
<hr/>		
60	Pkey	.CAT Number
	408229	1048482_1
	408432	1058667_1
	409679	114787_1
65	410483	1204995_1
	411320	1238624_1
	411332	1239102_1
	411356	1240273_1
	411426	1245515_1
70	411829	1260309_1
	411944	1266482_1
	413155	1351148_1
	413381	1365950_1
	413489	1373392_1
75	415054	151827_1
	415098	1522174_1
	415131	1523680_1
	415386	1535560_1
	415881	1564242_1
80	416628	1604848_1
	416935	163179_1
	419386	184356_1
	419896	1888662_1
	420778	196389_1
		AW176091 H24234
		AW195262 R27868 AW811262
		BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
		BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
		AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
		AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
		H45377 H21137 AW838640
		BE141714 AW845993 AW845989
		AW865749 BE179419 BE179492
		AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
		BE067952 BE067945 BE067942 BE067943 BE067944 BE067953 BE067956 BE067946
		BE090690 BE090688 BE090681 BE090693 BE090675
		BE144228 BE144291
		AI733907 AA159708 AI732614
		D59687 D59694 D59656 D59589
		D61119 D81508 D81734
		Z43087 F07410 H15506 H54108 R95033 H98000
		R35694 H12035 R53312
		W03955 H82332 H69247 H72486
		AA190712 AA190665 AA252564
		AA236867 AA237068 AA354236 AW957759 H08961
		Z99362 Z99363
		AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87796
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW458227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599
			C02215 AI6525
	423871	232749_1	AA331906 AA332484
10	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
	436190	41555_1	AK001059 AA633055
15	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
	447518	727487_1	T80061 AI382804
20	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
25	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072248 BE072229 BE072225 BE072210 BE072256 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	455887	1380836_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
50	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	89182-90053
	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
65	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
	402490	9797648	Plus	149982-150929
	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8469060	Minus	94723-94859
	403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
75	403649	8705159	Minus	27141-27247
	404260	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
	404678	9797204	Plus	115196-115448
80	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773



5	405152	9965561	Minus	137662-137969
	405258	7329310	Plus	129930-130076
	405422	7243869	Minus	101938-102079,102261-102443,102896-103202
	405564	2114222	Minus	16766-17344
	405678	4079670	Plus	151821-152027
	405735	9931101	Minus	29854-29976
	405770	2735037	Plus	61057-62075
	406003	8247800	Plus	42079-42516
10	406085	9123888	Plus	18665-18843
	406177	7279760	Minus	18930-19148
	406337	9213455	Plus	90117-90337
	406398	9256276	Minus	118691-118959
	406600	8248616	Minus	36296-36610

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Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

25	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of BPH tissue to normal adult body tissue		
30	Pkey	ExAccn	Unigene ID	Unigene Title
	420154	AI093155	Hs.95420	JM27 protein
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen
	419526	AI821895	Hs.193481	ESTs
	432441	AW292425	Hs.163484	ESTs
35	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti
	407202	N58172	Hs.109370	ESTs
	432101	AI918950	Hs.123642	EphA3
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen
	425075	AA508324	Hs.1852	acid phosphatase, prostate
40	414569	AF109298	Hs.118258	prostate cancer associated protein 1
	410929	H47233	Hs.30643	ESTs
	400287	S39329	Hs.181350	kallikrein 2, prostatic
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr
45	415989	AI267700		ESTs
	426336	AA503115	Hs.183752	microseminoprotein, beta-
	450693	AW450461	Hs.203965	ESTs
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of
	407168	R45175	Hs.117183	ESTs
50	408369	R38438	Hs.182575	solute carrier family 15 (H?? transport
	454119	BE549773	Hs.40510	uncoupling protein 4
	428819	AL135623	Hs.193914	KIAA0575 gene product
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278
55	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti
	433444	AW975324	Hs.128816	ESTs
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL
60	401424			NM_001172:Homo sapiens arginase, type II
	432435	BE218886	Hs.282070	ESTs
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1
	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_U04 Homo sapiens
65	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma
	432473	AI202703	Hs.152414	ESTs
	410330	AW023630	Hs.159425	ESTs
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH
	452792	AB037765	Hs.30652	KIAA1344 protein
70	418848	AI820961	Hs.193465	ESTs
	400292	AA250737	Hs.72472	BMP-R1B
	433647	AA603367	Hs.222294	ESTs
	453160	AI263307	Hs.239884	H2B histone family, member L
75	409262	AK000631	Hs.52256	hypothetical protein FLJ20624
	431474	AL133990	Hs.190642	CEGP1 protein
	429220	AW207206		ESTs
	428134	AA421773	Hs.161008	ESTs
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA
80	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu
	434792	AA649253	Hs.132458	ESTs
	433466	AA508353	Hs.105314	relaxin 1 (H1)
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 lino-1 pr
	428398	AI249368	Hs.98558	ESTs

	429260	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
5	429918	AW873986	Hs.119383	ESTs	9.1
	440260	AI972867	Hs.71130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450642	R39773	Hs.71130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
	446336	AW815036	Hs.151251	ESTs	8.4
20	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z <sup>3</sup> -1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.146625	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656859	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799909	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA: cDNA DKFZp564B083 (fr	6.9
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
	439569	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gbza32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
5	447156	AW274731	Hs.157920	ESTs	5.9
	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
10	438138	R98299	Hs.177502	ESTs	5.9
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
	434485	AI623511	Hs.118567	ESTs	5.8
15	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443950	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gbzv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902*:Homo sapiens progesterin induce	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gbxoc44f08.s1 NCI_CGAP_GC81 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AL049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.5
	426581	AB040958	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
60	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	423101	MB3941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
75	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
80	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
5	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.0
	407198	H91679		gb:yr04a07.s1 Soares fetal liver spleen	5.0
	403696			C4001100:gil5852342[gb]AAD54015.1 (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CLIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
10	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
15	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
20	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
25	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	4.7
30	452843	AI796769	Hs.208320	ESTs	4.7
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
35	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AI792628	Hs.133273	ESTs	4.6
	409731	AA125885	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
40	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small Inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	445024	AA993627	Hs.293907	hypothetical protein FLJ23403	4.6
45	447805	AW627932	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
50	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AI655499	Hs.161712	ESTs	4.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
55	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78968	Hs.14411	ESTs	4.5
60	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
65	418019	R68911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
	416705	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
75	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP0000020376*:PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 IMAGE resequences, MAGJ Homo	4.3

	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
5	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GC81 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001664:gil12698061[dbj]BAB21849.1 (AB	4.3
10	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
15	420905	AA521307	Hs.186651	ESTs	4.2
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
20	450597	AI701635	Hs.207077	ESTs	4.2
	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
25	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
30	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
35	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapia	4.1
40	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449907	AA004825	Hs.103281	ESTs	4.1
45	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
50	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
55	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
	442338	AI761976	Hs.156080	ESTs	4.0
	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
60	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
65	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	448131	AI675064	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partial	4.0
70	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
75	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW282779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
80	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

	416288	HS1299	gb:yp07c06.s1 Soares breast 3NbHst Homo	3.9
	420301	AA767526	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA888555	ESTs	3.9
5	435878	R08330	ESTs	3.9
	446862	AV660697	ESTs	3.9
	447530	AW192063	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403		Target Exon	3.9
10	448779	BE042877	ESTs	3.9
	420533	AI809510	ESTs	3.9
	411084	T18987	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	KIAA0888 protein	3.9
	423453	AW450737	CGI-09 protein	3.9
15	434833	AF156548	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420	gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AW848047	gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	ESTs	3.9
	421129	BE439899	ESTs	3.9
20	424332	AA338919	ESTs	3.9
	441766	R53790	hypothetical protein FLJ14393	3.9
	447033	AI357412	ESTs	3.9
	439306	BE220199	WD40 protein C1a01	3.8
	410352	AW969725	KIAA0373 gene product	3.8
25	407961	AW672939	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	microfibrillar-associated protein 1	3.8
	439560	BE565647	hypothetical protein FLJ12820	3.8
	440450	AI333129	ESTs	3.8
	458611	AI268407	DC-specific transmembrane protein	3.8
30	419589	AW973708	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
	431576	M76665	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE617907	ESTs	3.8
	438379	N23018	C-terminal binding protein 2	3.8
	416009	Z43062	gb:HSC12E041 normalized infant brain cDN	3.8
35	416534	H69043	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	423044	AA320829	protocadherin 18	3.8
	424701	NM_005923	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	ESTs	3.8
	437718	AI927288	ESTs	3.8
40	419831	AW448930	ESTs	3.8
	424830	AW270580	ESTs, Weakly similar to putative p150 IH	3.8
	426981	AL044675	KIAA0530 protein	3.8
	431447	AA505138	ESTs	3.8
	435932	W03928	ESTs	3.8
45	442447	AA999723	ESTs	3.8
	403242		Target Exon	3.8
	433908	AW298141	ESTs	3.8
	452323	W44356	ESTs, Weakly similar to T33468 hypothei	3.7
50	412095	AI624707	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
	418759	AA227879	ESTs	3.7
	422299	AK000181	hypothetical protein FLJ20174	3.7
	452462	BE173515	gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	423096	AA732684	progesterin induced protein	3.7
	454037	AW998716	gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420564	ESTs	3.7
	447785	AL041765	ESTs	3.7
	451746	M86178	ESTs	3.7
	453293	AA382267	ESTs	3.7
	436671	AW137159	ESTs	3.7
60	407437	AF220264	gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963897	KIAA1435 protein	3.7
	420092	AA814043	ESTs	3.7
	446947	AF146747	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	hypothetical protein FLJ23316	3.7
65	419875	AA853410	proenkephalin	3.7
	431231	AA653552	ESTs	3.7
	418348	AI537167	hypothetical protein FLJ23560	3.7
	419261	X07876	wingless-type MMTV integration site faml	3.7
	422899	D16471	Human mRNA, Xq terminal portion	3.7
70	429163	AA884766	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	ESTs	3.7
	440947	AA910403	ESTs	3.7
	404561		trichorhinophalangeal syndrome I gene (T	3.6
	430096	U91935	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	ESTs	3.6
	426991	AK001536	Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	ESTs	3.6
	414178	AW957372	ESTs, Weakly similar to I38022 hypothei	3.6
80	450630	AA010429	ESTs	3.6
	411057	AI681006	ESTs	3.6
	436326	BE085236	aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	six transmembrane epithelial antigen of	3.6
	423590	AW952412	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AJ381837	Hs.155335	ESTs	3.6
10	433563	AI732637	Hs.277901	ESTs	3.6
	425465	L18964	Hs.1904	protein kinase C, iota	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517::g[4758712]ref[NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
15	435177	AI018174	Hs.42936	ESTs	3.5
	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
20	427304	AA761526	Hs.163853	ESTs	3.5
	434763	AA648618		gb:ns07a11.1 r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
25	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9583	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AJ800041	Hs.190555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
40	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769::BG153Q3.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
50	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN81_HUMAN ZINC	3.4
65	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
70	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
75	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
80	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23605	ESTs	3.3

5	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AI215632	Hs.147487	ESTs	3.3
10	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
15	455710	BE072049		gb:PM4-BT0532-170100-004-f05 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
20	423412	AF109300		prostate cancer associated protein 5	3.3
	436962	AW377314	Hs.5364	OKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
25	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothe	3.2
	423595	R82826	Hs.220702	ESTs	3.2
30	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
35	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.2
	425557	T89839	Hs.119471	ESTs	3.2
	459546	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
40	401416			C14000338*gl 7459502 pir J574665 outer	3.2
	421928	AF013758	Hs.109843	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
45	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
50	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
	410870	U81599	Hs.66731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
55	415862	R51034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
60	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:lk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
65	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
70	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
75	420512	AA262886	Hs.143817	ESTs	3.1
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypothe	3.1
	423855	AA331761	Hs.254859	ESTs	3.1
	425805	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
80	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1



5	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL)	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.85447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
	433610	AA806822	Hs.112547	ESTs	3.1
	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
10	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogeni	3.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	Homo sapiens cDNA: FLJ22437 fis, clone H	3.1
15	410869	AW808361		gb:MR1-ST0111-111099-003-004 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
20	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	3.1
	433852	AI378329	Hs.126629	ESTs	3.0
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50955	Hs.159993	glycosyltransferase	3.0
	424690	BE538355	Hs.151777	eukaryotic translation initiation factor	3.0
25	405264			NM_030813*:Homo sapiens suppressor of po	3.0
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	3.0
	434497	AI821803	Hs.136580	ESTs	3.0
	420355	AW968263	Hs.123126	ESTs	3.0
30	403481			Target Exon	3.0
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547959	Hs.115838	ESTs	3.0
	430459	BE178539	Hs.278634	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	Hs.263478	ESTs	3.0
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
40	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	Hs.132950	ESTs	3.0
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450963	AI864668	Hs.48832	ESTs	3.0
45	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.0
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
50	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-l	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
55	437323	AA371145	Hs.194397	teplin receptor	3.0
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
60	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.0
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	428634	AA811845	Hs.106290	Kelch motif containing protein	3.0
65	431869	AA521136	Hs.190176	ESTs	3.0
	435008	AF150262	Hs.162898	ESTs	3.0
	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retroviri	3.0
	451391	AA017410	Hs.40668	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probe set identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808365 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934
80			AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
			AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528

411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
412988	1342150_1	AW848905 AW848214
413081	1348563_1	BE046680 BE046738 BE044958
413525	1374635_1	BE064415 BE064430 BE064448
415989	156454_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
416009	1566379_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
416288	1585983_1	Z43062 R13213 H14422
416882	162718_1	H51299 H44619 H46391 R86024 H51892 T72744
418259	173388_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
418866	179788_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24577 R40635 H05100 R40597
418948	180808_1	AA215404 AI990909 BE464132 AW271459 N74332 AI262061
419536	185688_1	T65754 AA228857 AA229658
420111	190755_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
420352	192979_1	AA603305 AA244095 AA244183
423412	228001_1	AA255652 AA280911 AW967920 AA262684
424200	236595_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
426413	266650_1	AF109300 AI299378 AI202654
426503	268283_1	AA337221 AA336756 AW966196
426991	27415_1	AA377823 AW954494 AI022688
428002	285602_1	AA380153 AA380233 AW963529
428342	290035_2	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
429163	300543_1	AA418703 AA418711 BE071915 BE071920 BE071912
429220	301384_1	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
430535	319643_1	AI092404 AI085630 AA731340
432600	350959_1	AA884766 AW974271 AA592975 AA447312
432765	353907_1	AW207206 AW341473 AA448195 AI951341
433523	368873_1	AW968485 AW968670 AA480922 BE350425
434763	392847_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
436295	41733_1	AJ003429 AJ003367 AA564825
436326	41795_2	H29682 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
437866	44433_2	AA648618 AW974389 H51771
439092	468554_1	N73895 AJ001872
439306	47088_1	BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281
440840	50357_2	AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706
440947	505904_1	AW270601 AW873282
442481	543588_1	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
445432	63943_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733
448044	747195_1	AA812489 AW874142 AI47188
449343	80517_2	AA830149 AW978407 M85983 AW503637
449570	81018_1	BE220199 W01813 AF086118 N70760 BE221405
449625	8113_1	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207
450317	831956_1	AA921877
450580	83929_1	AA910403 AI815593 W58361 AW162520 AI816550
450582	83933_1	N98828 BE079873 AI110738 AF074645
450687	84327_1	AV653771 BE089370
452462	918580_1	AI458682 H24240 R14537 R18426 AW867082
453682	977454_1	AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053
454037	996287_1	AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467
454096	1007449_1	H00789 R76925 AW1828
454171	1049240_1	AA001793 AA001871
454457	1207274_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760
454860	1237732_1	N48874 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
454968	1272541_1	AI692689 R14223 R18395
455276	1348557_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
455466	1352368_1	AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
457374	328758_1	AA164518 AA730973 W00417 W65303
458912	823104_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
		AA495800 AA495737 AA010736 AA654716 AA640726
		BE173515 BE173560 AI902860
		T79703 T96307 AL079725
		AW998716 AW022148 N68020
		AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
		AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
		AW753456 AW753036 AW854868 AW854862
		AW835767 AW835537 BE160187
		AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
		BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
		BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
		BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
		AA493862 AW897396 BE154814
		AI911066 AI933734 AI690888 AJ003599

TABLE 64C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
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	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
5	401403	7710966	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9865004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
35	R1:	Ratio of BPH tissue to prostate tumor tissue			
	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	428134	AA421773	Hs.161008	ESTs	9.4
	446336	AW815036	Hs.151251	ESTs	9.3
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	8.9
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	400533			ENSP00000209376*PRED65 protein (Fragmen	8.7
	418310	AA814100	Hs.86693	ESTs	8.7
	404592			NM_022739*.Homo sapiens E3 ubiquitin lig	8.1
45	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
	400080			Eos Control	7.4
	459646	AW883958	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	7.4
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
50	418387	R18085		gb:yg16b12.r1 Soares infant brain 1N1B H	7.2
	442481	N98828		gb:za32c04.r1 Soares fetal liver spleen	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	6.9
	404967			Target Exon	6.9
55	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	6.9
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	6.9
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	6.8
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	6.8
	400440	X83957	Hs.83870	nebulin	6.6
60	454171	AW854832		gb:QV2-CT0261-201099-011-405 CT0261 Homo	6.6
	400086			Eos Control	6.4
	440911	AA909536	Hs.143562	ESTs	6.4
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
65	419015	T79262	Hs.14463	ESTs	6.3
	453789	AA628517	Hs.118502	ESTs	6.2
	424940	AA985308	Hs.283902	ESTs	6.1
	403667			Target Exon	6.1
	429014	AI800518	Hs.118158	ESTs	6.0
70	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte	6.0
	419999	AI760942	Hs.191754	ESTs	6.0
	405348			C7001664:gi12698051 dbj BAB21849.1  (AB	6.0
	404003			Target Exon	5.9
	453200	AA033832	Hs.212433	ESTs	5.7
75	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
	432319	AW510770	Hs.128388	ESTs	5.7
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
	443361	AI792628	Hs.133273	ESTs	5.6
	411518	AW850246		gb:LL3-CT0219-291099-021-E07 CT0219 Homo	5.6
80	439079	AF085937	Hs.38348	ESTs	5.5
	422081	AW136820	Hs.195011	ESTs	5.5
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	5.5
	423529	T87318	Hs.120411	ESTs	5.5

	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW963551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084328	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720586	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293945	ESTs, Weakly similar to I38022 hypotheti	5.3
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
15	446495	D60923	Hs.153460	ESTs	5.2
	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST365595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
20	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RCS-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gl 4758712 ref NP_004659.1  al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
55	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE059128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stralagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
70	441620	R59595	Hs.26675	ESTs	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
75	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
80	430124	AW204994	Hs.253450	ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

5	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AJ741053	Hs.170770	ESTs	4.1
	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
	400746			Target Exon	4.1
10	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AJ761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QVO-DT0020-090200-106-g05 DT0020 Homo	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
15	431421	AW959118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	441568	AJ733322	Hs.127176	ESTs	4.0
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
20	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	454806	AW872430	Hs.273743	ESTs	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
25	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JCS238 galac	3.9
	407834	AW084991	Hs.28100	ESTs	3.9
	400398	AF137396	Hs.283879	ubiquitin 3	3.9
30	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482*gi 9790241 ref NP_062628.1  S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
35	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN IIII	3.8
40	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43052		gb:HSC12E041 normalized infant brain cDN	3.8
	434381	AA631834		gb:np77h05.s1 NC1_CGAP_Pr2 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
45	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QVO-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
50	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AI637649	Hs.196105	ESTs	3.8
55	443535	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
60	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
	448135	AJ470874	Hs.343799	ESTs	3.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
65	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
70	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
75	447458	AJ741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	417565	AI203405	Hs.47831	ESTs	3.6
80	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
80	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

5	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517*:g 4758712 ref NP_004659.1  a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:ns07a11.1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI339732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
50	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW292635	Hs.346145	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA059050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	3.3
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothe	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*:g 129092 sp P23270 OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447697	AI886036	Hs.213675	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

	451399	AL042110	Hs.326728	ESTs	AL042110	3.1
	450687	AA495800		gbzw05b07.s1 Soares_NhHMPu_S1 Homo sapi		3.1
	416812	H91010	Hs.44940	ESTs		3.1
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-		3.1
	434512	AW139932	Hs.188941	ESTs		3.1
	458251	AL040927	Hs.210422	ESTs		3.1
	439950	AW937417	Hs.293561	ESTs		3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th		3.1
10	403805			Target Exon		3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso		3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940		3.1
	429350	AI754634	Hs.131987	ESTs		3.1
	430454	AW469011	Hs.105635	ESTs		3.1
15	441817	AW969706	Hs.293332	ESTs		3.1
	427773	AA412290	Hs.98124	ESTs		3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1		3.1
	445758	R60715	Hs.25804	ESTs		3.1
	403291			Target Exon		3.1
20	436295	N73895		gbza52d06.s1 Soares fetal liver spleen		3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim		3.1
	418037	AI990212	Hs.85447	ESTs		3.1
	438142	T90309	Hs.269651	ESTs		3.1
	416423	H54375	Hs.268921	ESTs		3.1
25	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr		3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H		3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif		3.1
	420721	AA927802	Hs.159471	ZAP3 protein		3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L		3.1
30	441492	AI149998	Hs.146346	ESTs		3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo		3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti		3.1
	435628	W88732	Hs.36107	ESTs		3.0
	444326	AI939357	Hs.270710	ESTs		3.0
35	413774	AA131782	Hs.182314	ESTs		3.0
	434352	AF129505	Hs.85492	small muscle protein, X-linked		3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr		3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z		3.0
	416642	T96118	Hs.226313	ESTs		3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076		3.0
	418948	AI217097		gb:qcd43h07.x1 Soares_fetal_heart_NBH19W		3.0
	433796	AA810867	Hs.186997	ESTs		3.0
	427813	D29833	Hs.2207	salivary proline-rich protein		3.0
	405733			NM_021140: Homo sapiens ubiquitously tra		3.0
45	426743	AA383833	Hs.245022	ESTs		3.0
	449913	AA004696	Hs.333016	ESTs		3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo		3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Sla20-lik		3.0
	410929	H47233	Hs.30643	ESTs		3.0
	458187	D56919	Hs.265848	myomegalin		3.0
50	429430	AI381837	Hs.155335	ESTs		3.0
	451391	AA017410	Hs.40568	ESTs		3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600		3.0

TABLE 65B

**Pkey:** Unique Eos probeset identifier number  
**CAT number:** Gene cluster number  
**Accession:** Genbank accession numbers

	Pkey	CAT Number	Accession
60	408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263 AW810325 AW810443 AW8
65	409189	110687_1	AA125984 AA127189 AA056075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045 AW754192 W00554 AW857797 AW754203 AW754197 AW754193
	410559	1208283_1	AW803357 AW803423 AW812233 R05814
	410790	1221131_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
70	410859	1225123_1	AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411518	1248692_1	AW850246 AW850251 AW850302
	411552	1249255_1	AW851255 AW851432 AW850955
75	412701	1322288_1	AW984757 AW984797 AW984734 AW984745
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
80	416422	1593811_1	H60457 H68709 H73528 H54335 R87154
	418059	171879_1	AA211586 F35799 AA211641 F25720 AW937387 AW937408
	418387	174731_1	R18085 AA219028 R17712 Z44345
	418948	180808_1	AJ217097 AW886090 W38035 W38792 AA232835 AW936043

5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
	436295	41733_1	N73895 AJ001872
15	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	AI692689 R14223 R18395
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454086	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW866079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW953477 Z141970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NI_position:	Indicates nucleotide positions of predicted exons.		
55	Pkey	Ref	Strand	NI_position
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
	403305	8099945	Plus	114632-114805
65	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	106655-106050
	403433	9719611	Minus	72225-72437
	403481	9965004	Plus	93496-93633
	403510	7652047	Plus	61866-62027
70	403667	6850483	Minus	1344-1442,1545-1697
	403805	8140491	Minus	51483-51742,53429-53511
	404003	8655948	Plus	198349-199096
	404561	9796980	Minus	69039-70100
	404592	9943965	Minus	39067-39225
75	404848	8248647	Minus	23955-24034,25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
	405321	3419846	Minus	44654-45210
80	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051



5 Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

10 TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

15				
Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI990741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoiet	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-R05 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PRE065 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
435396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coo	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (f	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416502	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GC81 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA933571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3

	423101	M83941	Hs.123642	EphA3	5.3
	437587	AJ591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
5	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416705	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.1
15	445238	AA883971	Hs.187506	ESTs	5.1
	450582	AJ339732		G-rich RNA sequence binding factor 1	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
20	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:rh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AJ820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
25	450497	H64159	Hs.15328	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
30	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
35	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420831	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA933527	Hs.293907	hypothetical protein FLJ23403	4.6
40	405348			C7001664.gil12698061[kb]BAB21849.1] (AB	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	AI671141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
50	430188	AL049242	Hs.234794	Homo sapiens mRNA: cDNA DKFp564B083 (fr	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI093155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	458527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255652		gb:z21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z3-1 placenta expres	4.2
65	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256251	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	AI701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438875	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	4.0
5	435136	R27299	Hs.10172	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
10	448882	AJ001531	Hs.22404	protease, serine, 12 (neurolypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
15	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.9
	410186	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
20	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
25	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
30	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
35	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
40	432101	AI918950	Hs.123642	EphA3	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	436345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
50	450687	AA495800		gb:czw05b07.s1 Soares_NhiHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site faml	3.7
55	422899	D18471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
60	404561			trichorhinophalangeal syndrome I gene (T	3.6
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
65	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
70	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
75	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
	401132			C120005177:g 4758712[ref]NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.1 NCI_CGAP_Ew1 Homo sapiens	3.5
80	449588	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

5	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830060	Hs.124344	ESTs	3.5
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
10	436714	AA728964	Hs.293399	ESTs	3.4
	404848			ENSP00000240769:BG15303.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
20	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prol	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883958	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
40	448108	AW300021	Hs.170885	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
55	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1ao1	3.2
60	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
65	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI538323	Hs.52620	Integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/tn
	434512	AW139932	Hs.188941	ESTs
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-
	433444	AW975324	Hs.129816	ESTs
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypothe
	415861	Z43123	Hs.144513	ESTs
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174
10	432527	AW975028	Hs.102754	ESTs
	427773	AA412290	Hs.98124	ESTs
	441817	AW969706	Hs.293332	ESTs
	416812	H91010	Hs.44940	ESTs
	417958	AA767382	Hs.193417	ESTs
15	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL
	416423	H54375	Hs.268921	ESTs
	418037	AI990212	Hs.86447	ESTs
	419197	N48921	Hs.27441	KJAA1615 protein
	420179	N74530	Hs.21168	ESTs
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen
	405548			Target Exon
	423595	R82826	Hs.220702	ESTs
	412533	AA679863	Hs.69606	ESTs
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds
25	405264			NM_030813*:Homo sapiens suppressor of po
	410869	AW808361		gb:MR1-ST0111-111099-003-r04 ST0111 Homo
	425354	U62027	Hs.155935	complement component 3a receptor 1
	441492	AI149998	Hs.146346	ESTs
	447078	AW885727	Hs.9914	ESTs
30	435021	AA922192	Hs.54709	ESTs
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC
	450580	N40087		ESTs
	432319	AW510770	Hs.128386	ESTs
	453713	R20640	Hs.79133	cadherin 8, type 2
35	445784	AI253155	Hs.146065	ESTs
	416642	T96118	Hs.226313	ESTs
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W
	433796	AA810867	Hs.186997	ESTs
	439182	AF086030	Hs.21621	hypothetical protein DKFZp7620076
40	404995			ENSP00000251890*:Monocytic leukemia zinc
	444794	AI419991	Hs.145225	ESTs
	443634	H73972	Hs.134460	ESTs
	420133	AA426117	Hs.155543	ESTs
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197
45	426743	AA383833	Hs.245022	ESTs
	442326	H92962	Hs.124813	hypothetical protein MGC14817
	449913	AA004696	Hs.333016	ESTs
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo
	419622	AA452054	Hs.119338	ESTs
50	449745	AI668593		gb:yl38a05.x5 Soares breast 3NbHBst Homo
	428412	AA428240	Hs.126083	ESTs
	428200	AI039624	Hs.98388	ESTs
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600
	431869	AA521136	Hs.190176	ESTs
55	451391	AA017410	Hs.40568	ESTs
	452959	AI933416	Hs.189674	ESTs

TABLE 66B

60	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
65	Pkey,	CAT Number
	Accession	
	410790	1221131_1
	410869	1225123_1
70	411436	1245660_1
	411479	1247077_1
75	412988	1342150_1
	413081	1348563_1
	413525	1374635_1
	416009	1565379_1
	418948	180808_1
	420111	190755_1
80	420352	192979_1
	424200	236595_1
	424994	245786_1
	428002	285602_1

428342	290035_2	A1739168 AA426249 A1199636 AW505198 AW977291 AA824583 AA883419 AA724079 A1015524 A1377728 AW293582 A1928140 AA731438 A1092404 A1085630 AA731340
430535	319843_1	AW968485 AW968670 AA480922 BE350425
432765	353907_1	AJ003429 AJ003367 AA564825
433523	368873_1	H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320
434763	392847_1	AA648618 AW974389 H51771
436295	41733_1	N73895 AJ001872
439092	468554_1	AA830149 AW978407 M85983 AW503637
439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
440947	505904_1	AA910403 A1815593 W58361 AW162520 A1816550
442481	543588_1	N99828 BE079873 A1110738 AF074645
445432	63943_1	AV653771 BE089370
448044	747195_1	A1458682 H24240 R14537 R18426 AW867082
449570	81018_1	AA001793 AA001871
449745	814534_1	A1668593 A1820774 R86205 H39971 H22177 H26241
450317	831956_1	A1692689 R14223 R18395
450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
		AA164518 AA730973 W00417 W65303
450582	83933_1	A1339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
452462	918580_1	BE173515 BE173560 A1902860
453682	977454_1	T79703 T96307 AL079725
454037	996287_1	AW998716 AW022148 N68020
454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
454457	1207274_1	AW753456 AW753036 AW854868 AW854862
454655	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
454860	1237732_1	AW835767 AW835537 BE160187
454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
455067	1252050_1	AW854538 AW854418 AW854412
455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW888079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
457374	328758_1	AA493662 AW897396 BE154814
458912	823104_1	A1911066 A1933734 A1680888 AJ003599

TABLE 66C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
403657	6850483	Minus	1344-1442, 1545-1697
404003	8655948	Plus	198349-199096
404581	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034, 25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43452
405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435577	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249368	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M93119	Hs.89584	insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449625	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheu	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935962	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	LIM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to SS1797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421895	N62293	Hs.45107	ESTs	9.1
10	432101	AI918950	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
15	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	445100	AW967109	Hs.13804	hypothetical protein dJ462023.2	8.5
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.5
20	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
25	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0666 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
30	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	432586	AA568548		ESTs	7.3
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
45	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	cathepsin	6.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
60	450377	AB033091		KIAA1265 protein	6.6
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AI297436	Hs.20166	prostate stem cell antigen	6.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9



420092	AA814043	Hs.88045	ESTs	5.9
410268	AA316181	Hs.61635	sbx transmembrane epithelial antigen of	5.8
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	5.8
450244	AA007534	Hs.125062	ESTs	5.8
429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
451952	AL120173	Hs.301663	ESTs	5.7
429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	5.7
412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheli	5.7
434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
415621	AI648502	Hs.55468	ESTs	5.7
416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	5.5
418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	5.4
456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
410762	AF226053	Hs.66170	HSKM-B protein	5.4
440594	AW445167	Hs.126036	ESTs	5.4
413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
447805	AW627932	Hs.302421	gemin4	5.3
434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
453308	AW959731	Hs.323099	ESTs	5.3
421470	R27496	Hs.1378	annexin A3	5.3
418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
404632			NM_022490:Homo sapiens hypothetical prot	5.1
450861	AI523898	Hs.17617	ESTs	5.1
431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
410037	AB020725	Hs.58009	KIAA0918 protein	5.1
410240	AL157424	Hs.61289	synaptotagmin 2	5.0
403046			NM_005656*:Homo sapiens transmembrane pr	5.0
419647	AA348947	Hs.91816	hypothetical protein	5.0
450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
450164	AJ239923	Hs.63931	ESTs	5.0
417318	AW953937	Hs.240845	ESTs	4.9
417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
433852	AI378329	Hs.126629	ESTs	4.9
452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
453171	R76472	Hs.65646	ESTs	4.8
416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
427615	BE410107	Hs.178817	CGI-82 protein, PSDR1	4.8
419440	AB020689	Hs.90419	KIAA0882 protein	4.8
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
421685	AF189723	Hs.105778	ATPase, Ca transporting, type 2C, member	4.7
431724	AA514535	Hs.283704	ESTs	4.7
423242	AL039402	Hs.125783	DEME-6 protein	4.7
434485	AI623511	Hs.118567	ESTs	4.7
407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
414085	AA114016	Hs.75748	aldehyde dehydrogenase 1 family, member	4.6
422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
439735	AI635386	Hs.142846	hypothetical protein	4.6
420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
426006	R49031	Hs.22627	ESTs	4.5
451982	F13038	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.5
415082	AA160000	Hs.137396	ESTs, Weakly similar to JCS238 galactosy	4.5
409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
423583	AL122055	Hs.129836	KIAA1028 protein	4.4
452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
451752	AB032997		KIAA1171 protein	4.3
430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26087	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.3
5	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AJ694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
10	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
	442501	AA315267	Hs.23128	ESTs	4.2
	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
15	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
20	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55599	NK homeobox (Drosophila), family 3, A	4.1
25	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens	4.1
	447574	AF162666	Hs.18895	lousled-like kinase 1	4.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1521 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
30	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
35	438825	BE327427	Hs.79953	ESTs	4.0
	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
	415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
40	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
	432435	BE218886	Hs.282070	ESTs	3.9
45	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
	429259	AA420450	Hs.292911	Plakophilin	3.9
50	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.9
55	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
	432675	AF791855		ESTs	3.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.8
	427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
60	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.32793	ESTs	3.8
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AK479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
65	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
70	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
75	417081	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	exin 2 (conductin, end)	3.7
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.33010	KIAA0633 protein	3.7
	408063	BE086548	Hs.42346	caldesmon-binding protein calsarcin-1	3.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
80	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pro-B-cell leukemia transcription factor	3.6

	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
5	422424	AI186431	Hs.296638	prostate differentiation factor	3.6
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22552 fis, clone H	3.6
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
10	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
15	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
20	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (hls	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
25	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 6C	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
30	443884	N20617	Hs.194397	leptin receptor	3.4
	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
35	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
40	437617	AI026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
45	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
50	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
55	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
	433891	AA613792		gb:nc097h03.s1 NCL_CGAP_Pr2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
60	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
65	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (emlno	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
70	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476*:gij12737279[ref]XP_012163.1]	3.2
75	419517	AF052107	Hs.90797	Homo sapiens clone Z3620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upi3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
80	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
15	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
20	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
25	423453	AW450737	Hs.128791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
	436278	BE396290	Hs.5097	synaptogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	438705	AI049624	Hs.283390	ESTs, Weakly similar to T109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278962	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA: cDNA DKFZp564N0763 (f	3.0
45	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.211192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429638	AI916662	Hs.211577	kinecin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H56220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	445825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.0
	435032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78106	phosphodiesterase 6B	2.9
	412925	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	omithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
80	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
5	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.9
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
10	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	adonucleoside triphosphate diphosphohyd	2.9
15	423551	AA327598	Hs.89633	ESTs	2.9
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
20	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA: cDNA DKFZp564A072 (fr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
25	418166	AI754416		Cdc42 effector protein 3	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
30	425320	U29344	Hs.83180	fatty acid synthase	2.8
	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
35	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
40	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
45	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfolucosamine sulfolhydrolase (sulfa	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA609200		gb:af12a02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
55	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	2.7
60	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
65	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
70	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
75	409650	T08490	Hs.288969	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
80	420818	AW963635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	niban protein	2.6
	422717	AI557623	Hs.119475	cold Inducible RNA-binding protein	2.6
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
5	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*-HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
15	408157	AA047685	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulin 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
20	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75350	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
25	426180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
30	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	428343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
35	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
40	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor I	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
45	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
50	441128	AA570256		ESTs, Weakly similar to T23273 hypothei	2.6
	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
55	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypothei	2.5
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AI373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
60	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
65	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypothei	2.5
70	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (o-erb-b2,	2.5
	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC067 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
75	450628	AW382884	Hs.204715	ESTs	2.5
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
80	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
	418737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418649	AI095485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothel	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
	414556	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
10	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fls, clone NT	2.5
	443837	AI984625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
15	435021	AA922192	Hs.73962	ESTs	2.5
	435750	AB029012	Hs.4990	KIAA1089 protein	2.5
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	425976	C75094	Hs.334514	NG22 protein	2.5
20	449458	AI805078	Hs.208261	ESTs	2.5
	428013	AF151020	Hs.181444	hypothetical protein	2.5
	424369	R87622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
25	433586	T85301	Hs.194397	gbyd78d06.s1 Soares fetal liver spleen	2.5
	438682	AA354489	Hs.222103	EBF50-PDZ Interactor of 64 kD	2.5
	427515	T79526	Hs.179516	Integral type I protein	2.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5
30	TABLE 67B				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
35	Pkey	CAT Number	Accession		
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153		
			BG285837 AI720344 BF541715 AA355086 AA172236		
40	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259		
	412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514		
			AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538		
			BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721		
			AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815		
45	433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261		
			AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421		
			N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433		
	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526		
			BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360		
50	453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307		
			AA344186 AW952986 AA033609 AA037562 AA722183 R79452 H07775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991		
			AA084581 AA033610 AV742510 AV735788 R08336		
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756		
			AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727		
55	437124	59408_1	AL050013 BG939500 AW956191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010		
			N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860		
			AI219716 AA960926 H25544 BI851123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742		
			AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA869970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080		
			AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744		
			T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422		
60	432586	6633_1	BC022881 AI150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548		
	438869	52134_1	AF075009 R63109 R63068		
	450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695		
			BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384		
65			AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699		
			AL050294 BC010371 BF882270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398		
			BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866		
			AI699181 N73808 H08164		
70	436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970		
			N40094 N28596 AA884747 AA512890 BG436593		
	428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI337728 AW293582 AI928140 AI092404 AI085630 AA731340 BM469529 AW968804 AA425658		
			AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW529495 AW505314 W74704 AI356361		
			AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040		
			AI392620 Z40708 AI855564 AW263513 AA913892 AI633486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967		
			AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166		
75	424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377		
			AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096		
			BM045465 AL531028 BG437151 BE868021 AA179427		
	450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846		
			AI024796 AW020098 BI491127 AI336444 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192		
80	451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW259901		
			BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333		
	432363	1234917_1	AW970240 AA534489 AW970323		

422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264883 AW196918 AA948267 AI553735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI356013 AI867923 BG911906 D81142 C15616 AL538597 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603 AA196390 AA507837 AA196468 AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185 AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA805643 AW188870 BE705664 BE706539 BE153177 BF084925 AI133779 AW551788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826 AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610 AI973051 AI400921 AI796154 AW241817 AW290951 NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944397 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE050972 BF693195 AV738979 R65855 R80136 AA484677 BE644758 AI082238 BF940027 AI201079 AI435035 AW275956 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763897 AI565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA318136 AA514271 BF364291 AI515057 AV702312 AI307739 AL544217 AI341000 AW193583 AI350789 AA688338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM660872 AA319160 AA130778 AL514257 AW182329 AA613792 T05304 AW858385 BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695577 AL562079 AI700926 AI470561 BF063058 AW196387 AU132984 BI064046 AI970157 R02122 H55924 AI521721 AA080826 AA725223 BI756003 AW339821 AA805951 AI287969 AW664827 BC021085 AL527872 AL526296 AL557087 BI255090 AU143499 AI560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AL564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002624 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI204499 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78841 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284936 AA857926 BF372558 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 HA4325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106 AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI255452 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635 AF119847 AA437261 AA436987 AI132965 AF150424 AI861896 AA570057 AV738855 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF448023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N09081 AA771919 AI092259 AI028416 AI074114 BG656538 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 AK055915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376692 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI765892 BF108422 AI800361 T95129 F11313 R97946 R83989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 BF724237 AI216746 H11384 R38484 AA249043 AA249732 AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974 AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102 AA602964 AA609200 AW976637 AI033582 AA837085 AA745261 AA648395 BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW652760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI983299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA92453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AA440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954388 NM_015720 AF219137 AL534420 AL524055 AL537345 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF805256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE766903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867482 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833
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445636	8561_5	BF339388 AJ345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
419175	35068_1	AB018322 BC012480 BI524873 AW655554 AJ934469 AJ479916 BF096179 BF096162 BF096132 AA744972 AJ951988 AI858339 BE076331 AA886998 AJ570585 AJ916688 AJ678811 AJ693109 AJ308135 AA669046 AA961064 AJ018062 H80618 BE221942 R52609 AJ915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AJ275392 AJ273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AJ341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AJ364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AJ187299 AJ609644 Z40516 AW952314
441128	20932_1	BC014072 BE328850 AJ356567 AI148171 AJ022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AJ359827 BG674574 BE903322
406789	0_0	AI041403 Z49148
421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AJ922406 AA778161 BF345973 AW195853 AI687121 AJ336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI356396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AL567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569332 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559586 AL539326 T15481 AW895092 AL582684 BI519896 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AJ560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033488 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF698627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE833685 BE166758 BM452445 AJ937808 AW026128 N23684 AW006041 AJ337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE833973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118818, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5005246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165995, 166189-166314, 166408-16656
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	65.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen)	68.6
446057	AA20227	Hs.149358	Trp-p8 transient receptor potential cell	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AJ821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
	400292	AA250737	Hs.72472	BMP-R1B	31.4
5	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000531	Hs.52256	hypothetical protein FLJ20524	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	30.3
	407168	R45175	Hs.117183	ESTs	29.6
10	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	AJ733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
15	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
	407709	AA456135	Hs.23023	ESTs	24.7
20	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI267700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
	437052	AA861697	Hs.120591	ESTs	22.6
25	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	20.8
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
30	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
35	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW967646	Hs.23023	ESTs	17.3
40	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98558	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.50257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
45	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	14.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820961	Hs.193465	ESTs	14.3
	429918	AW873986	Hs.119383	ESTs	14.2
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
55	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
60	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
80	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFp434K1421	11.0

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
10	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
15	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
20	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
	443180	R15875	Hs.258576	claudin 12	9.5
	406964	M21305		GENES predicted novel secreted protein	9.5
25	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
	451684	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
	437124	AA554458		KIAA0666 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
35	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AJ655499	Hs.161712	ESTs	8.8
40	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofor	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	8.7
45	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoacidipate aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
	416239	AL038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP5641052 protein	8.4
50	450164	AJ239923	Hs.63931	ESTs	8.4
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AJ420611	Hs.153934	ESTs	8.3
	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
55	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
60	421928	AF013758	Hs.109643	polyadenylate binding protein-Interactin	8.1
	432596	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.183145	metallothionein 1E (functional)	7.9
65	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	7.7
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
70	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	7.6
75	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	necdin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
80	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AJ648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AJ623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
10	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
	422485	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
20	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
25	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490-Homo sapiens hypothetical prot	6.3
30	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410762	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
35	455508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
40	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
45	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
50	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
65	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GL004 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
70	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429638	AI916662	Hs.211577	kinecin 1 (kinesin receptor)	5.5
75	403046			NM_005656-Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
80	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
	417318	AW953937	Hs.240845	ESTs	5.3
5	429467	NM_004477	Hs.203772	FSHD region gene 1	5.3
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 28,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
	450832	AW970602	Hs.105421	ESTs	5.1
15	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
20	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
25	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
30	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
35	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432363	AA534489		gb:mf76g11.s1 NCL_CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA: cDNA DKFZp564O1763 (f	4.7
	447574	AF162666	Hs.18895	tousled-like kinase 1	4.7
50	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zfp99b10.s1 Stralagene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.7
55	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
65	420380	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
75	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
80	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	NZ3874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
5	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosaminopolyp	4.4
10	417958	AA767382	Hs.193417	ESTs	4.4
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	425092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
20	459284	AF155860	Hs.300496	mitochondrial solute carrier	4.3
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
30	432875	AI791855		ESTs	4.2
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AI246720	Hs.114390	ESTs	4.2
	410297	AA148710		tumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426547	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
40	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axl)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AI355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Cros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	4.1
	408063	BE088548	Hs.42346	calcineurin-binding protein calcarsin-1	4.1
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108842	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length Insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47166	HT021	4.0
	446791	AI632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	leptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476:gij12737279[ref]XP_012163.1]	4.0
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267695	UDP-Gal:beta-GlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AIW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubimucin 1	3.9
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
5	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AI249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
15	413010	AA393273	Hs.76133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AI186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nuclear protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AI861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	AI806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263:HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulon 1	3.7
	401886			Target Exon	3.7
	457183	H91882	Hs.118569	DNA-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
55	405387			NM_022170:Homo sapiens Williams-Beuren	3.7
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ck1 avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
60	454229	AW957744	Hs.278469	lacrimal protein rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
75	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753:Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H56220	Hs.278177	ESTs	3.6
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

	426695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.5
5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gbno97h03.s1 NCI_CGAP_P12 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Up3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300296	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
25	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
55	452295	BE379936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
60	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
70	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_016569	Hs.267182	TBX3-iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
75	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.3
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase I	3.2



5	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.2
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	3.2
10	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	3.2
	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019	3.2
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
15	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant 8 mRNA, complete	3.2
	406214			NM_016371:Homo sapiens hydroxysteroid (1	3.2
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
20	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
25	437179	AA393508		serologically defined colon cancer antig	3.2
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
30	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638:Homo sapiens hypothetical prot	3.2
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
35	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
40	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AI187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
	448044	AI458682		gb:tk13e01.x1 NC_CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
45	421254	AK001724	Hs.102950	coat protein gamma-cop	3.1
	424339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
50	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433036	AA574091	Hs.105964	ESTs	3.1
55	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
60	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437296	AA350994	Hs.20281	KIAA1700	3.1
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	RA3179	Hs.22695	hypothetical protein FLJ23548	3.0
65	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
70	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
75	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
80	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	3.0
	450937	RA9131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
5	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA853400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granula-associated RNA-bi	3.0
	445696	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.0
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
15	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	408927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
20	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CQI-83 protein	2.9
25	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	AI675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AI200281	Hs.123910	ESTs, Highly similar to B34087 hypothei	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	niban protein	2.9
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749855		ESTs, Weakly similar to I38022 hypothei	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	438165	AI373544	Hs.331328	Intermediate filament protein syncoilin	2.8
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CLTA	2.8
70	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA591508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
75	418196	AI745649	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
80	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypothe	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
15	440080	AW051597		ESTs	2.8
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506556	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA: cDNA DKFZp566L203 (tr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10600	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
25	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypothe	2.7
40	440340	AW895503	Hs.125276	ESTs	2.7
	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA: cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gbn178f05.x5 NCL CGAP_Pr3 Homo sapiens	2.7
50	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 poly	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypothe	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000061	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	intron ottrichorhinophalangeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AI823987	Hs.182285	ESTs	2.7
	411960	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypothe	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26530	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AJ096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
15	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
	404913			NM_024408*:Homo sapiens Notch (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibitor	2.6
35	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AJ373716	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
	417327	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.6
50	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110246	Hs.47367	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFp5660134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AJ378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated atlanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283476	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410645	Hs.164649	hypothetical protein DKFp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFp586P1622 (f	2.6
75	458946	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Aubergier b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
15	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188838	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalni	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothi	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90958	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypothi	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypothi	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypothi	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W05656	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [Hs	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101067	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
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		AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE695424 BF908060 BF962832 BF952020 BF963134 B1035538
		BF908052 BF908057 BF090026 BF943158 A1632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721
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		BC009612 NM_003526 B1597616 AV761592 AV760377 A1601008 B1604131 BE645918 BG187760 BG181525 BG210634 BG192999 A1263307
		AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H07775 BF674991 BE769437 BG007856 AA037483 AW572535 A1143991
		AA084581 AA033610 AV742510 AV735788 R08336
	420218	AW958037 R42557 A1337047 AA948360 A1638005 AA459950 A1624915 A1638047 A167856 A1521826 AA860305 A1932315 AW003092 AW271756
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	59408_1	AL050013 BG939500 AW969191 AA769925 A1377973 A1625545 AA811365 AA521114 N24705 A1379579 AA424899 A1684571 AA829715 A1543010
		N35401 AA677452 AA504340 A1209149 AA883574 A1379062 A1084455 A1280147 AA644327 BF432508 N27873 A147364 N34880 A1147024 T86860
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	451752	Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19503
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		BM128251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970
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65	432675	AW973834 A1791932 A1791855 A1732640 AA558833 AA559897 A1821610
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	2990_1	AW340368 AA928759 A1718737 BF513970 AA707807 BF435295 A1339463 A1373842 A1433809 BE222392 AA602308 AA428261 A1460355
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70		B1911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461951 BG681168 B1602483 BE889592 AW954311 BM052986 B1962893
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5	432908	452541_1	AF150424 A1861896 AA570057 AV738855	
	433891	647290_1	AW182329 AA613792 T05304 AW583855	
	409960	39576_1	BE644758 A1082238 BF940027 A1201079 A436035 AW275966 A1085394 A1291655 AW070441 A1474134 A1268978 A1769279 A1567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296858 A1268977 A1168133 BM352065 A1262769 BF941976 A1056920 AA481861 BF763597 AL555888 BM352383 AA427768 AA355346 A1186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 A1341000 AW193583 A1350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 A1004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257	
10	414222	18695_1	A021085 AL527872 AL526296 AL557087 B1255090 AU143499 AL560356 BG823170 BE736988 AU141388 AL580262 B1764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 B1770885 B1911394 BE901426 B1918039 BG760842 BE883026 B1254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726886 AL564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 B1222949 A458045 AW951537 BF196474 A1669049 A1042523 BE463928 AU160125 AU160580 AW069877 AW015214 A1948718 BE219706 A193605 BE217755 A1991382 A1245005 BF431179 A1521843 BE048908 A120449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 B1772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AU143835 A1635707 BF195492 A1280559 BF741685 AA385257 BE247655 W94974 BE163702 A1025167 A1827118 N78641 AL581093 AU158964 AU158917 A1282516 AU146399 AA713947 A1285028 AA101228 A1338522 AA832316 A1284986 AA857926 BF372568 AA570172 A1753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 B1259678 AA522554 N55172 AW013929 A1826274 A1871237 CT5260 AA934846 AA555036 AA526579 AA526466 N80270 A1538347 AW615805 AU158875 AU158883 AU159396 A1016667 AU159238 A182517 AA406317 A1285043 N53050 AA969446 N57718 H93323 W93374 A1873751 H55011 A1936174 AA937830 AW438877 A1800550 AW328268 A1244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106	
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	419175	35068_1	AB018322 BC012480 B1524873 AW665554 A1934469 A1479916 BF096179 BF096162 BF096132 AA744972 A1951988 A1858339 BE076331 AA886398 A1570585 A1916688 A1578811 A1693109 A1308135 AA669046 AA951064 A1018062 H80618 BE221942 R52609 A1915164 AA365626 Z44671 B1052776 BF882486 BG286184 A1589558 AA931663 AA543979 A1275392 A1273455 R52553 AA829920 H80652 AA360728 F10618	



5	421091	24941_2	AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 A1334004 BF057179 A1857450 A1341191 A1934143 A1917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 A1580157 A1364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 A1203159 N49403 F02090 A1187299 A1609544 Z40516 AW952314 AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 A1884867 BE858461 A1885227 A1935218 BE645596 A1922406 AA778161 BF345973 AW195853 A1687121 A1336147 A091364 A1769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 A1358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 A1935916 AA912295 BG910887 A1568301 AL567278 B1522445 B1754384 BG819375 BF835950 AA323718 AA860955 A1089847 AL520776 AL526045 A1538507 A1567798 AL535876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 B1913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 B1519896 BC014072 BE328850 A1356567 A1148171 A1022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 A1005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AA73237 BF033706 N90525 AW973623 A1359627 BG674574 BE903322 A1041403 Z49148 AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 B1917678 BG819395 BG911971 BG820167 A1174254 AA348720 AA364503 BG714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL583737 BG029709 W52882 A1439658 BE551237 AA283724 BF109530 A1457096 A1055992 BE467736 AA693467 A1697593 A1887863 A1167419 AW901980 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 A1418634 T31586 AA436630 A1365472 AA706191 A1422304 A1204899 A1041169 AA211402 AW827081 AA788593 T32736 A1676935 AA747914 T03534 AW959843 AL119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60090 N79906 D52685 T07735 BE702069 BE702172 T08671 BE767121 BE767117 BE767113 AA658826 A1821926 A1791191 AA635129 AA564492 Z11692 X51466 NM_001961 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935 BM016525 A1560409 AL562866 A1091978 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF869862 BG998348 B1011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756466 BG032392 B1859287 BM016990 BG332369 BE933685 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 B1199487 BF761700 B1261519 BF944452 BF898506 A1038390 BM044934 AW381142 BG743618 BE769206 BE893973 B1015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 B1000274 BG255503 BG674499 BG774174 B1015084 BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 B1042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09586 B1838226 BF034269 AA429173 BE741829 AW667495 A1123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 A1633815 BF921562 AA094230 BE092587 W86151 AA526153 A1672156 BF914496 R12579 BF852352 AA699780 T57386 BF030322 R09933 AA678298 BF339388 A1345516 BG391657 BE708867 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE667593 AA090310 AA090672 N27807 AA256634 BE276324 AF263306 BF951698 T66089 F11783 F11794 H29379 R19493 H18042 AL133995 AW134660 A1299437 AA057405 AA917450 A1002692 T09262 R43839 H29290 T65008 N78357 A1221207 A1659856 AA913591 A1220302 NM_000786 U23942 B1601050 BG771947 BG773455 B1561558 B1460206 BG714348 BM126447 AU129411 AU129401 A119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 A1217668 AA399409 BE182318 BM128040 A1693999 AW615411 AW070426 A1124550 AW778736 AA477781 AW263013 A1459619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 B1916393 BM470755 B133211 AA095636 B1256415 AU7727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H47580 R48858 T91611 H42019 B1869421 BG502073 BG425943 W37290 W371363 BE004451 BF208311 B1048717 N78122 AA226597 A1525334 A1953821 AA657925 AA935436 AW975068 BC000222 AL136871 NM_032261 BC009497 BM461705 BG470749 BG826905 BG285127 B1253235 BE397026 BG704967 AW961225 BM352817 B1227161 BG820180 AA454463 AA255685 N31549 AA326504 BC019924 BG257230 B1092368 B1869896 BG251883 BF034444 BG286577 BE260391 AA599912 BF686779 A1755222 AA452272 AW241170 A1156565 F28259 T16319 AA362506 N64153 BM016416 BM458963 BG739972 AV729565 BE268285 BE867433 BM011110 BG285856 A1922439 BE270975 AL119339 BF956085 A1565178 A1554305 AL573240 AL572917 A129627 AL546640 BE392285 A1092843 A1371057 BE302410 A1608753 AW674261 A1750057 A1052649 N47822 AL516249 A1589903 BG258439 A1123662 A126014 AA778101 AA243218 AW498837 AA748311 A1754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 A1061112 A1783806 AL569622 AA070466 BF229936 N58159 H80288 N32598 H80279 AL581253 AW571884 A1361698 AW073321 AA876464 H95640 T34421 AA331419 N99897 H80274 B1262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA362527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 B1085686 AA564566 A1221630 D52045 C14510 AA029390 W60153 H98743 A1682641 H28485 AA723093 A1081730 AA641309 AA687083 B1224818 AW204722 A1309186 A1215122 A1200785 BE467373 BM352502 A1304400 A193071 A1742483 AW003408 A1400201 A1656740 AW665173 A1215120 A1147599 A1803429 A1076110 A1754349 AW205103 A1262491 A1808243 A1281007 A1004801 AW768918 AW103289 A1474637 A1264446 A1699509 BE704420 AA989278 AA918256 AA830956 AA989425 AA911929 AA262598 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H48653 N69544 AA181762 D20132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 A1813809 AA933607 AA129695 AA548261 AA714393 AA775006 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489683 D52138 D51696 D55942 D52740 A1000118 AL516304 AL534259 N54940 AL579194 A1669399 A1342925 BE939201 AA633000 B1222963 A1619676 AW190306 BF035010 AW087897 A1864969 T57243 R48211 AA113880 R26594 C14467 C14444 A1195459 BE896346 BE270780 AL568073 BG389833 BE891549 B1223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304 A1380443 A1240179 AA977516 AA884643 AW079380 AW294316 A1913755 A1864320 A1685770 H25135 A1972654 A1538592 A1174783 R12271 R83569 A1274757 A1559500 AW022192 AW970134 AA516420 AA543007 BG057526 B1001430 A1498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60556 Z11692 X51466 NM_001961 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935 BM016525 A1560409 AL562866 A1091978 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF869862 BG998348 B1011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756466 BG032392 B1859287 BM016990 BG332369 BE933685 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 B1199487 BF761700 B1261519 BF944452 BF898506 A1038390 BM044934 AW381142 BG743618 BE769206 BE893973 B1015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 B1000274 BG255503 BG674499 BG774174 B1015084
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80

TABLE 68C

Pkey: Unique number corresponding to an Eas probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.



Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
5	403047	3540153	Minus	59793-59968
	401424	8176894	Plus	24223-24428
	401451	6634068	Minus	119926-121272
10	401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
	404632	9796668	Plus	45096-45229
	403046	3540153	Minus	55707-55859, 56369-56511
	404922	7341893	Plus	13248-13428
	401519	6649315	Plus	157315-157950
15	401197	9719705	Plus	176341-176452
	401866	8018106	Plus	73126-73623
	405387	6587915	Minus	3769-3833, 5708-5895
	403752	7678857	Plus	33704-33828
	404210	5006246	Plus	169926-170121
20	401785	7249190	Minus	165776-165996, 166189-166314, 166408-16656
	406214	7342036	Plus	86320-86523
	403532	8076842	Minus	81750-81901
	400860	9757499	Minus	151830-152104, 152649-152744
	404913	7341740	Plus	97717-97976

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Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

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Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

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TABLE 69A:  
 Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

40

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	424806	AA382523	Hs.105689	MSTP031 protein	1.51
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
45	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet	1.60
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
	417944	ALU077196	Hs.82985	collagen, type V, alpha 2	1.48
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
	452516	AA056630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
50	425139	AW630488	Hs.25338	protease, serine, 23	1.63
	402463			NM_014624:Homo sapiens S100 calcium-bind	1.50
	423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
	412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
	419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (	2.06
55	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
	441457	AW996651	Hs.43838	ESTs	1.30
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
60	413795	AL040178	Hs.142003	ESTs	1.64
	441689	AI123705	Hs.289068	ESTs	1.44
	412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
	424432	AB037821	Hs.146858	protocadherin 10	1.65
	432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
65	418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
	453085	AW954243		KIAA0251 protein	1.47
	438887	R68857	Hs.265499	ESTs	1.49
	436729	BE621807		transmembrane 4 superfamily member 1	1.91
	400494			ENSP00000238970*:ClG30 (Fragment).	1.34
70	442506	BE566411		ESTs	1.54
	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
	414476	AA301887	Hs.76224	EGF-containing fibron-like extracellular	2.65
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
	422389	AF240635	Hs.115897	protocadherin 12	1.38
	417124	BE122762	Hs.25338	ESTs	2.13
75	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
	450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
	449618	AI076459	Hs.15978	KIAA1272 protein	1.42
80	446098	AW072215	Hs.208470	ESTs	1.53
	413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
	448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
	407061	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	A1824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	A1750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
15	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
	433376	A1249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.43
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269551	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xa	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily 1 (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gb y65612.s1 Stratagene ovary (937217)	1.52
	412351	AL135890	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
40	433374	A1821409	Hs.304471	EST	1.45
	429113	D28235	Hs.195384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
45	406506			Target Exon	1.97
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.38
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-65kDa-associated protein 5	1.41
50	450152	A1138635	Hs.22968	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptotagmin 2	1.61
55	424711	NM_005795	Hs.152175	calcatonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 6730	1.81
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412564	X83703		cardiac ankyrin repeat protein	1.51
	414786	A1246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	A1554545	Hs.71832	angiotensin-2	1.91
	406627	T64904	Hs.163780	ESTs	1.78
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfamily	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
70	429276	AF055085	Hs.198512	G protein-coupled receptor 51	1.65
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	A1369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural era	1.55
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	1.74
	444409	AI792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1369	decay accelerating factor for complement	1.74
5	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AI380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AI834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443968	Hs.31595	ESTs	1.97
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
30	425811	AL039104	Hs.158557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AI878857	Hs.109706	hematological and neurological expressed	1.65
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs:similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypothe	2.33
45	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
50	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE280074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242687	Hs.118651	hematopoietically expressed homeobox	2.15
	406954	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AI701916	Hs.202509	ESTs	2.27
60	408989	AW381666	Hs.49500	KIAA0746 protein	1.43
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288757	v-rel simian leukemia viral oncogene hom	2.25
70	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX)	3.37
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI597655	Hs.49265	ESTs	3.08
	422424	AI186431	Hs.296638	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 698

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745542 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA802333 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI025328 AI284436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037325 AA375805 X75684 AL573167 AI445461 AI453743 AI983655 AI64644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI79814 AA129575 AI871727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI590245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI289935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI28364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156380 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545285 AL540643 AU118627 AL601379 BI259821 BG741788 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL555586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BC541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882 AA158151 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787	
442506	29197_1	NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882	
436772	123946_1	AA158151 Z25109 C05177 AW975688 AA731063 N67084	
434596	14701_1	AF147374 T59538 T59589 T59598 T59542	
412564	18571_1	X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787	
442006	1239046_1	AW975183 AA973583 AI365103 AI699495 AI301787	
TABLE 69C			
Pkey:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
NL_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	NL_position
402463	9796896	Minus	8818-8952
400494	9714719	Plus	169845-170272
401234	9929842	Plus	120173-120337
406506	7711374	Minus	6843-8077
405025	7107727	Plus	105267-105343, 106184-106294, 106387-10653
405121	8102330	Minus	35816-36004, 36587-36684
400666	8118496	Plus	17982-18115, 20297-20456
TABLE 70A:			
Pkey:	Unique Eos probeset identifier number		
ExAccn:	Exemplar Accession number, Genbank accession number		
UnigeneID:	Unigene number		
Unigene Title:	Unigene gene title		
R1:	Ratio of the mean of the vessel AI's to the mean of the HUVEC AI's		
Pkey	ExAccn	UnigeneID	Unigene Title
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v
412636	NM_004415		desmoplakin (DPI, DPII)
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v
414320	U13816	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)
417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fls, clone H
414572	AU077174	Hs.288181	cathepsin H
415314	N88802	Hs.5422	glycoprotein M6B
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac
406973	M34996	Hs.198253	major histocompatibility complex, class
456974	M12529	Hs.169401	apolipoprotein E
430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2
406828	AA419202	Hs.84258	CD74 antigen (invariant polypeptide of m
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein

5	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	A1223328	Hs.75335	glycine amidinotransferase (L-arginineg	2.12
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
10	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	A1193115	Hs.16611	tumor protein D52-like 1	2.27
	422639	A1929377	Hs.173724	creatine kinase, brain	2.29
	427451	A1690916	Hs.178137	transducer of ERBB2, 1	2.31
15	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	2.38
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	2.39
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
20	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75735	apolipoprotein D	2.50
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	2.51
25	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
30	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8503	p8 protein (candidate of metastasis 1)	2.62
	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
35	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	A1884911	Hs.32989	receptor (calstatin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
	452685	A1634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXRD domain-containing ion transport reg	2.73
40	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
45	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		platelet 4	2.94
	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
50	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425622	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	A1827976	Hs.24391	hypothetical protein FLJ13612	3.06
55	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
	414840	R27319	Hs.23823	halcy/enhancer-of-split related with YRP	3.14
	424651	AW93206		ESTs	3.17
60	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	perlestin(OSF-2os)	3.24
65	447384	A1377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.155007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	Integral membrane protein 2A	3.25
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
70	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	A1091195	Hs.65029	growth arrest-specific 1	3.35
75	451529	A1917901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
80	421913	A1934365	Hs.109439	osteoglycin (osteoductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
	407938	AA905097	Hs.85050	phospholamban	3.48
	418005	A1186220	Hs.83164	collagen, type XV, alpha 1	3.51
80	452877	A1250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	Integrin, alpha 8	3.52
	404277			NM_019111*Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypothei	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.86
	428957	NM_003881	Hs.194679	WNT1 Inducible signaling pathway protein	3.89
15	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
	449925	AI324293	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
20	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.295049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW939251	Hs.25647	v-fos FBI murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78085	complement component 7	4.37
30	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolaectin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
45	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426408	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
60	412636	1438_1
65		M77830 NM_004415 AF139065 BG681115 BG740377 BI712984 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI785807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149284 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI51766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW955615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AJ392926 AU158477 BI467252 AU159919 AU760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AG039975 AA946936 AA644381 BM314884 AA702424 AJ417612 AW190555 AJ220573 AI304772 AI270345 AI527383 AA552300 AI911702 AW166807 AJ346078 W95070 AA149191 AA026864 AI830049 AW780435 AJ078449 AI819984 AI858282 AI458588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AJ205263 BF082491 AW021347 AI568096 BE939862 AA088865 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026554 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067766 AV721320 AI022862 N29754 C03378 NB4767 AA131077 H30148 BE714290 AI666869 AI568892 AI915596 AW105614 AI887258 AI538577 BE826474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406

5	454042	30254_1	BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 B1089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG577157 BE009090 BG681378 BE712291 BG961498 BG578984 B1040941 AA337270 AW384371 AW847442 B1058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 A1284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 B1013292 BE001925 AW365156 AW365154 AW605653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 A1498487 A1420458 A1018523 AA708686 BF949533 AL119553 BF945960 A1081305 AA041432 A1921013 A1684910 A1654847 AW874199 A1206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 B1040435 BF831989 B1600000 AV722350 W27787 H45331 B1549761 R53955 B1549855 BG991583 B1491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 A1431587 BE858679 AW292267 A1421678 AA041195 BE466753 A1243913 A1358894 AW137298 A1366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17395 B1493714 A1880103 AW771447 A1202561 A1788851 A1494436 BF856114 H22570 AW964381 BG007409 BM314056 AA455642 T30661 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 A1267350 N64249 W67500 F07962 AA322394 B1489987 BE644965 BM313782 AA910364 A1809246 AA836750 BF115228 AA829730 N27413 BM141766 A1742325 AA455261 AA938708 A1420241 A1130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 N34898 A1678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 A1801368 AA971739 A1017351 AA760722 A1460007 A1458383 A1694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280 BG435302 BM083687 AA904035 AA488889 W76175 AA761874 H28767 AA910081 AA837086 A1521825 BG986378 A1478562 AA743152 AA746092 H88863 BG986375 AA635644 A1493206 AA669979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495
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20	TABLE 70C			
	Pkey:	Unique number corresponding to an Eos probeset		
25	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
30	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
	404277	1834458	Minus	91665-91946

TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
45	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
50	R1:	75th percentile of ewing sarcoma to 85th percentile of body map		
	Pkey	ExAccn	UnigeneID	Unigene Title
55	104659	AW969769	Hs.105201	ESTs
	101447	M21305		gb:Human alpha satellite and satellite 3
60	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro
	115881	NM_005756	Hs.184942	G protein-coupled receptor 64
65	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease
	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1
70	110278	AF061573	Hs.19492	protocadherin 8
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of
75	116752	AL008583	Hs.91622	neuronal pentraxin receptor
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro
80	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor
	110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin
85	121362	AF050147	Hs.97932	chondromodulin I precursor
	131291	NM_004350	Hs.170019	runt-related transcription factor 3
90	101063	D54745	Hs.80247	cholecystokinin
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri
95	122651	AW975398	Hs.293836	ESTs
	100299	D49493	Hs.2171	growth differentiation factor 10
100	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop
	123619	AA602964		gbcno97c02s1 NCL CGAP_P12 Homo sapiens
105	124006	A147155	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi]
	116301	AW969706	Hs.293332	ESTs
110	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!
	106533	AL134708	Hs.145998	ESTs
115	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbines
	131313	R96290	Hs.75874	ribosomal protein L44
120	116790	AW161357		microtubule-associated protein tau
	105316	A1671245	Hs.24835	hypothetical protein FLJ14594
125	102123	NM_001809	Hs.1594	centromere protein A (17kD)
	126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13
130	119791	AA554907	Hs.58291	ESTs
	113003	AW292315	Hs.7215	ESTs
135	102836	U94320	Hs.158330	neuropeptide Y receptor Y5
	126799	AW753865	Hs.74376	olfactomedin related ER localized protei
140	106298	BE387790	Hs.26369	hypothetical protein FLJ20287
	107160	AA314490	Hs.27669	KIAA1563 protein
145	115313	AA808001	Hs.184411	albumin
	123308	C14187	Hs.103538	ESTs

	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
5	110288	H40665	Hs.31564	ESTs	13.8
	106498	AJ221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;catyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
10	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AJ207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
15	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
20	104968	AJ249502	Hs.29669	ESTs	11.1
	123532	AA608733		gb:ae56106.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, 1	10.6
25	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	10.6
	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
30	110730	N67655	Hs.26411	ESTs	10.3
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AI204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	AJ940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-link	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AJ085153	Hs.143764	ESTs, Weakly similar to unknown [H.sapie	8.8
55	113903	AJ368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AJ347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106575	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AJ918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
70	107098	AJ823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
75	133063	AJ654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	106730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125934		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA: cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82265	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP566D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6



	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (	7.6
	118036	AJ471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	7.6
	131170	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	7.5
5	104548	R39398	Hs.91559	ESTs	7.5
	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRF (sex determining region Y)-box 11	7.4
10	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
15	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	7.1
20	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
25	118013	AI674126	Hs.94031	ESTs	6.9
	120147	AJ917116		hemoglobin, beta	6.8
	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
30	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
35	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
40	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
45	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
50	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
	106383	AA447453	Hs.27860	Homo sapiens mRNA: cDNA DKFZp568M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
55	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
60	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.0
	104689	AA420450	Hs.292911	Plekophilin	6.0
	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
65	109841	H01052		gb:yj32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AI088691	Hs.208414	Homo sapiens mRNA: cDNA DKFZp564D0472 (f	5.8
	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
70	113494	T91451	Hs.85538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
75	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AA680004	Hs.276956	hypothetical protein FLJ12929	5.7
80	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gbyp88h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transpos	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
5	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	R49390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109605	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
15	131185	BE280074	Hs.23960	cyclin B1	5.4
	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
20	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
	115121	AJ634549	Hs.325422	ESTs	5.3
	125464	N71807		gb.yz29d09.r1 Soares_multipia_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
25	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 femi	5.3
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	M41367	Hs.173002	ESTs, Weakly similar to I38022 hypothe	5.2
30	120830	AJ568170	Hs.96886	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
40	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AJ927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothe	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102627	AL021918	Hs.158174	zinc finger protein 184 (Krueppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
50	116814	H50834	Hs.77899	gbyp88a10.s1 Soares fetal liver spleen	5.0
	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4H1D1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RJ2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AJ476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	126769	AA083456		gbczn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gbyp77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.8
	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL056739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.178833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	126521	AJ475110	Hs.203933	ESTs	4.7
	110343	AW135703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

	113974	AW959756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
5	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
10	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
15	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
20	108489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
25	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AI031650		ESTs	4.4
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
30	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
35	115167	AA749209	Hs.43728	hypothetical protein	4.3
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
40	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
45	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
50	129550	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
	106073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
55	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
	106012	AI240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130832	AW838005	Hs.20082	zinc finger protein 3 (A8-51)	4.2
60	125860	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-IRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
65	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101266	L36845	Hs.73964	EphA4	4.2
	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
70	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothetic	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
	119271	AI081118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
75	115333	BE241812	Hs.87850	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca <sup>++</sup> transporting, plasma membra	4.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
80	129948	AI537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.283316	ESTs	4.1

5	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23550 retrovira	4.0
	127153	AI732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
10	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.0
	126965	AI470523	Hs.133336	ATP-binding cassette, sub-family C (CFTR	4.0
15	103100	NM_005574	Hs.184585	UM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
20	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
25	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133515	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gbvyy54c08.s1 Soares_multiple_sclerosis_	4.0
	126522	W31912	Hs.21168	gbzcc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
30	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
	105808	AI133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
35	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
	118967	AI668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
40	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	3.9
45	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
50	120820	AA347417	Hs.96869	EST	3.8
	105459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
	105476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
55	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gbzbb80d09.s1 Soares_senescent_fibroblas	3.8
60	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
65	103319	X83492	Hs.82359	tumor necrosis factor receptor superfami	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA296874	Hs.77494	deoxyguanosine kinase	3.8
	127262	AA828125		gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UI-H-B13-ala-a-12-O-UI.s1 NCL_CGAP_Su	3.7
70	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasmn 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
	116203	AW137166	Hs.87306	ESTs	3.7
	123377	AW569183	Hs.271297	ESTs	3.7
75	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
80	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW969731	Hs.323099	ESTs	3.7
	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0543 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	AI300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
15	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.6
	125174	W51835	Hs.231082	EST	3.6
	104799	AA029703		gbze95h08.s1 Soares_fetal_heart_NbHH19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X16866	Hs.333497	cytochrome P450, subfamily IID (debrisoq	3.6
20	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AI738810	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78799	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1N1B H	3.5
	117265	AA451966		RAB9-like protein	3.5
45	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
	109482	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R59958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
60	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AI580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	105367	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
70	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
75	109734	AI927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
80	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AI141426	Hs.8706	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
5	126671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
10	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
15	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal effact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
25	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Soares infant brain 1N1B H	3.3
30	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
35	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21801	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
50	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
55	121292	AA401807		gb:zv65f11.s1 Soares_tetal_fetus_Nb2HF8_	3.3
	123284	AA488988	Hs.283796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GCB1 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
70	126770	AI282320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	129284	AA318224	Hs.296141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

5	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14205 fis, clone NT	3.2
	105103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein I3	3.2
10	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
15	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N65148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
	109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
20	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2453 protein	3.2
25	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
	129056	AI769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN IIII	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
30	103038	AA926960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
	132305	AI806090	Hs.44344	hypothetical protein FLJ20534	3.2
	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
35	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothei	3.2
40	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S66657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A, pancreatic	3.2
45	115536	AK001468	Hs.62180	anillin (Drosophila Scrapie homolog), act	3.2
	119551	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
	134964	AI803516	Hs.272891	hippocalcin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease HI, large subunit	3.1
50	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group I, m	3.1
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
55	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14957 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
60	108807	AI652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
65	112369	AW968243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
70	128403	AI908008	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AI914699	Hs.13297	ESTs	3.1
	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:cn57d02.s1 Stratagene muscle 937209 H	3.1
75	117997	N52030	Hs.47420	EST	3.1
	104558	R56878	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297208	Hs.164018	ESTs	3.1
80	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOPS/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
	123485	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	UIM domain binding 2	3.1
	115348	AA281562	Hs.768	ESTs	3.1
	117297	AW779829		gb:cn88a05.x1 NC1_CGAP_Jd11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173584	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88357	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
15	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA589362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128560	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133966	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105552	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129928	AI338993	Hs.134535	ESTs	3.0
	118922	AW208193		hypothetical protein DKFZp76182423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:cc81h08.s1 Pancreatic Islet Homo sapi	3.0
	122219	AA436002	Hs.183161	ESTs	3.0
40	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp5640043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
45	128902	AA036637	Hs.107052	ESTs	3.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-II	3.0
	108711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
50	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	105735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
55	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:aa38f04.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 6	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	125887	H20832		gb:ym48d03.s1 Soares infant brain 1N1B H	3.0
70	117960	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109568	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81655	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 718

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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	123619	371681_1		AJ686662 AW389079 AA602099 AW134567 AW517843 AI682674 AI474874 AA374167
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	101445	1650_5		AA812434 AI831542 AA766261 AI769894 N63376 AA214392 AA135833 AW605017 AA135965 AW450072 H04812 AA446459
	100944	25682_2		AW439151 AA426273 AI061423 AA598549 Z40087 AI753216 AA743075 AA854268 AA458920 AA843893 AI565516 AI864957
15	117297	647718_1	15	AJ566634 AW971760 AA211796 AA430089
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25			25	AL121500 AW291763 AI732432 AA129708 AA133309 AI733750 AI225224
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30			30	AA476718 AW772454 AI807703 R44253 AA976667 AI985186 AI650254 H38942 R84829 AA018724 AA010000 H85934 AA019126
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65			65	T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
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				M79088 N88221
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				N95428 W24040 AW751366 H81987
				R59305 R19748
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129012	22280_4	H46534 H51478 H20702 H46515 H40200 H50046 H23647 H50439 H18383 H21846 H23849 H40182 R21924 H01290 H01283 H42464 W31497 W39660 AA046219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 AA42481 AA088608 R69918 R36334 H80281 N58483 A1075154 A1086754 AA595787 H81051 H01187 A1057251 T96992 H59584 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 R92416 H89486 R36617 R65795 A1088338 A1373324 H66992 R96235 A1494132 R16678 AA088178 AA705356 AA962143 AA148933 R09231 A1160937 R70525 T46980 A1200046 H02301 AA367587 R35968 T97106 D78703 N78072 D78668 D63268 R26197 AA085579 R63766 R92415 W00998 R80766 R67875 R27583 R09343 H13646 R27682 T89007
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123470	8785_29	AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630166 AL041326 AA780690 L40517 U21556 A1093182 AW062487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389484 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 A1673095 AA599106 AW601545 A1538739 A1538730 A1521786 AW366369 AW021010 AA362576 A1289927 AA382592
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123808	genbank_AA620552	AA620552
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118129	genbank_N57493	N57493
109841	genbank_H01052	H01052
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124250	314220_1	AA350256 H68126
101447	entrez_M21305	M21305
117357	genbank_N24829	N24829
103392	entrez_X94563	X94563
135029	H58818_at	H58818
105225	genbank_AA211777	AA211777
121292	genbank_AA401807	AA401807
105909	82840_1	AA195191 AA190578 A1532307 AA195227 AA743633 A1823408 A1832203 A1653114 AA205307 AW021913 A1687980 A1674198 A1675563 A1417935 AA707350 AA135157 A1434721 A1151038 A1038305 R52643 AA780141 AW207645 D19691 A1474370 AA401739 N22905 N70378
100237	entrez_D30715	D30715
114988	genbank_AA251089	AA251089
123423	genbank_AA598484	AA598484

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title

Seq ID No: Seq ID number correlation for those sequences in Table 73

Pkey*	ExAccon	UnigeneID	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82932	Seq ID No B1 & B2
	410102	AW248508	Hs.279727	Seq ID No B3 & B4
	101104	AW862258	Hs.169266	Seq ID No B5 & B6
	447761	AF061573	Hs.19492	Seq ID No B7 & B8
	428183	AW969726	Hs.98381	Seq ID No B9 & B10
10	439221	AA737106	Hs.32250	Seq ID No B11 & B12
	121619	AA528339	Hs.178062	Seq ID No B13, B14, & B15
	104659	AW969769	Hs.105201	Seq ID No B16
	105782	H09748	Hs.57587	Seq ID No B17 & B18
	129977	NM_000399	Hs.1395	Seq ID No B19 & B20
15	100299	D49493	Hs.2171	Seq ID No B21 & B22
	116301	AW969706	Hs.293332	Seq ID No B23 & B24
	106533	AL134708	Hs.145998	Seq ID No B25-B27
	131313	R96290	Hs.75874	Seq ID No B28 & B29
	105316	AI671245	Hs.24835	Seq ID No B30 & B31
20	113003	AW292315	Hs.7215	Seq ID No B32
	102836	U94320	Hs.158330	Seq ID No B33 & B34
	102745	AW753865	Hs.74376	Seq ID No B35-B40
	123308	C14187	Hs.157208	Seq ID No B41 & B42
	120147	AI917116		Seq ID No B43
25	123049	BE047680	Hs.211869	Seq ID No B44 & B45
	119082	AF252297	Hs.91546	Seq ID No B46 & B47
	105301	AW352357	Hs.7457	Seq ID No B48 & B49
	128478	AA708205	Hs.100343	Seq ID No B50-B53
	106111	AW875398	Hs.6451	Seq ID No B54 & B55
30	131307	NM_000025	Hs.2549	Seq ID No B56 & B57
	120830	AI568170	Hs.96886	Seq ID No B58 & B59
	127654	AA806164	Hs.116502	Seq ID No B60
	102725	AB026187	Hs.159156	Seq ID No B61 & B62
	132520	AA257992	Hs.50651	Seq ID No B63 & B64
35	130637	AA356764	Hs.17109	Seq ID No B65 & B66
	117602	N35020	Hs.44685	Seq ID No B67 & B68
	128797	NM_002975	Hs.105927	Seq ID No B69 & B70
	129703	BE388665	Hs.179999	Seq ID No B71 & B72
	125770	AA143045	Hs.81665	Seq ID No B73 & B74
40	414761	AU077228	Hs.77256	Seq ID No B75 & B76
	420462	AF050147	Hs.97932	Seq ID No B77 & B78
	410268	AA316181	Hs.61635	Seq ID No B79 & B80
	104691	U29690	Hs.37744	Seq ID No B81 & B82
	416836	D54745	Hs.80247	Seq ID No B83 & B84

Table 72B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

50	Pkey	CAT Number	Accession
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Table 73: Sequences

Seq ID NO: B1 DNA sequence  
Nucleic Acid Accession #: NM\_053056.1  
Coding sequence: 210..1097

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	TCCCCAGCTG	CCCAGGAAGA	GCCCCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCCG	CCGCGGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAATGT	GTGCAAGAGG	360
15	AGGTCTGTGC	GTCCATGCGG	AAGATCGTCG	CCACCTGGAT	GCTGGAAGTC	TGCGAGGAAC	420
	AGAAATGAGA	GGAGGAGGTC	TTCCCGCTGG	CCATGAACTA	CCTGGACGCG	TTCTGTGCGC	480
	TGGAGCCCGT	GAAAAAGAGC	CGCTGCGAGC	TGCTGGGGGC	CACCTGCAATG	TTCTGTGGCT	540
	CTAAGATGAA	GGAGACCATC	CCCTGACGCG	CCGAGAAGCT	GTGCATCTAC	ACCGACAACCT	600
	CCATCCCGCC	CGAGGAGCTG	CTGCAAATGG	AGCTGCTCCT	GGTGAACAAG	CTCAAGTTGA	660
20	ACCTGGCGCG	AATGACCCCG	CACGATTTCA	TTGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
	CGGAGGAGAA	CAAAAGATC	ATCCGCAAC	ACGCGCAGAC	CTTCGTGCCC	CTCTGTGCCA	780
	CAGATGTGAA	GTTCAATTTCC	AATCCGCCCT	CCATGCTGGC	AGCGGGGAGC	GTGGTGGCCG	840
	CAGTGCAAGG	CGTGAACCTG	AGGAGCCCCA	ACAACTTCCT	GTCTTACTAC	CGCTCCACAC	900
	GCCTTCTCTC	CGAGGTGATC	AAGTGTGACC	CAGACTGGCT	COGGGCTGAC	CAGGAGCAGA	960
25	TGGAAGCCCT	GCTGGAGTCA	AGCCTGCGCC	AGGCCACGCA	GAACATGGAC	CCCAAGGCCG	1020
	CGGAGGAGGA	GGAAGAGGAG	GAGGAGGAGG	TGGAAGTGGC	TTGCACACCC	ACCGACGTGC	1080
	GGGAGCTGGA	CATCTGAGGG	CGCCAGGCAG	GCGGGCGCCA	CCGCCACCCG	CAGCGAGGGC	1140
	GGAGCGCGGC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGGAGCATTT	TGATACCAGA	1200
	AGGGAAAGTG	TCATTTCTCT	TGTTGTGGGT	TGTTTTTTCC	TTTGCTCTTT	CCCCCTTCCA	1260
30	TCTCTGACTT	AAGCAAAAGA	AAAAGATTAC	CCAAAAACTG	TCTTTAAAG	AGAGAGAGAG	1320
	AAAAAAAAAA	TAGTATTTGC	ATAACCCCTGA	GCGGTGGGGG	AGGAGGGTGT	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATAATCAAC	TCGTTTTTAT	ATTAAATGAT	TTGTTTCTCT	1440
	GTGTGAAGAA	TAGGCATTAA	CACAAAGGAG	GCGTCTCGGG	AGAGGATTAG	GTTCATCTCT	1500
	TTACGTGTTT	AAAAAAAGCG	ATAAAAAAT	TTTAAAAACA	TAGAAAAAT	CAGCAAAACA	1560
35	TTTTTAAAGT	AGAAGAGGGT	TTTAGGTAGA	AAAACATATT	CTTGTGCTTT	TCCTGATAAA	1620
	GCACAGCTGT	AGTGGGGTTC	TAGGCATCTC	TGTACTTTGC	TTGCTCATAT	GCATGTAGTC	1680
	ACTTTATAAG	TCATTGTATG	TTATTATATT	COGTAGGTAG	ATGTGTAACC	TCTTCACTTT	1740
	ATTCTATGCT	GAACTCAGCT	CTTGTTTACA	GTAGCGTAGC	GTGGCGGTGT	GCATGTCTCT	1800
	TGCGCCTGTG	ACCACCACCC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1860
40	TGCGGCACCA	GCCAGCGTAG	CAGGTCGCGG	AAAGGCCACC	TGTCCACTC	CTACGATACG	1920
	CTACTATAAA	GAGAAGACGA	AATAGTGACA	TAATATATTC	TATTTTATA	CTCTTCTCT	1980
	TTTTGTAGTG	ACCTGTATTAT	GAGATGCTGG	TTTTCTACCC	AACGGCCCTG	CAGCCAGCTC	2040
	AGGTCCAGGT	TCAACCCACA	GCTACTTGGT	TTGTGTTCTT	CTTCATATTC	TAAAAACATT	2100
	CCATTTCCTA	GCATTTTCAG	TCCAATAGGT	GTAGGAAATA	GCGCTGTTTT	TGTTGTGTGT	2160
45	GCAGGGAGGG	CAGTTTCTTA	ATGGAATGGT	TTGGGAATAT	CCATGTACTT	GTTTGCAAGC	2220
	AGGAGTTTGA	GGCAAGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2280
	TGCGTGTGTT	TCAGAAGAGA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCTT	2340
	TTCTTTTCTT	TAAAGAAAGT	TGAAGTTTAG	GAATCCTTTG	GTGCCAAGTG	GTGTTTGAAA	2400
	GTAGGGACCT	CAGAGGTTTA	CCTAGAGAAC	AGGTGGTTTT	TAAGGTTTAT	CTTAGATGTT	2460
50	TCACACCGGA	AGGTTTTTTAA	ACACTAAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2520
	ATTATATGCA	GAGGATGTTT	ATAAGGCCAG	TATGATTTAT	AAATGCAATC	TCCCTTGAT	2580
	TTAAACACAC	AGATACACAC	ACACACACAC	AAACCTCTG	CCTTTGATGT		2640
	TACAGATTTA	ATACAGTTTA	TTTTTAAAGA	TAGATCCTTT	TATAGGTGAG	AAAAAACAAA	2700
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55	ATCTGATTGG	ACAGGCAATG	GTGCAAGGAA	AATTAGGGTA	CTCAACCTAA	GTTCGGTTCC	2820
	GATGAATTCCT	TATCCCTCTG	CCCTTCTCTT	AAAAAACTTA	GTGACAAAT	AGACAATTTG	2880
	CACATCTGGG	CTATGTAATT	CTTGTAAATT	TTATTAGGA	AGTGTGAAG	GGAGGTGGCA	2940
	AGAGTGTGGA	GGCTGACGTG	TGAGGAGGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGGTC	3000
	CGGAGGGGAA	GGGCGGTGCG	CCACACCGGG	GACAGGCGCG	AGCTCCATTT	TCTTATTGCG	3060
60	CTGCTACCGT	TGACTTCCAG	GCAAGGTTTG	GAAATATTCA	CATCGCTTCT	GTGTATCTCT	3120
	TTACATTTGT	TTGCTGCTAT	TGGAGGATCA	GTTTTTGTGT	TTACAATGTC	ATATACTGCC	3180
	ATGTACTAGT	TTTGTGTTTC	TCTTAGAACA	TTGTATTACA	GATGCTTTT	TTGTAGTTTT	3240
	TTTTTTTTTT	ATGTGATCAA	TTTTGACTTA	ATGTGATTAC	TGCTCTATTC	CAAAAAGGTT	3300
	GCTGTTTTC	AATACCTCAT	GCTTCACTTA	GCCATGTTGG	ACCCAGCGGG	CAGGTTCTGC	3360
65	CTGCTTTGCG	GGGCAGACAC	GCGGGCGCGA	TCCACACAC	GCTGGCGGGG	GCCGGCCCGG	3420
	AGGCGCGGTG	CGTGAGAAC	GCGCGGTGT	CCCCAGAGAC	CAGGCTGTGT	CCCTCTTCTC	3480
	TTCCCTGCGC	CTGTGATGCT	GCGCACITCA	TCTGATCGGG	GGGTAGCAT	CATAGTAGTT	3540
	TTTACAGCTG	TGTTATTCTT	TGCGTGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3600
	ATTATAACAA	GTGTGCTCTA	CGTGCCACCA	CGGCGTTGTA	CCTGTAGGAC	TCTCATTCGG	3660
70	GATGATTGGA	ATAGCTTCTG	GAATTGTTC	AAGTTTTGGG	TATGTTTAA	CTGTTATGTA	3720
	CTAGTGTCT	GTTTGTATT	GTTTGTGTTAA	TTACACCATA	ATGCTAATTT	AAAGAGACTC	3780
	CAAACTCTCA	TGAAGCCAGC	TCACAGTGCT	GTGTGCCCGG	GTCACTAGC	AAGCTGCCGA	3840
	ACCAAAAGAA	TTGCAACCCC	GCTGGGGGCC	CACGTGGTTG	GGGCCCTGCC	CTGGCAGGGT	3900
	CATCCTGTGC	TGGAGGCGCA	TCTCGGGCAC	AGGCCCAACC	CGCCCAACCC	CTCCAGAACCA	3960
75	CGGCTCAAG	TTACCTCAAC	CATCTGGCT	GCGGGTCTG	TCTGAACAC	GCGGGGGCCT	4020
	TGAGGGACGC	TTTGTCTGTC	GTGATGGGGC	AAGGGCACAA	GTCTGTGATG	TTGTGTGTAT	4080
	CGAGAGGCCA	AAGGCTGGTG	GCAAGTGCAC	GGGGCACAGC	GGAGTCTGTC	CTGTGACGGG	4140
	CAAGTCTGAG	GGTCTGGGCG	GCGGGCGGCT	GGGTCTGTGC	ATTCTGTGTT	GCACCGCGCG	4200
	GCTTCCAGC	ACCAACATGT	AACCGGCATG	TTTCCAGCAG	AAGACAAAAA	GACAAACATG	4260
80	AAAGTCTAGA	AATAAACTG	GTAACACCCC	AAAAA			

Seq ID NO: B2 Protein sequence  
Protein Accession #: NP\_444284.1

1 11 21 31 41 51  
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5 MEHQLLCCEV ETIRRAYPDA NLLNDRVLRA MLKABETCAP SVSYPKCVQK EVLPSMRKIV 60  
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 AEKLCIYTDN SIRPEELLQM ELLLVNKLKW NLAAMTPHDF IEHFLSKMPE AEENKQIIRK 180  
 HAQTFVALCA TDVKFISNPP SMVAAGSVVA AVQGLNLRSP ENFLSYRYLT RPLSRVIKCD 240  
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10 Seq ID NO: B3 DNA sequence  
 Nucleic Acid Accession #: XM\_044166  
 Coding sequence: 1..1576

1 11 21 31 41 51  
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75 Seq ID NO: B4 Protein sequence  
 Protein Accession #: XP\_044166.2

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 PMVTGRREDV ATARREIISA AEHPSMIRAS RNKSGAAGFV APALPGQVIT RVRVYRVRVG 240  
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 EYNNENDFLA GSPDAIDSR YSDANRVHQP GCKPLSTFRQ NSLGCIGEGC VDSGFAPRL 360  
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KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPIQGFSLKG GGGLRSPGGG RDCMVCPESE 480  
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5 Seq ID NO: B5 DNA sequence  
Nucleic Acid Accession #: NM\_000909.1  
Coding sequence: 209..1363

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55 TGTTTGATT TAAAGGGGCG GACATTTTAT TAAATCAAT ATGTGTTTGT CTTTTCTGTA 2700  
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Seq ID NO: B6 Protein sequence  
Protein Accession #: NP\_000900.1

60 1 11 21 31 41 51  
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65 CVSITVSIFS LVLLAVERHQ LIINPRGWRP NNRHAYVGLA VIWVLAVASS LPFLIYQVMT 180  
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70 Seq ID NO: B7 DNA sequence  
Nucleic Acid Accession #: NM\_002590.2  
Coding sequence: 204..3416

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80 GGATCGCACT TGAGGCTGGA GCATGAGTCT CTGTGAGGCG TTGGGCGAGC CCTTGCCTTT 240  
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5 AGGAGCAGTT CCGGCTGGTG CACGTGGAGG TAGAGQTGAG GGACGTCAAC GACCAAGCGC 600  
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Seq ID NO: B8 Protein sequence  
 Protein Accession #: NP\_002581.2

65 1 11 21 31 41 51  
 MSFVRRNGSP CLFLQLFSL CWLVSVAQSK TVRYSTFEED APGTVIGTLA EDLHMKVSGD 60  
 TSFLRKQFN SLLLRVREGD GQLTVGDAGL DRERLCQAP QCVLAFDVVS FSQEQFRLVH 120  
 VEVEVRDND HAPRFPRAQI PVEVSEGAIV GTRIPLEVPV DEDVGANGLO TVRLAEPHSP 180  
 70 FRVELQTRAD GAQCADLVLL QELDRESQAA YSLELVAQDG GRPPRSATAA LSVRVLDAND 240  
 HSPAPPGAV AEVELAEDAP VGSLLLDLDA ADPDEGPNGD VVPAFGARTP PEARRLFRID 300  
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 APGAPATSPF AAAAAAALG GADASSPAGA GTPEAGATSL VPEGAARESL VALVSTSDRD 420  
 SGANGQVRCA LYGHEHFRLO PAYAGSYLVV TAASLDRETI AEYNLTVAE DRGAPPLRTV 480  
 75 RPYTVRVGDE NDNAFLFTRP VYEVSVRENN PPGAYLATVA ARDRDLGRNG QVYRLLLEAE 540  
 VGRAGGAVST YVVDPATGA IYALRSFDYE TLRQLDVRIQ ASDGGSPQLS SSALVQVRVL 600  
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 AFATGRRTGE ILLTGDSQE PPGRVFRALL VISDGRPFPL TTTATVSFVV TAGGGGPPAA 720  
 PASAGSPERS RPPGSRGLVS GSVLQMDTPL IVIIVLAGSC TLLLAIIAI ATTGNRRKE 780  
 80 VRKGGALREE RPAAGGGAS APGSPERAAR GAGPRPNMPD VLTFFGTGKA PFGSPAADAP 840  
 PPVAAAAEV PSEGGSATGE SACHFEGQOR LRGAHAEPYG ASPGFGKEPA PPVAVWKGHS 900  
 FNTISGREAE KFSGRDSGKG DSDFNDSDD ISGDALKKDL INHMQSLGWA CTAECKILGH 960  
 SDRCSWSPCS GPNRHPSPHP PAQMSTFCKS TSLPRDPLRR DNYQAQLPK TVGLQSVYEK 1020  
 VLHRYDRTV TLLSPPPRGR LFDLQZIGVP LYQSPFGRYL SPKKGANENV

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10	GATCTCAGCT	GACAGTGCCT	TGCGGGACCA	AACAAGCTCG	GCAGGACCAA	ATTAGAAGAT	180
	CAAAATGCAA	AATATGCTGC	TTTGTGTGAT	ATTTTTCAC	CTCGGTGGGA	CCCTCATTTA	240
	TGGATCTGAA	ATGGAATGGG	ATTTTATGTG	GCACITGAGA	AAGGTACCCC	GGATTGTCTA	300
	TCAAGGACTT	TTCCATCTCA	CCAGCCCGCG	ATTTGAGGCA	GATGTCTAAGA	TGATTGGTAA	360
	TAGAGTGTGT	GGCATCGAAT	GCAGGAAGA	ACTCCCAAT	CCGACGCTTT	CTGAATTGGA	420
	GGATTATCTT	TCCTATGAGA	CTGTCTTTGA	GAATGGCACT	CGAACCTTAA	CCAGGGGTAA	480
15	AGTTCAAGAT	TTGGTCTCTG	AGCCGACTCA	AAATATCAC	ACAAAGGAGG	TATCTGTTAG	540
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	AACTCAATTC	CCTTTCAGCA	CAGCTGTGAA	CGTTTCCACG	GGCTGTAGTG	GCATTCTCAT	660
	TTCCCTCAG	CATGTCTTAA	CTGCTGCCCA	GCTGTGTCAT	GATGGAAGAG	ACATGTGCAA	720
20	AGGGAGTAAA	AACTCAAGGG	TAGGGTTGTT	GAAGATGAGG	AATAAAAGTG	GAGGCAAGAA	780
	ACGTGCGAGT	TCTAAGAGGA	GCAGGAGAGA	AGCTAGTGGT	GTGGACCAA	GAGAGGGTAC	840
	CAGAGAGCAT	CTGCAGGAGA	TGCGGAGAGG	TGGGATAGGA	AGTAAAAAT	CTGGCGCGGG	900
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	TCCGAAGGCT	TGGGCACGAG	GAGGATCAAG	GGGCGTACC	TGGGACTATG	ACTATGCTCT	1020
25	TCTGGAGCTG	AAGCGTGCTC	ACAAAAAGAA	ATACATGGA	CTTGGAAATC	GCCCAACGAT	1080
	CAGGAAAAAT	CCCTGGTGA	TGATCACTT	CTCAGGATT	GATAACGATA	GGGCTGATCA	1140
	GTGTGCTAT	CGGTTTTCGA	GCTGTTCYGA	CGAATCCAA	GATCTCCTT	ACCAATAYTG	1200
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	AGGGCGGTGT	ATCATCTAAA	TCACAGAGAA	AACCCAGCTC	GCTTACCGTA	GTGAGATCAC	1500
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	GGAGATTTTC	GTCCATTTAA	AAAAATGTATA	GGTGCAGATA	TTGAAACTAG	GTGGGCACIT	1620
35	CAATGCCAAG	TATATACTCT	CTTTTACATG	GTGATGAGTT	TCATTGTGAT	AAAAATTTTG	1680
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	TTGTGTATTA	AATGTGAAAT	YGCATAGATA	AAGGTAGATG	GTAAGACAT	TAGTATGACA	1860
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40	GCCCTCAATG	TTTATATTGT	GTTATCTGTT	GCGTCTGGGA	CATTAGTTT	AGTTTTTTGT	1980
	AGAAATFACA	ATTCAGAGAA	AAAAGCAAGC	ATTATAAAC	AAACTAATA	CTGTTTACT	2040
	GCTTTAAGAA	ATAACAATTA	CAATGTGTAT	TTTATAAAA	TGGGAGAAAT	AGTTTGTCT	2100
	ATGAAATAAA	CCTAGTTTAA	AAATAGGGAA	GCTGAGACAT	TTTAAGATCT	CAAGTTTTTA	2160
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45	GCTACATTTT	TAGGACAAG	AATCTGTAA	TCCTTTTCAA	GAAGAGGTCT	TTTTCTCCT	2340
	GACAAAATCC	AGCTTTTGT	TGAGGACTAT	AGGGTGAAT	CTCTGATGAT	TAATTTTAGA	2400
	TATGTCTCTT	CCTAAAAAT	ATAAAATTT	TGAAATATGA	CTTAAAAAAA	AAANWCGACG	2460
	CGCGCGCGAA	TTTAGTAGTA	GTAGTGCACC	CGGGAATTC	GGACCGGATC	CTGCAGGCGT	2520
	ACCGC						

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	VCIGIEQDQL	PTPSLSLELD	YLSVETVFEN	GTRTLTRVKV	QDLVLEPTQN	ITTKGVSVRR	120
	KRQVYQKSR	PSILDKPLFT	NFPSTPAVLK	STGCGSILQI	PQFVLTAACH	VHDGKDYVRG	180
	SKGLRVGLLK	MNRKSGGKKR	RQSKRSRREA	SGDQREGTR	HLRILREAKG	RRRKSGRGQ	240
60	RIAEGRPSFQ	WTRVINTHIP	KGWARGGMGD	ATLDYDVALL	ELKRAHKYKY	MELGISPTIK	300
	KMPGGMIHFS	GFDNDRADQL	VYRFSVSDSE	INDLLLYQCD	ABESGTSGSV	YLRLKQDPDK	360
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	1	11	21	31	41	51	
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	CTGCGCGCT	CTCGTGCGC	TCTGTCTGCG	TGCTGTACAT	GGTGTCTCCG	CTCATCAGCC	180
	CCAGAGCCCT	CGCCCTGCCC	GGGGCGCATG	TGGTGGTTAC	AGGAGGTTC	AGTGGCATCG	240
	GGAGATGCAT	TGCTATGAG	TGCTATAAAC	AAAGAGCTTT	TATAACTCTG	ATTGGCCAGAA	300
75	ATAGGATAT	CTGCTCGCAG	CAGAAAGAA	AAATTGAAAT	CGACTCTATT	AATGACAAAC	360
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	TAAATCAAGC	CACAGAGAAA	TGGGTGCTG	TCCAGATGCT	GTGAAATTTG	CGAGGAATGG	480
	CAGTGTGCGG	AAAAATTGAA	GATCTTGAAG	TTAGTACCTT	TGAAAGGGTA	ATAGGATCA	540
	ATTACTGGGG	CAGCGTGTAC	CCACGCGCGG	CGGTGTACAC	CACCATGAAG	GAGCGCCGGG	600
80	TGGCGCAGAT	CGTGTTTGTG	TCTCTCCAGG	CAGGACAGTT	GGGATTATTG	GGTTTACAG	660
	CTACTCTGCG	ATCCAAAGTT	GCCATATAGG	GATTGGCAGA	AGCTTTGACG	ATGGAGGTGA	720
	AGCCATATAA	TGTCATCAT	CACAGTTGCT	AACCCACAGA	CACAGACACA	CTGGGCTTTG	780
	CGGAAGAAAA	CAGAACAAAG	CCCTTTGGAG	CTCGACTTAT	TTCAGAGAGC	ACATCTTGTG	840
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10  
15  
20  
25

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Seq ID NO: B12 Protein sequence  
Protein Accession #: NP\_002026.1

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1 11 21 31 41 51
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CAGMAVSGKF EDLEVSTFER LMSINYLGVS YPSRAVITM KERRVGRIVF VSSQAGQLGL 180
FGFTAYSASK PAIRGLAEAL QMEVKPYNVY ITVAYPPDID TPGFAEENRT KPLETRLISE 240
TTSVCKPEQV AKQIVKDAIQ GNFNSSLGSD GYMLSALTGC MAPVTSITEG LQQVVTMGLF 300
RTIALFLVGS FDSIVRRMM QREKSENADK TA

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Seq ID NO: B13 DNA sequence  
Nucleic Acid Accession #: CAT Cluster

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50

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TTTGATTTGG TTAAGTCCAA TTATTAATATG CTGCGGTTTC AAATTCACAG CTGGAAGGAC 180
CACCATTTA AAAACTTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAAAATT 240
CCAGGCATTG GTTTGACATA TTTCCAGAGC TCAAACTCTG AGTGTTCCAC ATGCACATAC 300
AAGATCCAGA GTCTCATGTT AAAATCACTT ACATACCCAG AAAGACCACC ACTTTGCAGG 360
TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420
AAGAACACAT AAGATGCCTT CTTCATCAA ATGCACCTGC TTGTGAATTA ATGGACTTGT 480
AAATGAACAT ATGCAATCAG TCTTTTATAA TGCACTGTTT AATTTGAGAT TCAAGTATTT 540
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AACATTTCCA AAAAAAAGAA AA

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Seq ID NO: B14 DNA sequence  
Nucleic Acid Accession #: XM\_086767.1  
Coding sequence: 276..611

60  
65  
70  
75

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1 11 21 31 41 51
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TCGCTGGGT TATCAAGCCA AGCTATTATA AGGTGTTTAA AAAGAAAGGA TGGAAAGGAAG 180
ACCTCTTAGG ACCACTGTGT TTTTGGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT 240
ATTTTGTTCT CAGTATAATT GTTCCAGATA AAATATGAT GGATGGCTCG TTTTCATTTA 300
AATTATTAAT TCAGCTTGGG ATGATTGAAG AGCCAAAGCT TTATGAAAG AACAAACCAT 360
TTTATAAAT TCAAGAAAGT AAGATCTCTG CTCAATTTTA TAATGACTTT GTAAATATTT 420
CAAGCATTTG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCCACA TGCACATACA 480
AGATCCAGAG ACTCATGTTA AAATCACTTA CATACCCAGA AAGACCACCA CTTTGCAGGT 540
ATAATATTGT ACTTAAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCAA 600
AGAACACATA AGATGCCCTC TTCCATCAAA TGCACTTGCT TGTGAATTA TGGACTTTGA 660
AATGAACATA TGCAATCAGT CTTTATAAAT GCACGTGTCA AATTGAGATT CAAGTATTTT 720
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AACATTCG

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Seq ID NO: B15 Protein sequence  
Protein Accession #: XP\_086767.1

80

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1 11 21 31 41 51
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Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

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AAGTGCTATT AGCCCAAGCT TCTTACATTC ATTAAGAGAG TGACTATCAA AAACAGCAAC 180
ATGCACAATG GTACATATGC ACRAAATGGA ATTATATCAA CAAATATACA AAATACCCAA 240
AATAAAATAT TTACAGGTTT AAAAATATAA ACATTGATTC CTCTATCCCA TTAACCATTT 300
10      GGAGTGGAGA AAGGAGGAAA GACCCATTGG CTATTAGAA TCCTTTTAA AACAGTTTT 360
TAAAAATAG AATTAGTTCT AGGAGACAAT TTTTGATGTT TTTGAGGGT TTAACATTCT 420
ATTATAAAAA TAACATCTAT AAACCTACTA ACAATTTTCC TCCTGTGCAC AAAAATAATA 480
CTGCCAAAAC CTGTCTCAA AGACATGCCCT GACTTTCAGG AAAGCTAATT ATGGAATG 540
AGTTTCTCGT TTGGGTTATC TTTGTTACTA TTTTCAAATA ACCAGCAACT CCTATATTA 600
15      CACTGAGATA CTTTATATAA ATAAAGTGGG CGAAACCTGA AGTTCACAAT GAGCCTGCTA 660
GGTAGCTGCT GTCAAGTACA AATGATAGGA ATTGACTTTG CCAACACAT CAAAAGCATT 720
TTCCCTGATA TTCTGATAG ACCTACCACT ATCAGATCCT CCATATTCAA TAAGATTAT 780
CCTGGAAACA ATGAAATGT TAAATATTAC TTTGCTAGAG TTTCTCTCC TTTATTAGA 840
20      AATAAATGTG TAGTGGGAC CAGTGGTGT AATGTAGATA CTTGAGAAGT TTCATTGATT 900
CCTTCAGACC CATGCCG

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Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM\_022898.1

Coding sequence: 268..2739

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GCCCTGGACA AGGACAGCCC GCCACCTTCC TCAGCTCCG AGCTCAGGAA AGTGTCCGAG 600
CCGCTGGAGA TCGGATGCCA AGTCACCCC GACGAAGATG ACCACCTGCT CTCACCCAG 660
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70      AAGGTGTTCA AGAAGTGCAG CAACTTGACG GTGCAACGCG GAGCCACAC CCGCGAGCG 2520
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CAGGTACTTT TTATTATTAT TTTTCTGTT TGAATTCCTT TAAGAGATT TGTGGGTAT 3060
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5 GAGATGTAGC ACTCATGTGG TCCCGAGTCA AGCGGCCCTTT TCTGTGTTGA TTTCGGCTTT 3480  
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 15 TACTGGCACT ATAAAGAAAC AAATAAAATA ATAATTATA GGACAGTTT TCTACTGCCA 4320  
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 20 AGATAGAGGA TATGAAATGC CATAAGACCC AATCAATGA AGAAATAAAC CCAGCACAA 4560  
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 30 TAACTGTAAA GTCCGAGTTT TAGTAAATTT TTTTCTGCTT TGGGTGTGTA ATTTTATTAT 5160  
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 60 CCCACTGAGG TCCTCAGAGT CCTCCAGGGT GGTCTTCTG TAGTCATAAC AGCTAGCCAG 6780  
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 65 TTAGAGGGTC TTTTATGGG AGAGAAGGAG ACTGAATTAC TCTAAGCAA ATGTGAAAAG 7080  
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 70 ACTTATTGTA TGAGCTTTT TGTTTACTT GGAGGTTTGT TCTTTTACTA CAAGTTTGA 7320  
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Seq ID NO: B18 Protein sequence  
 Protein Accession #: NP\_075049.1

75 1 11 21 31 41 51  
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 QMNFPLGDI LVFIEHKRQK CGSLGACYD KALDRDSPPP SSRSELKRV EPVEIGIQVT 120  
 PDEDDLHLSF TKGICPKQEN IAGKDEPSSY ICTCKQPFN SAWFLQHAQ NTHGFRIYLE 180  
 80 PGPASSSLTP RLTIPLPLPG EAVAQSPLMN FLGDSNPFNL LRMTGPILRD HPFGGEGRLP 240  
 GTPPLFSPFP RHLDLPHRLS AEEMGLVAQR PSADFVRNRL NPMADSPAM DFRRLRELA 300  
 GNSSTPPFVS PGRGNPMHRL LNPFPSPKS PFLSTPPLPP MPPGGTTPPP PPAKSKSECF 360  
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 LSAASSPEPG TSELAGEGLK AADGDFRHE SDPSLGHEPE EDEBEEREE EELLLENESR 480

5 PESSFSMDSE LSRNRENGGG GVPGVPGAGG GAAKALADEK ALVLGKVMEN VGLGALPQYG 540  
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 KPAPLPSPGL NSAAKRIKVE KDLELPPAAL IPSENVYSQW LVGYAASRHF MKDPFLGFTD 660  
 ARQSPFATSS EHSSENGSLR FSTPPGDLDD GGLSGRSGTA SGGSTPHLGG PGPGRPSSKE 720  
 GRRSDTCBYC GKVPKNCNL TVHRRSHTGE RPYKCELCNY ACAQSSKLTR HMKTHGQIGK 780  
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10 Seq ID NO: B19 DNA sequence  
 Nucleic Acid Accession #: NM\_000399.2  
 Coding sequence: 339..1769

1 11 21 31 41 51  
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 AGCGAGGGAG TTGGGTCTCC AGGTTGTGCG AGGAGCAAAAT GATGACCGCC AAGGCCGTAG 360  
 20 ACAAANTCCC AGTAACCTCT AGTGGTTTTG TGCACCAGCT GTCTGACAA ATCTACCCGG 420  
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 25 ACCCAGAAGG CATAATCAAT ATTGTGAGTG CAGGCATCTT GCAAGGGGTC ACTTCCCCAG 720  
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 30 ATCCATCCCC CCAAGCCAGC ACGGACCCAG GTCTCTTCCC AATGATCCCA GACTATCCCTG 1020  
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 TCCGTAACCT TACCTTGGGG GCGCCCACTG CTGGGGTGAC CGGACCAAGG GCCAGTGGAG 1200  
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 35 CCGCCTATAA CCAACACCA CCGCCACTGC GCGCCATTCT GAGGCGTCC AAGTACCCCA 1320  
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 45 TCCCTCTCTC CCTTTGTTGG GCAAAGGGCT TTGGTGAGG TAGCACTGCC CCTTTCCAC 1920  
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 60 TAGAAAGTAT ATTTTGTAT GCCTTGTGTT GTGACTTAAA AGTGTACCT TTGTAGTCAA 2820  
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65 Seq ID NO: B20 Protein sequence  
 Protein Accession #: NP\_000390.2

1 11 21 31 41 51  
 70 MMTAKAVDKI PVTLSGFVHQ LSDNIYFVED LAATSVTIFP NAEELGGPFDQ MNGVAGDGM 60  
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 LQGVTSFAST TASSSVTSAS FNPLATGFLG VCTMSQTQPD LDELVSPPPP PPPYSGCAGD 180  
 LYQDPSAELS AATTSSTSSL AYPPPPSYPS PKPATDPLGF PMIPDYRGFF PSQOQDLLEG 240  
 75 TAGPDRKPFP CPLDTRLVPP PLTPLSTIRN FTLGSPSAGV TGPASGGSE GPRLPSSSSA 300  
 AAAAAAAYY NPHFLPLRPI LRPRKYPNRP SKTPVHERPY PCPAEGCDORR FSRSEDLTRH 360  
 IRIHTGKFF QCRICMRNFS RSDHLTTHIR THTGEKPFAC DYCGRKFPARS DERKRHTKIH 420  
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80 Seq ID NO: B21 DNA sequence  
 Nucleic Acid Accession #: NM\_004962.2  
 Coding sequence: 457..1893

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Seq ID NO: B22 Protein sequence  
 Protein Accession #: NP\_004953.1

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 SMQDSEMITL ATFHFYSEPP RWPRALEVLK KPRAKNASGR PLPLGPPTRO HLLFRSLSON 180  
 TATQGLLRGA MALAPPPRGL WQAKDISPIV KAARRDGELL LSAQLDSBER DPGVPRPSPY 240  
 APYILVYAND LAISEPNSVA VTLQRYDPPF AGDPEPRAAP NNSADPRVR AAQATGLPLQD 300  
 NELPLGLDERP PRARAHQPHK HQLHPSPPRA LKPRPGRKDR RKKGQEVFMA ASQVLDPDEK 360  
 TMQKARRKQW DEPRVCSRRY LKVPDFADIGW NEWIISPKSF DAYYCAGACE FPMPIKVRPS 420  
 NHATIQSIVR AVGIIPGIPE PCCVPDRMNS LGVLPDENR NVVLKVYPNM SVDTCACR

Seq ID NO: B23 DNA sequence  
 Nucleic Acid Accession #: AK026322.1

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80

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 CTTTCTTCTA TTATGTGTTT ATCTCTGGCA GTTTGAGCCA AGAGAGGGCA CGGAGAAGTA 900  
 CAATGACTAG AGAGCACTTC TGTGAGGCT CATTCAATGA CCCCTACCCC AGTGTCTTAT 960  
 GAATGTGTGC TGCAGATGTC ATACAGCATC ACAGCTTCTT CTCTAATTTA TGAGCCATAA 1020  
 TTTTCTTTT TGTATTTTGA TTGTATTACC TGCTTGGTTG CAAGAGGATG ATGAGGAGGA 1080  
 CTACTATAGG ATAAATTTGT TTTTATAGAG CAATTCTCA TGGGTACAGA GGGATAGTAC 1140



TCCATTTTCC TCACGTATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200  
 TATGGAATCC TTTATGCTTT TTCTCAGGCT GCTTCGTGA CATGAATAA AGCCAGAGTT 1260  
 GATTGTGAAA AAAAAAAAAA AAAA

5 Seq ID NO: B24 DNA sequence  
 Nucleic Acid Accession #: cat cluster

1 11 21 31 41 51  
 10 TGTATACATT CCTTTCAAAAT AAAGACCTTG AGAAAAACAGC AGAGCCCAAGT GAAGATCACC 60  
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 15 AAATTATTGG ACTACAACT AATATACTAG AAAAGCATAC ACTTATTTTA TTTGAATGCA 300  
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Seq ID NO: B25 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 45 Coding sequence: 1..1144

1 11 21 31 41 51  
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 CCTT

70 Seq ID NO: B26 Protein sequence  
 Protein Accession #: FGENESH predicted

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Seq ID NO: B27 DNA sequence  
 Nucleic Acid Accession #: cat cluster



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Seq ID NO: B28 DNA sequence  
Nucleic Acid Accession #: NM\_002581.2  
Coding sequence: 368..5251

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Seq ID NO: B29 Protein sequence  
 Protein Accession #: NP\_002572.1

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 Coding sequence: 61..1008

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Seq ID NO: B31 Protein sequence  
 Protein Accession #: NP\_116197.1

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 40 LDSPFLACDC RLLWVPRRRW RLNFNRQOPT CATPEFVQKG EFKDFPPDVL PNYFTCRRAR 120  
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Seq ID NO: B32 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

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 55 TGGCAGCAGA CTGACAAAGG TAGAGGGAAA TGTAATAGCA CATCTACGCT GCAGTCTGGT 300  
 GAAAGTGGCC GGGGTGCTCC TTGGAAACA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC 360  
 AGCCTTTCG TACGCGGCAG GGACGCTTG ATTTAAAAA AATAAATAA TAAACGCTCT 420  
 GGGTATAGAA A

Seq ID NO: B33 DNA sequence  
 Nucleic Acid Accession #: NM\_006174.1  
 Coding sequence: 71..1408

1 11 21 31 41 51  
 | | | | |  
 GAAAGGCTAT CGGTAAACAAC TGACCTGCCA CAAAGTTAGA AGAAAGGATT GATTCAAGAA 60  
 65 AGACTATAAT ATGGATTAG AGCTCGACGA GTATTATAAC AAGACACTTG CCACAGAGAA 120  
 TAATACTGCT GCACTCGGA ATTCTGATT CCCAGTCTGG GATGACTATA AAAGCAGTGT 180  
 70 AGATGACTTA CAGTATTTTC TGATTGGGCT CTATACATTY GTAAGTCTTC TTGGCTTTAT 240  
 GGGGAATCTA CTTATTTTAA TGGCTCTCAT GAAAAAGCGT AATCAGAAGA CTACGGTAAA 300  
 CTTCTCTATA GGCAATCTGG CTTTCTGA TAICTTGGTT GTGCTGTTTT GCTCACCTTT 360  
 CACACTGACG TCTGTCTTGC TGGATCAGTG GATGTTTGGC AAAGTCATGT GCCATATTAT 420  
 GGCTTTTCTT CAATGTGTGT CAGTTTGTGT TTCAACTTTA ATTTTAAATAT CAATTGCCAT 480  
 75 TGTTCAGGTAT CATATGATAA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540  
 CTTTCTGATA GCTACTGTCT GGACACTAGG TTTTGCCATC TGTTCTCCCC TTCCAGTGT 600  
 TCACAGCTT GTGGAACTTC AAGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATTT 660  
 ATGTGTTGAG TCATGGCCAT CTGATTCATA CAGAAITGCC TTTACTATCT CTTTATTGCT 720  
 AGTTCAGTAT ATTTCTGCCCT TAGTTTGTCT TACTGTAAGT CATACAAGTG TCTGCAGAAG 780  
 80 TATAAGCTGT GGAATGTCCA ACAGAGAAAA CAGACTTGAA GAATATGAGA TGATCAACTT 840  
 AACTCTTCAAT CCATCCAAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG 900  
 GAGTTATTCA TCTTCAAAA AACACAGAAG AAGATATAGC AAGAAGACAG CATGTGTGTT 960  
 ACCTGCTCCA GAAAGACCTT CTCAAGAGAA CCACTCCAGA ATACTTCCAG AAAACTTTGG 1020  
 CTCTGTAGA AGTCAGCTCT CTTTATCCAG TAAGTTTATA CCAGGGGTCC CCACTTGCTT 1080  
 TGAGATAAAA CCTGAAGAAA ATTCAGATGT TCATGAATTG AGAGTAAAAAC GTTCTGTTAC 1140

AAGAATAAAA AAGAGATCTC GAAGTGTGTTT CTACAGACTG ACCATACTGA TATTAGTATT 1200  
 TGGTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAATCT 1260  
 TATTTCAAAT AGGCATTCCA AGTTGGTGTA TTGCATTGTT CATTGTGTGG GCATGATGTC 1320  
 CTGTGTCTT ATATCCAATTC TATATGGGT TCTTAATAAT GGGATTAAAG CTGATTAGT 1380  
 GTCCCTTATA CACTGTCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence  
 Protein Accession #: NP\_006165.1

1 11 21 31 41 51  
 MDLELDEYNN KTLATENNTA ATRNSDFPVN DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60  
 LILMALMKKR NQKTTVNPLI GNLAFSIDL VLFCSPTTLT SVLLDQWMPG KVMCHIMEPL 120  
 QCVSVLVSTL ILISIAIVRY EMIKHPISNN LTANHGYFLI ATVWTLGFAI CSPLPVFHSI 180  
 VELQETFGSA LLSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240  
 GLSNKENRLE ENEMINLTLH PSKSGSPQVK LSGSHKWSYS FIKKHRRYS KKTACVLPAP 300  
 ERPSQENHSR ILPENFGSVR SQLSSSKFKI PGVPTCFEIK PEENSVDVHEL RVKRSVTRIK 360  
 KRRSRVFYRL TILILVFAVS WMLHLFHV TDFNDNLISN RHPKLVCIC HLLGMSCCL 420  
 NPILYGLNN GIKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence  
 Nucleic Acid Accession #: NM\_014279.1  
 Coding sequence: 286..1689

1 11 21 31 41 51  
 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCGCG CCAGCCCAGC 60  
 CCTGCCCCAGC CCTGCCCGGA GGCAGACGCG CGGGAACCGG GACGCGATAA ATATGCAGAG 120  
 CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGTGTCTGAA TCAGGCGGTG 180  
 GGGACACGAG LLSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240  
 TCCGCGTCCA CGCAGCCGCC GGCAGGCGAG CAGGAGGCGG CAGGAGGCGG CAGGAGGCGG 300  
 AGGTGGCAGC GAGACATGCA CCCGCGCCCG AAGCTCTCTCA GCTCTCTCTT CCTCATCTCT 360  
 ATGGGCACTG AACTCACTCA AGTGCTGCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420  
 AGCTCTGCCC AGGACAGCGA GGCAGGTGT ATCTGCACAG TGTGCGCCCC ACAGCAGACC 480  
 ATGTGTTCAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540  
 ATGTCTCAAT CCATAGAGGT CTGAGCAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600  
 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCA 660  
 AAGCAACACC TGGCCAGGCA GTTTAAGGCG ATAAAGGCGA AAATGGATGA ACTTAGGCCT 720  
 TTGATACCTG TGTGGGAAGA GTACAAGGCC GATGCCAAAT TGTATTGCA GTTTAAAGAG 780  
 GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATTGG CGCCTATGAC 840  
 TACGATGAAC TTCAGAGCAG AGTGCTCAAT CTGGAAGAAA GGTCTCGTGC ATGCATGCAA 900  
 AAATAGCTT GCGGGAAGTT GACGGGCACT AGTGACCCCG TGACTGTCAA GACCTCCGCG 960  
 TCGAGGTTCG AACTCTGGAT GACAGACCCCT CTGCGCCCTG AAGGCGATAA CCGGTGTGCG 1020  
 TACATGGAGC GCTATCACAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGTGACTC 1080  
 ATGAACACCG ACAATTTTAC CTCCCACCGT CTCCCACACC CCGTGTGGCG CAGGCGCGG 1140  
 GTGGTCTACA ACGGTCTTAT CTACTTCAAC AAGTTCAGG GCCACATCAT CATCAGGTGT 1200  
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCCGG TTACAACAAC 1260  
 ATGTACCACT ACGCCTGGGG TGGCCAATCG GACATCGACC TCATGGTGA CGAGAGCGGG 1320  
 CTGTGGGCGG TGTAGCCAC CAACCCAGAAC GCTGGCAACA TCGTGTTCAG TAGGCTGGAC 1380  
 CCGGTGTCCC TGCAGACCTG GCAGACCTGG AACACGAGCT ACCCCAGCG CAGGCGCGG 1440  
 GAGGCTTCA TCATCTGCGG CAOGCTGTAC GTCAACCAAG GCTACTCAGG GGTATCCAG 1500  
 GTCCACTATG CATACAGAC CAATGCTGCC ACCTATGAAT ACATGACAT CCCATTCCAG 1560  
 AACAAATACT CCACATCTC CATGCTGGAC TACAACCCCA AGGACCGGGC CCGTATGACC 1620  
 TGAACAACG GCCACAGAT CCTCTACAAC GTGACCTCT TCCAAGTCAT CCGCTCCGAC 1680  
 GAGTTGTAGC TCCTCTCTCC TGAAGGCCAA GGGGCCAAGT CCTCACCACA AAGGACTCC 1740  
 TGTGAATCG CTGGCAAAAA GATACCAATA ACCTAACCAA TACGATCTT GAAAAATCAT 1800  
 CAGCAGTGGC GATCTGAGA TCGAGGGATG GCATTACCTC CGTGTTCCTC CTTTCCGAGC 1860  
 CGGCGGGCCA CAGGCTGGG AAGAACTCC GGTATTGCA GCTGGAAGT CAGCCCAAG 1920  
 CGCCCCGGTT TTCTCCCGG CCCTGTCCCT CTCTGGTCAA ACAACATACT AAAGAGGCGA 1980  
 GGCAATGACT GTTGGCCAGT TCTCACCGGG GAAAAACCA CTGTAGGAT GGCATGAACA 2040  
 TTCTCTAGA TCGTGTGAG CTCCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG 2100  
 GCTGCACCGG GCGTAGGCT AGTGTAACTC GCATCCCAT GCAGTGGCGT TCTTGTACTG 2160  
 TGTGTCTGTC TCTTAGATTA ACGTGTCTGA GGCTCCCAT AGCTCTGGA CCTGTGTCTA 2220  
 GTACATACTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGCTGTGCCC ACATTGTTG 2280  
 AACTCGCGTA CCCCGTAGAT ACATTGTGCA ACGTCTCTCT GTTATTCCCT TGAGGTGGTA 2340  
 ACTTGTATG TTCAGTTTAT GCGATGATTG TGTAAATGC AATGCCGTAG TTTGGATTAA 2400  
 TAAGTGGATG GTTTTGTGTT CTAATAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2460  
 CATAGTCAAG TTCATGTTGA TAATAATCAA AGGAATTACT CTCTCTGTGT TAAATTAGCT 2520  
 AAATCATGTA ACGGCAGATA GGAAGGGCTC ACCTGGGGAA ACTCTGTTTT COGATGGGAC 2580  
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTTAAGTAA AAAACAAAGG 2640  
 CAAACTTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAGG 2700  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: B36 Protein sequence  
 Protein Accession #: NP\_055094.1

1 11 21 31 41 51  
 MPGRWRWRD MHPARKLLSL LFLILMGTEL TQVLPTNPPE SWQVYSSAQD SEGRICITVV 60  
 APQQTNCSDR ARTQQLRLQLL EKVQNMSSQI EVLDRRTQRD LQYVEKMNQ MKGLESKFKQ 120  
 VEESHQHLA RQPKAKAKM DELRPLIPVL KEYKADAKLV LQPKVEQVNL TSVLNELOEE 180  
 IGAYDYDELQ SRVSNLEERL RACMQKLACG KLTGISDPVT VKTSGSRFGS WMTDPLAPEG 240  
 DNRVWYNDGY HNNRFVREYK SMVDFMNTDN FTSRHLPHFW SGTGGVVYNG SIYFNKFSQH 300  
 IIRFDLKTE TILKTRSLDY AGYNNMYHYA WGGHSDIDLM VDESGLWAVY ATNQNAAGNIV 360

VSRLDPVSLQ TLQWNTSYP KRSAGEAFII CGTLYVTNGY SGGTKVHYAY QTNASTYEYI 420  
DIPFPQNKYSH ISMLDYNPKD RALYAWNNGH QILYNVTLFH VIRSEDL

5 Seq ID NO: B37 DNA sequence  
Nucleic Acid Accession #: NM\_006334.1  
Coding sequence: 286..693

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1      11      21      31      41      51
|      |      |      |      |      |
10 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
   CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
   CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
   GGGACACGAG CCAGGCGCGG CCGCGGAGGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
   TCCGCGTCCA CGCAGCGCGG GCGCGGCCAG CACCCAGGGC CCTGCATGCC AGGTCGTTGG 300
15 AGGTGGCAGC GAGACATGCA CCGGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTTG 360
   ATGGGCACTG AACTCACTCA AGTGTCTGCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420
   AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC 480
   ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
   ATGTCTCAAT CCATAGAGGT CTTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
20 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
   AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACTTAAAA GAGTTTTTTC AATGCTGCAG 720
   TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTTGCA 780
   CCATGCATT TTAATAATTAT TTTCCAATAC TTAGCACCAT TTCCTAAGG AACCTTGAAT 840
   ACAACACAGA TCCTCCTTTG CATGCGACTG TAGCTGCATT TCATGAATAG TTTGAACCCCT 900
25 TGTCAATGCA TTTTTTGAAA AAGAAAGAAA AAAAAAAGCTT CGTGTATGTG ACTCAAGACA 960
   TGTAACTTAA AGATGTGCA TTCTAAACTG ACAATAAAGA CCTTTCCTCC
```

30 Seq ID NO: B38 Protein sequence  
Protein Accession #: NP\_006325.1

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1      11      21      31      41      51
|      |      |      |      |      |
35 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPPE SWQVYSSAQD SEGRCTCTVV 60
   APQQTMCSDR ARTKQLRQLL EKVNQMSQSI EVLDRRTQRD LQYVERMENQ MKGLESKFKQ 120
   VEESHKQHLA RQPKG
```

40 Seq ID NO: B39 DNA sequence  
Nucleic Acid Accession #: NM\_058199.1  
Coding sequence: 286..795

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1      11      21      31      41      51
|      |      |      |      |      |
45 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
   CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
   CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
   GGGACACGAG CCAGGCGCGG CCGCGGAGGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
   TCCGCGTCCA CGCAGCGCGC GCGCGGCCAG CACCCAGGGC CCTGCATGCC AGGTCGTTGG 300
   AGGTGGCAGC GAGACATGCA CCGGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTTG 360
50 ATGGGCACTG AACTCACTCA AAATAAAAGA GAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
   GAGAGCGAGA GGAAGACCAC AGGAGAGAAG ACACTGAACG AGCTTCCCTT GTTTTGCCCTG 480
   GAAGCCCAAG CTGGCTCCCT GGCTCTGCC AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
   GTGGGGTTAT GTGGTCCCGC TTACCTCTAG AGCCCTTCTC CTGGTCTGTC CCAGACGATC 600
   AGCCAGTCCC TCGTGGAGAG GTTCTGCATG GCCTCTAGGA GAGAAGTTTT CTTGGCCCCA 660
55 GGAAGGCGCT GTGGAGGGTG GTGGTTGTGC ACTGTGTCTG GACAGATGCA TTCATTCTAT 720
   TGCACACACA CACACACACA TGCACACACA GGGGAGCAGA TACCTGCAGA GAAGAGCCAA 780
   CCAGTCTCTG ATTAGTGGCA AGCTGCCCA CAAAGGGCTA TGCTGTGTCT TTATTGAGAC 840
   ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTCTGAC ATGGCCGCAC CCAAGGGCCC 900
   TCAAAGCCTT AATGGCACC TGAAGCCTCC ATGCCAGGC CAAAGATGC TTTTCTCTCC 960
   TAAAAA AAAA
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60 Seq ID NO: B40 Protein sequence  
Protein Accession #: NP\_478106.1

```
1      11      21      31      41      51
|      |      |      |      |      |
65 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQNKRENAE KMGFPESERK TTGEKILNEL 60
   PLFCLEAHAG SLALPRMCSP NPNPAVGLCR PAYPQSPSPG AAQTISQSLI ERFPMASRRE 120
   VFLAPGRPGG GWWLCTVAGQ MHSFMCETHH THARTGBQIP AEKSQPGPD
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70 Seq ID NO: B41 DNA sequence  
Nucleic Acid Accession #: AY038071.1  
Coding sequence: 1..1686

```
1      11      21      31      41      51
|      |      |      |      |      |
75 ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC COGAGTGCAA AAGTAAATCT 60
   CCAACTTTGC TCTCCTCTTA CTGCATCGAC AGCATCTCGG GCGGAGGAG CCGTGCATAA 120
   ATGGGTTTGC TGGGAGCGCG GCAGAGCTTG CCTGCTCCCG TGACCAGCCG CGCCGACCCG 180
   GAAAAGGCCG TGCAGGCTTC CCCTAAGAGC AGCAGCGCCC CGTTGAGGCG CGAGCTGCAC 240
   CTGCGGCCCA AGCTGCGCGG CCTGTACGGC CCGGCGGGGG GCGGCTCTCT TCAGGTTGGG 300
   GCAGCGCGCG CGGCGCGCGG GCGGCGGGG GCGGCGAGCG CGGCAAGGCG CACGGCGGGT 360
   CCACGCGGGG AGGCCCCCTC GCCGCCACCG CCAACCGCGC GGGCGGGGGA ACGGCGGGAC 420
   GCGCAGGGG CGGCGCGCGG AGCGCGGGC GCGGCGCGG CGGCTCTGGA CAGGCTCAAG 480
   ATCAGCCAGG CGCGCGAGGT GAGCATCAGC CGCAGCAAGT CGTACCGCGA GAAAGGGGCG 540
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CCCTTGCTGC CGCGCGCGCC CGCGCTGGAC GAGCTGGGCG GCCCGGGGGG CGTCAAGCAC 600
CCGGAGGAGC GCCTCGCGGT GCGCGGCGGC CGGGGAGCG CCCCGGCTGC GGTGTGTGGC 660
ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAGATGA GGACGAGGAA 720
GAGGAAGTGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACGACGCGCG CGCGCTGCTC 780
AAGGAGCCCC GCGCTGTGCT TGTGGCCCGC ACTGGCGCGC TGGCGCGCAG AGCTGCGGCT 840
GCAGTGGCCA CAGAGGGCGG GGAGCTGTCA CCCAAGGAGG AGCTGCTGCT GCACCGGAA 900
GAGCTGAGG GCAAGGACGG CGAGGACAGC GTGTGCTCT CTGCGGGCAG CGACTCGGAG 960
GAGGGGCTCG TGAACGCAA ACAGAGGCGC TACCGCACA CGTTCACCAG CTACGAGCTG 1020
GAGGAAGTGC AGCGGGCCTT CCAGAAGACG CACTACCCGG ACGTCTTAC CAGGGAGGAA 1080
CTGGCGATGA GGCTGGACTT GACCGAGGCC CGAGTCCAGG TCTGGTTCCA GAACCGTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGACAGC GCGCAGACCC ACCCCCTGG GCTGCCCTTC 1200
CGGGGGCGCG TCTCGGCAC CACCCGCTC AGCCCTACC TGGAGCCAG CCCCTTCCT 1260
CGCACCACC CGCGCTCGA CTCCGCTTGG ACTGCGCTG CGCGCGCGC CGCGCGCGC 1320
TTCCCGAGCC TACCTCGGCC TCCGGGCTCG GCCAGCTGCG CGCCAGCGCG GCGCGCGCTG 1380
GGCTGAGCA GTTTCCTCG AGCGGACATG TTCGACACC CAGCTTTCAT GACCCGCGCA 1440
TTGGGACGCG TCTTTTCCAC AATGGCCCCC CTGACCAAGC CGTGCAGCGG GCGCGCGCTC 1500
CTGAGACAG CCAACCGCG CGTGGAGGCG GAGTGGCAT CGGGCGCGCT GCGCGAGCCG 1560
GCCACGCGCG CGCAGACAG ACGCGCTCT AGCATAGCGG CGCTGAGGCT CAAGGCCAAG 1620
GAGCACGCGG CGCAGCTCAC GCAGCTCAAC ATCTGCGCGG GCACGAGCAC GGGCAAGGAG 1680
GTGTGC

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Seq ID NO: B42 Protein sequence  
Protein Accession #: AAK93901.1

25  
30  
35

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1 11 21 31 41 51
MSNQYQEGEC SERPECKSKS PTLSSSYCID SILRRSPCK MRLGAAQSL PAPTSTRADP 60
EKAVQGSFPGK SSAPPEABSLH LPPKLRLRYG PGGRLLQGA AAAAAAATAA AAAAAATATAG 120
PRGEAPPFPPT PTARPGERPD GAGAAAAAAA AAAAANDTLK ISQAPQVVIS RSKSYRENGA 180
PFVPPFPALD ELGGPGGVTH PEERLGVAGG PGSAPAAAGG TGTEDEEEL LEDEDEDEE 240
EBLLEDEDEE LLEDDARALL KEPRRCFVAA TGAVAAAAAA AVATEGGEELS PKELELLHPE 300
DAEGKDGEDS VCLSAAGDSE EGLLKRKQRR YRTTFTSYQL EELEERAFQKT HYPDVFTRFE 360
LAMRLDLTEA RVQVWFQNRK AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASPPF 420
PHEPALDSAW TAAAAAATAA FPSLPPPPGS ASLEPPSGAPL GLSTFLGA AV FRHPAFISPA 480
FGRLESTMAP LTSASTAAL LRQPTPAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
EHAALQLTQLN ILPGTSTGKE VC

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Seq ID NO: B43 DNA sequence  
Nucleic Acid Accession #: CAT cluster

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45  
50  
55  
60

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1 11 21 31 41 51
CGCTGCGCCC CCGCTGTGCTT CTCTCTCTTC CTTCTGCTCT GGTGCTCGC CGTCTTTGG 60
TTCCGCGCGT TCCGTGCGCC CTCTCTGCGC TTCGCTCTCA CCTCGCTCT GGTCTGCTG 120
CTGCTCTCTT CCGCTCTCAT GCCCTTTTCA GCTCTACTC TGGTGTGCTC CCCCTCCCTC 180
GCTCTGTTCT CTGTGTTCTT TCCTTCCCGG TCGTGTGCTT GCTTCTGCT GTTCCCTCTC 240
GTCTGTGTTT GTGGGTGCTC CTCTGCGTCC TGCTCTCTTC TCTTGTGCTT CGCGGCGCTT 300
CTGTGTTTGG TCCCTCTGCT TCTGCGCGCG TCTGTGTGTC GCGGGCGCGC CGGTCTCTTC 360
TTGGTGTCTT GCTCTGCTC TCTGTCTGCT GTTCTCGGCC GTCTGTGCTT TTTCTCTTT 420
ATCTCTCTGT TTCTCTTTT CTGTGTTCTT CTGTGTTT TTGTCTTTG TTTCTCTTA 480
GCTGAGGTTG GGGAGAGATA ACGCTGTAAA CTTTTATTTT TCAGGAAATC TGGAAACCTA 540
CAGTCTCCAT GCTCTGCTAG CCAAGAAAGG GCTCACTGTG GGCACAGAG ACAGGGAACC 600
AATGTGGAGA CCGTGTGAGC TGTGTCCGCG CCTGAACCTT CAAGCACAGG CGAGGCTTCC 660
TGAGCATTTG AGAGAAATAG TGGAGAACAA AAACAGAAAC TGAAAGAAAT TGCAAGGTGT 720
CTTCTCTTGA TGTATTTCCT TGATAGATAG TAGGGGCGAG AGTGAGAGAG GCTGACTAGG 780
TCTGGACATG GAGCTGAGGA GAGTCAGGCT GTGATTGCGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GGCTGGAAT CTGAGGGTCA GTGTGCAAG TCACTCAGAG ACAGATCAC 900
AGCATAGCCC TTGCTGATGG CAA

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Seq ID NO: B44 DNA sequence  
Nucleic Acid Accession #: NM\_014421.1  
Coding sequence: 718..1497

65  
70  
75  
80

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1 11 21 31 41 51
CCACGCGTCC GCGGGGAGCC CGCGGCGAGC GTAGCGCAAG TCGCTCCCT AGGCATGCT 60
GCGCTGGCAG CGATTGCGTG TCTCTGTGTA GTCAGGGGAC AAGCTCTCGG GCAACTGTG 120
AGTGCAGCTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTGCTG CCGGGAGCTC 180
TCTGATCCCT CTAATAAGC GCCTGCTAAC TTTGAAAAGG AGCACTGTGT CCTGCAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTTGA AGGAGAGGGA 300
GCTGATCGCG GCTCTGTGAT CAATTAAGAG GAGAGTTAAA CGCCGAGAT CCGGGCGGGA 360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTCT 420
TGCACCTTGG GTACGCGCTC CTGCGCGAGA AAGCGCCTCG CATTTGATTG CTTCCAGTTA 480
TTGCAGAACT TCCTGTCTCG GTGGAGAAGC GGGTCTGCTG TGGTTCCGCG TAATTTCTGT 540
CCTGAGGCGT GAGACTGAGT TCATAGGGTC CTGGTCCCGG GAACACAGGA GGGTTGAGGG 600
AACACAATCT GCAAGCCCCC GCGACCCAAG TGAGGGGCGC GTGTGTTGGG TCCTCCCTCC 660
CTTTGCAATC CCACCCCTCC GGGCTTTGCG TCTTCTGCGG GACCCCTCG CCGGGAGATG 720
GCGCGGTGTA TGGCGAGCAA GGATTGCTCC TGCTGCTGCT TCCTACTGCG GCGGCTGCTG 780
ATGGTGGAGA GCTCACAGAT CGGCAGTTCC CGGGCCAAAC TCAACTCCAT CAAGTCTCT 840
CTGGGCGGGG AGACGCTCTG TCAGGCGCGC AATCGATCTG CGGCGATGTA CCAAGGACTG 900
GCATTGCGCG GCACTAAGAA GGGCAAAAC CTGCGGCGAG CTAACCTTGT TAGCACTGAT 960
AAGGAGTGTG AAGTTGGGAG GTATTGCCAC AGTCCCCACC AAGGATCATC GGCCTGCATG 1020
GTGTGTGCGA GAAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCCC CAGTACCCCG 1080
TGCAATAATG GCATCTGTAT CCCAGTTACT GAAAGCATCT TAACCCCTCA CATCCCGCT 1140

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CTGGATGGTA CTGGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200  
 TGGCAGAAATC TAGGAAGACC ACACACTAAG ATGTACACATA TAAAGGGCCA TGAAGGAGAC 1260  
 CCTCGCTAC GATCATCAGA CTGCATTGAA GGGTTTTGCT GTGCTCGTCA TTCTGGAGCC 1320  
 5 AAAATCTGCA AACCACTGCT CCATCAGGGG GAAGTCTGTA CCAACAAACG CAAGAAGGGT 1380  
 TCTCATGGGC TGGAATTTT CCAGOGTTGC GACTGTGCGA AGGGCCTGTC TTGCAAGTA 1440  
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTCAGAA AATTGTATCA 1500  
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTAAATGC ATTATAGCAT 1560  
 GGTGGAATAA AAGGTTGAGA TGCAGAAGAA TGGCTAAAT AAGAAACGTG ATAAGAATAT 1620  
 10 AGATGATCAC AAAAAGGGAG AAAGAAAACA TGAAGTGAAT AGATTAGAAT GGGTGACAAA 1680  
 TGCAGTGCAG CCAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 1740  
 GGAATAATGT ATTATTAAGA GAACAAGCAC ACAGTGGAAA TTACTGATGA GTAGCATGTG 1800  
 ACTTTCCAAG AGTTTAGGTT GTGCTGGAGG AGAGGTTTCC TTCAGATTGC TGATTGCTTA 1860  
 TACAAATAAC CTACATGCCA GATTCTTATT CAACTTAGA GTTTAACAAA ATACTCTTAG 1920  
 15 AATAACTTGT TATACATAG GTTCTAAAAA TAAATTTGCT AAACAAGAAA TGAACACATG 1980  
 GAGCATGTGT AATTACAAAC AGAAAAATTAC CTTTGTGATT GTAAACACTAC TTCTGTCTGT 2040  
 CAATCAAGAG TCTTGGTAGA TAAGAAAAAA ATCAGTCAAT ATTTCCAAAT AATTGCAAAA 2100  
 TAATGGCCAG TTGTTTAGGA AGGCCTTTAG GAAGACAAAT AAATAACAAA CAACAGCCCA 2160  
 CAAATACCTT TTTTCAAAA TTTTAGTTTT ACCTGTAAAT AATAAGAACT GATACAAGAC 2220  
 20 AAAAACAGTT CCTTCAGATT CTACGGAAATG ACAGTATATC TCTCTTTATC CTATGTGATT 2280  
 CCGCTCTAGA ATGACATTATA TTTTCCAAAG TATAOCCATA AATTGTGACT AGTAAAAATC 2340  
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 25 GGATCTGTAC TGCACCTGGG TAAGCAAGAA AATTGGGAAA ACTTTTTCGT TTGTTCAAGT 2580  
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 30 TCTTCCCAA ACCTCTGCAG CATCTGCTTT ATTGCCAAAG GGCTAGTTTC GGTTTCTGTC 2940  
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 35 TTTAACTTTT TGTAGACCAA AATTCACCTT TTAGTTTTCT TTTACTTAAA TCCCATCTGC 3180  
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 40 TTATATTAC AATTTGGTTT CTGCAATATT TTTCTTATGT CCACCTTTT AAAAATTATT 3480  
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45 Seq ID NO: B45 Protein sequence  
 Protein Accession #: NP\_055236.1

50 1 11 21 31 41 51  
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 RCNNGICPV TESILTPHIP ALDGRHRDR NHGHYSNHL GWQNLGRPHY KMSHIKSHG 180  
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55 Seq ID NO: 46 DNA sequence  
 Nucleic Acid Accession #: NM\_019885.1  
 Coding sequence: 1..1539

60 1 11 21 31 41 51  
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 70 AAGCGCAAGG TCTTCTCCAA GATCTTCAGC CAOGAGGCC TGGAGAGTTA CCTGCCAAG 480  
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 75 CAGATCCTCG AGAAGGGGCT GGAGAAGGCC ATCCGGGAGA AGCTGCAGTG CACACAGGGC 780  
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 80 GGCACATCGC GCTTGGACAC GCTCAGTGGG CTGCGCTACC TGGAGTGGGT CATCAAGGAG 1080  
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5 ACCAGCGCGT TTGAGCTGGC TACAOGGACC TTCCCCCGCA TCACCTTGGT CCCCCTCCTG 1440  
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 10 GAGCGGTGCC CCTTGGGGG CACTCTTCAG CGTCTCTCC TCCTGGCGCC CCACTGCGTC 1980  
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 15 GCGCCAGGCG CTGTCTCCCC AGCATCCTCC CTGGTGGCCC TGGGCAGGTG CACTGACACC 2220  
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 20 GAAAGCCTTC CCGGCTCCG GGCATTATT GGGTTAATC TOGGAGCCTC ACTCCTGGAC 2520  
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 40 AATTGTTTTT GACTGAGTAT CTAGGAGAGC AGTAAGTGA ACTTCAGACA AGCCCACTGG 3660  
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 50 TTTGTTATAA TTCAAATAG ATATTAGTA TAAAGTTTT GCTGTAAAT ATTGTTTAT 4260  
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 CACAGTCGTT TTAATATTGA AAAAGCACTT GTGTGTTTTG TTTTGATATG AAACGTGTAC 4380  
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Seq ID NO: B47 Protein sequence  
 Protein Accession #: NP\_063938.1

1 11 21 31 41 51  
 60 MLFEGLDLVS ALATLAACLIV SVTLILLAVSQ QLWQLRWAAT RDKSCKLPIP KSGMGFPLIG 60  
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 TRMLLGNTV SNSIGDIHRN KRKVPFKIFS HEALESYLPK IQLVIQDTRL AWSHPRAIN 180  
 VYQEAQKLF RMAIRVLGFP SIPEEDLGLH PEVYQQFVDN VPSLPVDLPF SGYRRGIQAR 240  
 QILQGLEKA TREKLQCTQG KDYLDALELL IESSKEHGKE MTMQELKDTG LELIFAAAYAT 300  
 65 TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGCPCE GTLRDLTSLG LRYLDCVIKE 360  
 VMRLFTPISG GYRTVLQTFE LDGFQIPKGV SVMYSIRDTH DTAPVFKDVN VPDPRFSA 420  
 RSEDKGRFH YLPFGGVRV CLGKHLAKLP LKVLAVELAS TSFELATRT PPRITLVPVL 480  
 HPVDGLSVKF FGLDSNQNEI LPETBAMLSA TV

Seq ID NO: B48 DNA sequence  
 Nucleic Acid Accession #: AB040527.1; AL136582.1  
 Coding sequence: 94..2319

1 11 21 31 41 51  
 75 GCGGCTGCGG GGTTCCTGGT GCTGAGGACG GAOGCCATTG GAGTTOCCGA GAAGCATGGC 60  
 TGAGGGAGGC TTCAGCGTGC AATCGGAAG CTACAGTGTT GAAGACATGG ATGAGGGTAG 120  
 CGACCAAGTC GGGGAGGAG AGATGGTTGA AGGCAAGAC TATGAAGAAT TCGGTGCGTT 180  
 TGGTGGCTAT GGCACCTCA CCAGCTTGA CATCCATATC CTCAGAGCCT TCGGAAGCTT 240  
 80 GGGTCCAGGC CTTCGCATCT TATCGAATGA GCCCTGGGAA CTGGAAGACC CTGTGCTGGC 300  
 CCAGACCTG GTGGAGGAT TGCACTGGA TCGGAACA CTGCAATG AGACGGCCGC 360  
 CGTGTGCGC AACGTAGCC GCGCGCCGC CTCACACGT GCGCTCGGG CCGCTGCCGC 420  
 CGCTGCCGT ACCGCTTCA GTCAGGTGGT GCTAGCCAC CGGTGGCCA CGCGCAGGT 480  
 CTCAGGAGAG GATACCCAG CCACGACCTA GCGCGCGAG GCTCAGGGG CACCCCTCA 540  
 GCCACCCCTT GCTTCTCCG AGACCTCCA GATGTTAGTC ACCAGTAAGA TGGCTGCCCC 600



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 CAACCGGGCC AGCAGAGCCT TCCTGGGCCA GAATGATGTC TTGATTTCA CTCAGCGGCG 780  
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 5 CACAGAGGGC CCAGTGTCTG CCTCTGCTGT GCCCCAGCG GGACCTGGCA GGGAGGTGGC 900  
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 GCCTCAGAAAT GTTGTGGCAG CAGCTGTCTG CAAGGCCAAG ATGGCCACGA GCATCCCTGA 1020  
 GCCGAGGGGT GCAGCTGTCT CCACTGTCTA GCACAGTGCT GAGCCCTGGG CCAGGATGGG 1080  
 10 AGGCAAGAGG ACCAAGAGT CCAAGCACCT GGATGATGAG TATGAGAGCA GCGAGGAGGA 1140  
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 15 TGTCTATGAG GAATATGATG AACATTTCCG TGAGATCATT GAACGAGCAA CGTACACCTT 1440  
 GGAAAGAAG TTTGGGATCC ACCTGAAGGA GATGACAAG GAAGAACACC TGTATATTCT 1500  
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 20 GAAGATCCCC AACAGCAACC CACCTGAGTA TGAATTCCTC TGGGGCTGCG GAGCCCGCCA 1800  
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 30 ACGAATGCA GCGATCTTAC TGGCCAAGCC AGAGCGCCTC CTCTCAGATT CTTTCTCGAC 2340  
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Seq ID NO: B49 Protein sequence  
 Protein Accession #: BAB33378.1; CAB66517.1

1 11 21 31 41 51  
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 40 MAEGSPFSVQS ESYSVEDMDE GSDEVGHEEM VEGNDYEEFG AFGGYGTLS FDIHILRAFG 60  
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 AAAARTAFSQ VVASHRVATP QVSGEDTQPT TYAAEAQGPT PEPPLASPT SQMLVTSKMA 180  
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 45 VEPQNVVAAA AAKAKMATSI PEPGAAAAAT AQHSAEPWAR MGGKRTKKSK HLDDEYESS 360  
 EERETPAVPP TWRAQSLT VRAQLAPRPP MAPRSQIPSR HVLCLPRNV TLLQERANKL 420  
 VKYLMIKDYK KIPKIRADML KDVIREDYDEH FPBIIERATY TLEKKGPIHL KSIDKBEHLY 480  
 ILVCTRSSA RLKGTIKDTP RLKLLLVILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540  
 FLGDLRLKIT DDFVKQKYLE YKKIPNSNPP EYEFWGLRA RHETSKMRLV RFTAQNRD 600  
 50 PREWKAHFE AVDDAFKIMD VDMABEHARA QMRAQMNIGD BALIGRWSWD DIQVELLTD 660  
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Seq ID NO: B50 DNA sequence  
 Nucleic Acid Accession #: XM\_084965.1  
 Coding sequence: 356..2014

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 65 AGTGGCCTGG CGGAGGCCCA CTGCTGACGA AAGCGGCTTA TCCCGCGCGG TTCCATGGA 360  
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5 CGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA 1620  
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 ACGTTTCCTT CCTTCCCTTC TTTCTCTTT CTTTCCAGT T

Seq ID NO: B51 Protein sequence  
 Protein Accession #: XP\_084965.1

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 25 EEPGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLIKKN GRSENGKGEF 180  
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGILPLGSL TASLECVKEE 240  
 TPRAAREPEE PSQDAPRPPA GCGDIIADQE EEAGPSCDKH VPGPGKPLAS KKNPGVVAYQ 300  
 GGGEEAMSPD EVDDTYLQEF WDMLSQTEQ GPEPQEGAAK VAAALETKV PETPKDTRCV 360  
 30 EAAKDASSVK RRRILNRIPIE PHPKKEPKHP EKEQQEGVFN SDEGYWDSST PGPEEDSSSS 420  
 GKAGIPRDS YSGKHLVDLY ADPDGSPATL PGKEDNEETS SLRLKVPSP GTTTCPLRTP 480  
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 RATACHDSAK KL

35 Seq ID NO: B52 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..2016

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 GCAGACATGG ACTTGCATTG TGACTGTGCC GCGGAAACGC CGGCCGCCGA GCCCGCTCG 180  
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 45 CCAGCATTTT TTGGGGTCAA AAACAAAGGG GACGGGAAAA GCTCGGGTCC GACGGGGCTG 300  
 GTGAGGAGCA GGAACCAAGA CGGACTTGCC GAGGTGTCTG TGCTGGAGAG CCGCAGGAAG 360  
 GAGGAGCCGC GCGGCGGGGG CGACAGCGGC GGGGCGGGGG GGGGCGGGCC GAACCCGGGG 420  
 CCCCCAGAG CCGCAGGGCC CGGCGGGGGC TCCTTCGCCA GCAGCTCGGT GGCCAAAGTC 480  
 CACAGCTTCT TCTGCTGCT GAAGAAGAAC GGGCGCTCGG AAAACGGCAA GGGAGAGCCT 540  
 50 GTGACGCGGA GCAAGCCCGG CGGCAACAA AAGCGGGGGC TGCGGGGGCT GTTCAGCGGC 600  
 ATGCGCTGGC ACAGGAAAGA CAAGCGGGCC AAGCGGAGG CCGCGGAGG GCGCGCGCCC 660  
 GGGGCGGGCT TGATCTTACC CGGCTGCTC ACCGCCAGCC TGGAGTGGT CAAGGAGGAG 720  
 AGCGCCAGAG CCGCGCGCGA GCGGAGGAG CCCAGCCAGG ACGCCCGCG AGACCCAGCA 780  
 GGTGAGCCCG CAGGGGGAGA GGAGGTGCCG GCGCCCGCGG ACGCGCGCCC AGCGCGGAGC 840  
 55 TGCCGAGAGG CAGAGGGGCT CGCGCACCCC GCGCACACCG GCGCCCGGGG AGAGGACGCC 900  
 GCGGGGCATC GCGCGGCCGA GCGCGGGCCC GGGGAGGTCC GCACGGCAGA GGACGCTTCC 960  
 AGGACGGGGC CGTTCCTCGT AAAGACGCTC CCGCTTGTG ACTCCGAGG CCGCAGCGGC 1020  
 CGGCGCGCGG CCGCGCCAGA CCCTGCTCT GTGATCCAC CCTCAGACCC GTCCGCGAGT 1080  
 CGTATTGTGT TGATGTTTTT TGACGTGACT TCACTGAAAA GCTTTGACTC TCTTACAGGC 1140  
 60 TGTGGAGATA TTATTGCAGA CCAAGAGGAA GAGGCAGGTC CCAGCTGTGA CAAGCATGTC 1200  
 CCGGGGCCAG GCAAGCCGGC TCTGTCTAAA AAGAACCCTG GGTGGTGGC CTACCAAGGA 1260  
 GCGGGGGAAG AGATGGCCAG CCGGACGAG GTGGACGACA CCTATCTACA GGAGTTCTGG 1320  
 GACATGCTCT CCGACAGCGA GGAGCAGGGA CCGGAGCCCC AGGAGGGCGC GGCTAAGGTG 1380  
 GCAGCTGCGC TGGAAACCAA GGTGGTGCCC GAGACCCCCA AAGACACCAG GTGTGTGGAA 1440  
 65 GCGGCCAAGG ACGCGTCTCT GGTCAAGCGC AGGAGGCTCA ACCGATTCC CATCGAGCCC 1500  
 CATCTTAAGG AGGAGCCCAA GCACCCGAGG AAGGAGCAGC AGGAGGCGT CCCCACAGC 1560  
 GACGAGGGCT ACTGGGACTC CACCAAGCCA GCGCCAGAGG AAGACAGCTC GAGCAGCGGG 1620  
 AAGAAGGCGG GCTATCCCGG GGATAGCTAC AGCGGGGACG CGCTCTATGA TCTCTATGCT 1680  
 GACCGGACG GAGTCCAGC AACCTTCCT GGAGGGAAGG ACAACGAGGA GACGTCCTCC 1740  
 70 CTGTCCCGGT TAAAGCCCGT ATCTCCAGGC ACCATCACCT GTCCACTGCG AACACAGGC 1800  
 AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAGC ACCTGACCAA CCTTCCATCT 1860  
 AGCCATCCCG TGGTGCACCA GCAACCTTCC AGGAGTGAGA TGCCACAGAA AAAAATCCCG 1920  
 GTTTCCAAAG TGCTGTGTCG CAGAGTCAGC AACCGGGGCT TGGCTGGGAC CACCATCAGA 1980  
 GCAACGGCCT GCCACGACAG TGCCAAAAG TTGTGA

75 Seq ID NO: B53 Protein sequence  
 Protein Accession #: FGENESH predicted

80 1 11 21 31 41 51  
 METSRSRGGG GAVSERGGAG ASVGVCRRA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60  
 GKINKAFLK FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120  
 EEPGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLIKKN GRSENGKGEF 180  
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGILPLGSL TASLECVKEE 240  
 TPRAAREPEE PSQDAPRPPA GEPAGGEEVP APADRAPARS CREAEGLAHP GDTGARGEDA 300

5 AGHRRASPGP GEVRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPSPDPSAD 360  
 RICLMFSDVT SLKSPDSLTV CGDIIADQEE EAGPSCDKHV PGPKPALSK KNPGVVAYQG 420  
 GGEEMASPE VDDTYLQEFW DMLSQTEEQG PEPQEGAAKV AAALTKVVP ETPKDTRCVE 480  
 AAKDASSVKR RLRLRIPIEP HPKEEPKHPE KEQEGVPNS DEGYNDSTTP GPEEDSSSSG 540  
 KKAGIPRDSY SGDAILYDLYA DFDGSPATLP GGDNEETSS LSLRLKPVSPG TITCPLRTPG 600  
 SLLKDSKIPI SKHLTNLPS SHPVVHQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660  
 ATACHDSAKK L

10 Seq ID NO: B54 DNA sequence  
 Nucleic Acid Accession #: NM\_014138.1  
 Coding sequence: 60..854

15 1 11 21 31 41 51  
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 AGGGGCTGCT CGGCCAGCGG TACAGAGAGG AGAAGACCTT GGAAGAGCGG CGGTGGGAGA 180  
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240  
 ATCAGATGGC CCCCTATGCT GTTGGGAGGG AAGCCAGAAT CTCCCCATTA GGTGACAGAA 300  
 20 TCAGAAATCG ATTCGATGAT GAATGTCGAT ACTGCCAGAG CCACAGGCGG AATCTTTCTG 360  
 GGATCCCTGG GGAGAGTAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGACGG 420  
 GCCTCAGTGG CTGACTCTC AGCCTAGGCA CCAACCAACC CGGGCCTCTG CCTGAAGCGG 480  
 CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540  
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCATAT 600  
 25 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGGTGTGGGC 660  
 CCATTTTGGG GACCAACAG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG 720  
 ACACGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCCG AGGAAGGTCC TCATGTTTCG 780  
 TGCTCTGTCAT TCTCGGATGG CTGTGAGGCA TTCCTTGGCA AGGGACGCTG CGTACCAGCG 840  
 GCTCTCACCG CATCTCACAT GGCTCCTGTG ATGCATGTTG TCGCTTTCCC ACCCGGGATC 900  
 30 TCCATCTCTC TTCCCTTCCT GCTGTGAGTA AGAGATCACA TGTCTGTGTA GTGTGAATCG 960  
 CTGTGCTGTG TCCTGTGCTT TTGCACCATT GAGTTGACTG CCTCTGAGAA GCAGCACTAG 1020  
 GCCTGTGTAA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAATGGGC AGTAAACGC 1080  
 AGTGTGGGAA AGGAATGTGG AATGAGAACT TGGTGGTTCA CCGCTGTACT ATTTGTGTAA 1140  
 ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG 1200  
 35 TAGTATCTC CCTTACAGGA ATTTTGTACG GGGTTCTCTA TCATCAATAC CAAATAAATA 1260  
 TATGTAGGAA TGGAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 1320  
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 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA

40 Seq ID NO: B55 Protein sequence  
 Protein Accession #: NP\_054857.1

45 1 11 21 31 41 51  
 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEPLQRKKA FLRHVRRRHR 60  
 DHMAPYAVGR EARISPLGDR SQNRFRBCBR YCQSHRPNLS GIPGESNRAP HPSSWSTLVQ 120  
 GLSGLTLSLG TNQPGPLEPA ALQPQETEEK RQRERQESK IMFQRLKQW LEEN

50 Seq ID NO: B56 DNA sequence  
 Nucleic Acid Accession #: NM\_000025.1  
 Coding sequence: 198..1424

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 CCAAGCGGGA CCGGGGATG GCTCCGTGGC CTCACAGAA CAGCTCTCTT GCCCCATGGC 240  
 60 CGGACCTCCC CACCTGGGCG CCCAATACC CCAACACAG TGGCTGCCA GGGGTTCCGT 300  
 GGGAGGCGGC CTAGACCGGG GCCCTGTGCG CGCTGGGGGT GCTGGCCACC GTGGGAGGCA 360  
 ACCTGTCTGT CATCGTGGCC ATCGCCTGGA CTCGAGACT CCAGACCATG ACCAACGTGT 420  
 TCGTGAATTC GCTGGCGGCA GCGGACCTGG TGATGGGACT CTGGTGGTG CCGCGCGGG 480  
 CCACCTTGGC GCTGACTGGC CACTGGCCGT TGGGCGCCAC TGGCTGGAG CTGTGGACCT 540  
 CGGTGGACGT GCTGTGTGTG ACCGCCAGCA TCGAAACCTT GTGCGCCCTG GCGCTGGACC 600  
 65 GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GGTCAACCAAG CGCTGCGCCC 660  
 GGACAGCTGT GGTCTGTGTG TGGGTCTGTG CGGCGCGGT GTGCTTTGCG CCCATCATGA 720  
 GCCAGTGGTG GCGGTAGGG GCGGACCGCG AGGCGCAGCG CTGCCACTCC AACCGCGGCT 780  
 GCTGTGCTCT CGCCTCCAAC ATGCCCTAGG TGCTGCTGTC CTCCTCGCTC TCCTTCTACC 840  
 TTCTCTTCTT CGTGATGCTC TTCTGTCTAG CCGCGGTTTT CTGTGTGGCT ACGGCGCAGC 900  
 70 TGCGCTTGTG GCGCGGGGAG CTGGGCGGCT TTCCGCCCGA GGAGTCTCG CCGGCGCGCT 960  
 CGCGCTCTCT GCGCCCGGCC CCGGTGGGGA CGTGCGCTCC GCGCGAAGGG GTGCGCGGCT 1020  
 GCGGCGCGCG GCGCGCGGCG CTCCTGCTCT TCGGGGAACA CCGGCGGCTG TGCACTTGG 1080  
 GTCTCATCAT GGGCACCTTC ACTCTCTGCT GGTGCGCTTT CTCTGCGCTG AACTGCTAG 1140  
 75 GCGCCCTGGG GCGCCCTCTT CTAGTCCCGG GCGCGGCTTT CCTTGCCTG AACTGCTAG 1200  
 GTTATGCCAA TTCTGCTCTT AACCCGCTCA TCTACTGCGG CAGCCCGGAC TTTCGCGAGG 1260  
 CCTTCGCGCG TCTCTGTGTC CGCTGCGGCC GTGCGCTGCC TCGGAGGCCC TGCGCGCGCG 1320  
 CCGCGCGGCG CTTCTTCCCC TCGGCGGCTT CTGCGCGCG GAGCAGCCCA GCGCAGCCCA 1380  
 GCGCTTGGCA ACGGCTCGAG GGGGCTTCTT GGGGAGTTTC TTAGGCTGGA AGGACAAGAA 1440  
 80 GCAACACTCT TGTGTATCAG AACCTGTGGA AACCTGTGCG CCTGTGTTCA GAATGAGTCC 1500  
 CATGGGATTC CCGCGCTGTG CACTCTACCC CTCCAGAAC TGACGACTGG GCCATGTGAC 1560  
 CCAAGGAGGG ATCTTACCA AGTGGGTTTT CACCATCTCT TTGCTCTCTG TCTGAGAGAT 1620  
 GTTTTCTAAA CCGCGCCTTT GAACCTCACT CCTCCCTCAG TGGTAGTGTG CAGGTGCGGT 1680  
 GGAGCAGCAG GCTGCTTTTG GTAGGGGAC CCATCACCCG GCTTGCTCTG GCAGTCAGTG 1740  
 AGTGCTTAGG GCAAGAGAG CTCCCTGGT TCCATCTCTT CTGCCACCA AACCTGATG 1800

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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
AAGATTGGG GTTTTATCTC TGGTTCCCTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAAGAC TTCGCCAGGG 1980
TTTTGGAGC TCAGGGGTTT ATAAGAAGGT GAACCAITAG AACAGATCCC TTCTTTTCTT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTGGGCCCA CTTCCTCTCC 2100
GTTTGTTTTC TTTTCATAAT CCACCTACTC CCTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAACAAAAA 2220
AATGAAAACT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCTTCTCTG AAACCTCTGA AATCCAGITG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGGCCA CAGGGGGATG GGCTGGCTGT GGGCAGGTTT AGGGCAGGGG 2400
GCATTGTGCC CCTCCATGCT ATAATCCAGT GGTGCCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGCCTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTG CTGGGTTGG 2520
TCAATGTCTT TGTGTCTATA ATATATTCTG ATGTTTCCCA GCCTTTCCAC AACCTCTACC 2580
TTCCCACTCA CTTCCTCCAG CTACAAAAAT CTGTATTATC CTCTTAAAGT AAACTGGAG 2640
TTAC

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Seq ID NO: B57 Protein sequence  
Protein Accession #: NP\_000016.1

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AIAMTPRLQT MTNVEVTSLA AADLVMLGLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120
VTASIELTCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VVVVSAAVSF APIMSQWVRV 180
GADAEARQCH SNPRCCAFAS NMPYVLLSSS VSFYLPGLVM LPVYARVVFV ATRQLRLRG 240
ELGRFPPEES PPAPSRSLAP APVGTCAPEE GVPACGRRFA RLLPLREHRA LCTLGLIMGT 300
FTLCWLPPFL ANVLRALGGP SLVPGFAPLA LNNLGYANSA FNPLIYCRSP DFRSAFRRL 360
CRCGRRLPPE PCAAARPALP PSGVPAARSS PAQPRLCQRL DGASWGV

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Seq ID NO: B58 DNA sequence  
Nucleic Acid Accession #: NM\_032553.1  
Coding sequence: 37..1038

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ATTCTTGTGC CAGGCTCATAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG 180
AAAGAACCAA AACGAGCTGT GATATTATAT ATAACTTAGC CCATTGCTGA CTTACTACAA 240
GTCTTTTCTT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT 300
GGTCTCTGCA TGTTCGTGTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGGTCTGCA TCAGTGTGCG ACGATTTTGG TTTCTCATGT ACCCCTTTCT CTTCCATGAC 420
TGCAACACGA AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCCTGCC 480
TGTGACTACT TTCCACTCCT CAGAACCAGT GATGATACCT CTGGCAATAG GACCAATATG 540
TTTGGGATC TTCTTACCAG GAATGTCAAC CTGGCCAGT CCGTTGTTAT GATGACCATT 600
GGCGAGTTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG 660
GTTTATACAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
TTGAAGATGA TTCTAACCTG TGCAAGGGTA TTCTTAATTT GCTTTGCACC TTATCATTTT 780
AGTTTCTCTT TAGATTCTCT GGTGAAGTCC AATGAAATTA AAAGCTGCTT AGCCAGAAGG 840
GTGATCTTAA TATTTCATTC TGTGGCATTG TGTCTTGCTA GTCTGAATTC ATGCTCTGAC 900
CCAGTCATAT ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCTTTCAAG ACNAGATTGT 960
CATGACAGCA TCCAACCTCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020
ACACCTGAAT TAGCTTAAAC CAAAAAACCA AACTGAATGT GACCTGAAAT GCAAGTACAT 1080
CAGAACATAT CTGCAATACC CAAGCCACAG GGAAGAACTT GCAAAACAAC ACAGCTTTTC 1140
AGTTCGTCTC TATCTTACTG CTATGGGGAA TTCATCTCTT CAAAGCAGGA CCTATTGGA 1200
GCATTACGAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTTT CTTCAGAT

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Seq ID NO: B59 Protein sequence  
Protein Accession #: NP\_115942.1

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65  
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LAIALDLQVL SLPLRIFFYL NHDWPFPGPL CMFCPYLYKV NMYASIFLV CISVREFWFL 120
MYPRFPHDCK QKYDLYISIA GWLIICLACV LPFLLRTSD TSGNRTKCFV DLPTRNVLNA 180
QSVMMTIGE LIGFVTPLLI VLYCTWKTVL SLQDKYPMAQ DLGEKQKALK MILTCAGVFL 240
ICFAPYHFSF PLDFLVKSNE IKSCLARRVI LIHFSVALCL ASLNSCLDFV IYFSTNEFR 300
RRLSRQDLHD SIQLHAKSFV SNHTASTMTP ELC

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Seq ID NO: B60 DNA sequence  
Nucleic Acid Accession #: CAT cluster

75  
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CCCGAGGGTT AGACATTAA CTGAGTCTTT TTCAATACAC GGTATGCTTT TATTTTACC 120
TCATATATAA TTAATTTTCA TCTGGGCATA TATTTCCAGA TTAGAAATCA TTTCTTTTCA 180
TACATTTTAA GGAATTTATA CATTTGCATC TGAAATTTGA TTCAATATCT TCTAGAAACC 240
AAGAGTGGAC TTGGTATCCG TCTGATTATA TTTTCTTTGT TGGTAAAGAG CCTCTTTTTT 300
CCTTTTTTAT TTTCACTCTC TCTTCTCTTA GTGTTTATAA TCTTATTTTT ATGAATGTAG 360
TCTAATATT TAGAACCTG TCTCGAGTA TGTGTTTATT TGGGTTTGTG TTTTGAACAT 420
TGCTCCAGG TGCGAGTTTA TGTGTGTTTA TGTTCCTAT TTGAGGTTGG ACCTTAGAA 480
AATTTTCTCA ATTCGAAAC TATTTTCTTT CAGCACTCAG AAATTTTAT CAAAGATTAT 540
TTCCAGGATT ATTTCTCTGC CTGGTTTTTT OGRGTTCTTA ACCTAGAATT CAATTGTTA 600

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5	ATGTTAGACC TTACACATCT TCAATGTATC ATATATATTT CACTCATATT ATTTATTGTC 660
	ATATCTTTTG GACTATTGTG TGAAGCAAT AAATGTATAT TACTTTAAAA AAAAAAATAA 720
	AAACTHCAT TTTCAAATTT AATACACACA AATTGTGCAT ACCCACACAC ATATACCACA 780
	GATATATTCA TTTTCAGSAT TTCTTTAAGT GTTATTTTAA AAATAATCAT ATTCTTATT 840
	TGTGAACGTG GGGATTTCCT GAAACTTTTT GAAACTCTC ATTAGTCTGT GTTTGTGTGG 900
10	TTCTTTAAA TTATCTCTTC CTTCAGAAAT ACTTTTGTGT TTGAATTTG AGTCTTTGCC 960
	ATTCATAAGG CGGGCTTTCC TTGAATACCA GATAACTCTG AGTTCTCTGT TCATATTTTA 1020
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	Seq ID NO: B61 DNA sequence
	Nucleic Acid Accession #: NM_014522.1
	Coding sequence: 846..3911
15	1 11 21 31 41 51
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	ATATTAATAG CTATTCTTGT TTTTCTTATC CAAAGAAAAA TCCTCTAATC CCTTTTTCAC 180
	ATGATAGTTG TTACCATGTT TAGGCATTAG TCACATCAAC CCTCTCTCTC TCCCAAACTT 240
20	CTCTCTTCA AATCAAACTT TATTAGTCCC TCCTTTTATA TGATTCCTTG CCTCGTTTAA 300
	TCAGATACAA TTTTCTTCA CTTTGATGCC CAGAGCTGAA GAAATGGACT ACTGTATAAA 360
	TTATTCATTG CCAAGAGAA AATTGCATT TAAACCCATA TTATAACAAA GAATAATGAT 420
	TATATTTTGT GATTGTAAAC AAATACCCCT TATTTTCCCT TAACATTGA ATTAATATT 480
	TTAATATTIT GTATTCTCTT TAACATCTCT GGTATATTAA AGTATTATCT TTTATATATT 540
25	TATCAATGGT GGACACTTTT ATAGGTACTC TGTGTCAATT TTGATCTGT AGGTATCTTA 600
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	CACATATTAA CAGAGTGTCA ATTATGCTAA CATCTCATT ACTGATTITA ATTTAAAAACA 720
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	CTCTCTCTCT CTTTTGTGTA GTTGTGTGGG GGTAAATACA ACAAACTGTA ACAAGTGTAC 840
30	CTGATATGGA CTGTGTGTCC GGGACGTACA TTTTGGCGGT CTGCTAGCA TGGCTGGTGT 900
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40	CACAACTGAT TGTTCAAAAG GAGTTAGATA GGGAAAGAGG GATACCTAC GTGATGAAAG 1500
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	ACATGTCAAA TCCCTGCAAT GACACAGTTG TTCTTTCAGA AAATATTCCA CTCAACACCA 1980
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	CAGATGCTGG CAAACCTCCT TTGAATCAGT CAGCAATGCT CTTCATCAA GTGAAAGATG 2220
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	ACTCTCCTGG CATCCAGTTG ACGAAAGTAA GTGCAATGGA TGCAGACAGT GGGCTTAATG 2340
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	CAATCTGGC AAAAGATAAC GGGGTACCA CTTTAAACCA CAATGTGACA GTCTTTGTAA 2520
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	ATTCAACAAC TGGTGTATC OGACCAATA TTTCAATTGA TAGAGAAAAA CAAGAATCTT 2760
	ACACTTTCTA TGTAAAGGCT GAGGATGGTG GTAGAGTATC ACGTCTTCTA AGTGCCAAAG 2820
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	ACTGTTCTTA TGAATTGGTT CTACCGTCCA CTAATCCAGG CACAGTGGTC TTTCAAGTAA 2940
65	TTGCTGTTGA CAATGACACT GGCATGAATG CAGAGGTTGG TTACAGCATT GTAGAGGAG 3000
	ACACAAGAGA TCTGTTTGCA ATCGACCAAG AAACAGGCAA CATAACATTG ATGGAGAAAT 3060
	GTGATGTTAC AGACCTTGGT TTACACAGAG TGTGGTCAA AGCTAATGAC TTAGGACAGC 3120
	CTGATTCTCT CTTCAGTGT GTAAATTGTC ATCTGTTGCT GAATGAGTGG GTGACCAATG 3180
	CTACACTGAT TAATGAACTG GTGCGCAAAA GCACTGAAGC ACCAGTGACC CCAAACTATG 3240
70	AGATAGCTGA TGTATCTCTA CCAACTAGTG ACTATGTCAA GATCTCTGTT GCAGCTGTTG 3300
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	CACCACACCT TAAGGCTGCT CAGAAAAACA AGCAGAAATC TGAATGGGCT ACCCAAACCC 3420
	CAGAAACAG CGAGATGATA ATGATGAGA AAAAGAAAAA GAAGAAGAG CATTCCCTTA 3480
	AGAACTTGCT GCTTAATTTT GTCACTATTG AAGAAACTAA GGCAGATGAT GTTGACAGTG 3540
75	ATGGAAACAG AGTCACTCTA GACCTTCTTA TTGATCTAGA AGAGCAAAACA ATGGGAAAGT 3600
	ACAATTGGGT ACTACACCT ACTACTTTCA AGCCGACAG CCCTGATTG GCGGACACT 3660
	ACAAATCTGC CTCTCCACAG CTGCGCTTCC AAATTCAGCC TGAACCTCCC CTGAATTGCA 3720
	AGCAACCAT CATCCAGAA CTGCGCTCTG ATAAACACTT TGTGGCCTGT GACTCTATCT 3780
	CCAAGTGTTC CTCAAGCAGT TCAGATCCCT ACAGGTTTC TGACTGTGGC TATCCAGTGA 3840
80	CGAUCTTGA GGTACCTGTG TCGTACACA CAGACCGGT AGGTATCCAA GTTTCTAACA 3900
	CAACTTTCTA ACTATTTTTT TATTATTATT TTAGTTGAT GTAGAATCTT ACAAAATCTA 3960
	TTGACTTCAA AGAGGGATCA AAACAATCAT ATTCTACAGA TGTACCCAAT AGATATATGG 4020
	ATTCAAATTA GTTTGGTAGA AGATGAGAAC AAAATAACTA CTGATTTAGG AAAATTGGAT 4080
	GCAGAATAAT AATTATAGTA GGGGCAATT TGTCTGTAGA TGGCAGTATG ACAATCTTGT 4140

5 CTAGAGAATA TATTGAAAAA AACTTCAACA CAAAGGGTTG TAGCACTGTC CTCAGTACCA 4200  
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10 Seq ID NO: B62 Protein sequence  
 Protein Accession #: NP\_055337.1

15 1 11 21 31 41 51  
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 RLVKIRFLIE DINDNAPLFP ATVINISIEP NSAINSKYTL PAAVDPDFGI NGVQNYELIK 180  
 SQNIFGLDVI ETPGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT 240  
 DTNDNHPVFK ETEIEVSIPE NAPVGTSTVQ LHATDADIGE NAKIHPSFSN LVSNIARRLF 300  
 20 HLNATTLGIT IKESPLDREEST FNHKLVLAS DGLMPARAM VLVNVDVDND NVPSIDIRYI 360  
 VNPVNDTVVL SENIPLATKI ALITVTDKDA DHNGRVCTPT DHEIPFRLRP VFSNQFLLET 420  
 AAYLDYESTK EYAIKLLAAD AGKPLNQSA MLFIKVKDEN DNAPVFTQSF VTUSIPENNS 480  
 PGIGLTQVSA MDADSGBNAK INYLLGPDAP PEFSLDCRTG MLTVVKLLDR EKEDKYLFTI 540  
 LAKDNGVPPL TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDFY 600  
 25 DNSAVTLLSL DENDDPTIDS QTGVIRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT 660  
 INVVDVNDNK PVFIVPPSNC SYELVLPSTN PGTVVVQVIA VDNDTGMNAE VRYIVGGNT 720  
 RDLFAIDQET GNITLMERCD VTDLGLHRVL VKANDLQPD SLFSVVIVNL FVNESVTNAT 780  
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 30 HLKRAQKNKQ NSEWATPNPE NRQMIMMKKK KKKKKHSPKN LLLNFVTIEE TKADDVDSG 900  
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35 Seq ID NO: B63 DNA sequence  
 Nucleic Acid Accession #: XM\_059180.2  
 Coding sequence: 276..3740

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 GCGGCGTAGC GAGCCTGCGG GTGCGACCCA GCGAGCGCAG CGACGCGGGG CTGCGCTGGCC 180  
 CAGGCGGCACA CGGAGTGGCG CTTCTCTGAA GTAGCTTTGG AAAGTAGAGA AGAAAAATCCA 240  
 45 GTTTGCTTCT TGGAGAACAT TGGACAGCTG AATAAATGCA GTATCTAAAT ATAAAGAGG 300  
 ACTGCAATGC CATGGCTTTC TGTGCTAAAA TGAGGAGCTC CAAGAAGACT GAGGTGAACC 360  
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 GGCTGGGCGG TGGAGAGTAC ACAGCAGAGG AACTGTGCAT CAGGGCTGCA CAGGCATGCC 480  
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 70 AGGGTGCCCA GAAGCAGTTC AAGAACTTTC AGATCGAGGT GCAGAGGGGC CGCTACAGTC 1800  
 TGCAOAGTTC GAGCGGCGC TTCCCGAGCT TGGGAGACCT CATGAGCCAC CTCAGAAGC 1860  
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GGTGAGGCC AGTGACACCA TCATGTAAGG AGCTGGCTGA CCTCATGACC CGCTGCATGA 2760
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CTCTTTATAC AAATAAATAT ACTAAGACT TT
  
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Seq ID NO: B64 Protein sequence  
 Protein Accession #: A39577

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DNEQSVWRHS PKQKNGYEK KKIIPDAPLL DASSLEYLFA GGQYDLVKCL APIRDPKTEQ 180
DGHDIENECI GMAVLAISHY AMMKMQLPE LPKDISYKRY IPETLNSIR QRNLLTMRI 240
NNVFQDFLKE FNNKTCIDSS VSTEDLKVKY LATLETLLKH YGAEIPETSM LLISSENEMN 300
WFHSNDGGNV LYEVMTGNG LGIQWRHEPN VSVBKERKN LKRRKLENKD KDBEKNKIR 360
BEWNNFSEFF EETHIVIKES VVSINKQDNK KMLKLSSEH EALSFSVLVD GYFRLTADAH 420
HYLCTDVAPP LIVHNIQNGC HGPICTEYAI NKLRQBSSE GMVYLRWST DFDNILMTVT 480
CFEKSQVQAG AQKQFKNFQI EVQKGYSILH GSDRSFPLSG DLSHLKQKI LRTDNISFML 540
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TLMYKDDDEG TSEEKKIKVI LKVLDPSHRD ISLAPPEAAS MMRQVSHKHI VYLYGVCVRD 660
VENIMVEEFV EGGPDLDFMH RKSDVLTTPW KFKVAKQLAS ALSYLEDKDL VHGNCVCKNL 720
LLAREGIDSE CGPFIKLSDF GIPITVLSRQ ECIERIPWIA PECVEDSKNL SVAADKNSFG 780
TTLWEICVNG EIPLKDKTLI EKERFYESRC RPVTSPCKEL ADLMTROQNY DPNQRPFRA 840
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TGEQVAVKSL KPESGGNHIA DLKKEIEILR NLYHENIVKY KGICTEDGGN GIKLIMEFLP 960
SGSLKEYLEK NKNKINLKQQ LKYAVQICKG MDYLGSRQYV HRDLAARNVL VESEHQVKIG 1020
DFGLTKALET DKEYYTVKDD RDSVPFWYAP ECLMQSKFYI ASDVWSFGVT LHELLTYCDS 1080
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Seq ID NO: B65 DNA sequence  
 Nucleic Acid Accession #: NM\_004867.1  
 Coding sequence: 140..931

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CGCAGCCGCA AGATTACTA TGGTGAAAAA CGCCTTCAAT ACCCTACCG CGGTGCAAAA 180
GGAGGAGGGG CGGCAAGAGG TGGAGGCCCT CCTGAGCCGC ACGGTGAGAA CTCAGATACT 240
GACCGGCAAG GAGCTCCGAG TTGCCACCCA GGAAGAAAGAG GGCTCCTCTG GGAGATGTAT 300
GCTTACTCTC TTAGGCTCTT CATTATCTT GGCAGGACTT ATTGTTGGTG GAGCCTGCAT 360
TTACAAGTAC TTCAATGCCA AGAGCACCAT TTACCGTGGG GAGATGTGCT TTTTGTATTC 420
TGAGGATCTC GGAATATCCC TTGTTGGAGG AGAGCCTAAC TTCTGCTGCTG TGACTGAGGA 480
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Seq ID NO: B66 Protein sequence  
 Protein Accession #: NP\_004858.1

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 DNIAIIDVPV PSFSDSDPAA IHDPEKGMT AYLDLLLGNC YLMLPLNTSIV MPPKNLVELF 180  
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 IDKCWKIRHF PNEFIVETKI CQE

Seq ID NO: B67 DNA sequence  
 Nucleic Acid Accession #: XM\_083862.1  
 Coding sequence: 121..813

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Seq ID NO: B70 Protein sequence  
Protein Accession #: NP\_002966.1

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5      1      11      21      31      41      51
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MQAANLLGAL VVPQLLGFH GARGAEREWE GWMGGAQEEREREREALMLKH LQELGLPAG 60
RGDENPAGTV EGKEDWEMEE DQGEHEEEEA TPTPSSGSPSPTPEDIVTY ILGRLAGLDA 120
GLHQLHVRHL ALDTRVVELT QGLRQLRNA GDTRDAVQAL QEAQGRAERE HGRLEGCLKG 180
10    LRLGHKCPFL SRDFAQAAA QARCTARGGS LAQPADRQOM EALTRYLRAA LAPYNWVWL 240
GVHDERAEGE YLFENGQVRV FFAWHRSPRP ELGAQPSASE HPLSPDQPNG GTLENCVAQA 300
SDDGSWNWDH CQRRLYVCE FPF

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Seq ID NO: B71 DNA sequence  
Nucleic Acid Accession #: BC000839.1

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15      1      11      21      31      41      51
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20    TGGGGCTTTG TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGGTCCCCC TTCCTATGAT 120
GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AAGTAACTCT GAGGAGATGG 180
GCCCTGCAAG CCTCTTCTT AGCGCTCTGT TCAGAAAATA GCGTTTTCGA AATGCCCTGA 240
GTTGACCTAA TGCTCTATTG GCCTCTGTCT TGCAGGATTT ACGCGCACGT TGAACCGGAA 300
GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGCTGAAGG AATGGGACAA 360
25    GACCCATCTT TATGCAAAGC CAGCGTTACA GTAATGTTCC AGCATCTCAT AATCTATCCT 420
GGGGAATTCG GCTGCCCTCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCCCTCTAT 480
CTTACAGAGC AGCTTGTGTG TATATACCAT TGAAAAGCCT TCAGAGCTGA GAGGTACTAC 540
TAACCAATAA CCTGCTTGGC TCAAAAGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT 600
TTCAGGAAAA CTAGGTGTCT GTGTTCACCT CAGGCTGAAG TTACAGGTCT GAGCAATAAA 660
30    GGTGTATATA AATGGGAATC TGTCTTGGAG GACATCAGAA GGTGAATTTT CCAAGTTCTT 720
GGACAACCTA GCTGTTGAAA AGCTTTCTGG GTTTGGGGGG TATTTCAGAT GTACCTTAAA 780
GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT 840
GTGTATCACA TTTCTGTATT TTATCACCCT CTCTCTGCAA CATTATTTAT CTGGAATCTA 900
CCTGCCCTTT TGTTTTTTAG ATACAAGGGC TTGGTTTTGT TACCCAGGCT GGTTCAGAG 960
35    CCATAGCTTT AAGATGACCT CTCACACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA 1020
TTCTATGACG CCAGACTTTG CTGCCCTTCT TACATGATCC AGGCCAGAA CCAAACTCA 1080
GGCACTGTAT AGATGACCACT TTCTGTAAAC TACTGACCTA GCTTGTGGCC AATGTGTGAT 1140
TGAACITCCC ATAACCTCAC TTCTGTCTGT TTCTCTGTA TACAGCCACC TTCTGTTCCT 1200
30    GTCATGAGCC TTAGGTCTC CATTTGCATA TTGCAAAATC TATGTTCCAT GTAGGTAGCT 1260
40    CATTCAGGCG CTGCTCTCTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCAATTTG 1320
TGTTCGTGTG TTGTTGTTG ATGAAAATAA TAAATGATT GATTACATAA AAAAAAATAA 1380
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Seq ID NO: B72 DNA sequence  
Nucleic Acid Accession #: CAT cluster

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50    CTTGTACTT GTCTTTTCT TTTATTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA 120
CGCACTATGG CACGAGGCTC GTGCTGCTG CCGAGGGCGA CTGGCGGATA AGGCTCTGTG 180
CGTGCCCTGG AGGCTTAAAA GTAGCAGTGG GGCCTTTGTA AGGACAAAAT GCGGATGGCG 240
GGCGGTGTAG GTCCGCCCTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG 300
TGAGGATATA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC CGTCTGTCTA 360
55    GAAAATAGCG TTTTCAAAAT GCCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC 420
AGGATTTAGC CGCAGCTGG AACCAGAGAG ASCTCTGTTG TTGCAATGTT CAGCCCAACA 480
GAGCTTACTG GTGAAGGAAT GGGACAGAC CCATCTTTAT GCAAGGCCAG CGTTACAGTA 540
ATGTTCCAGC ATCTCATAT CTATCTGGG GAATTCAGCT GCCTCCAGG GTGAATACAG 600
GTATTCTTGA TGACAGTCTG CCTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCATTGA 660
60    AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGCCAGC 720
ACCTTCTCTC TAAAGCCCAA GAGGAGTTG AGGAAAACCT GGTGTCGTG TTACTCCAG 780
GCTGAAGTTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAACTCTG CTGGAGGAC 840
ATCAGAAGGT GAATTTTCCA AGTTCTTGA CAACCTAGCT GTTGAAGAGC TTTCTGGGTT 900
65    TGGGGGATAT TCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAGA CACTGGGAGC 960
CAATGAAACA GCAGTTGAGG GTTTGCTGTG TATCACATTT CTGTATTTTA TCACCCCCTT 1020
CCTGCAACAT TATTTATCTG GAATCTACCT GCCCTTTTGT TTTTATGATA CAAGGGCTTG 1080
GTTTGTGATC CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT 1140
70    TCCAAGTGC TGGGATTGCA GGTGTGATTC ATGGCACCCA GACITTGCTG CCTTCTTAC 1200
ATGATCCAGC CCCAGAACCC AAACCTAGGC ACTGTATAGA TGACCACTTT CGTAAACTAC 1260
TGACCTAGCT TGTGTCGAAT TGTGATTGA ACTTCCATA ACTCCACTTC GTGCTGTCTC 1320
CTCTGTATAC AGCCACCTTC TGTCCCGTC ATGAGCCTTT AGGTCTCCAT TTGCTATTG 1380
CAATACTACT GTTCCATGTA GGTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG 1440
TTCCCTTGA GACTGGCTGT CAATTTGTGT TGCTGTGTG GTTGTGTATG AAAAAATAAA 1500
75    AATGATTGAT TACATAAAAA AAAAAAATAA AAAAAAATAA CAAAAAATAA 1560
GCGCGGCTT TTTCCCGGGC GCACAAAGTT ATAAACGCC GTCCATC

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Seq ID NO: B73 sequence  
Nucleic Acid Accession #: NM\_000222.1  
Coding sequence: 22..2952

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CTGCTCTCTAC TGCTTCGCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120

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	CCGTCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCCGT	GGGCGAOCGAG	180
	ATTAGGCTGT	TATGCACTGA	TCOGGGCTTT	GTCAAATGGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACAGGT	GCACCAACAA	ACAOGGCTTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCCAAGC	TTTTCTCTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTC	CTCTCAGAGA	CCCAGAAGTG	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGGCGGGCAT	CATGATCAAA	540
	AGTGTGAAAC	GGCGCTACCA	TCGGCTCTGT	CTGCATTGTT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGTCTG	CGGAAAAATT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAGGC	TGTGCTGTT	660
	GTGTCTGTGT	CCAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTCCAC	AGTGACGTGC	720
	ACAATAAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAACGTGGA	AAAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGGTGACT	TCAATTATGA	ACGTCAGGCA	840
	ACGTTGACTA	TCAGTTTCAGC	GAGAGTTAAT	GATTCTGGAG	TGTTTCATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCACACAA	ACCTTGGAA	TAGTAGATAA	AGGATTCATT	960
	AATATCTTCC	CCATGATAAA	CACCTACAGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTG	1020
	ATTGTTGAAT	ATGAAGCAAT	CCCCAARCTT	GAACACCAAGC	AGTGGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAAGTAA	TATCAGATAC	1140
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	CCAGAGCCCA	CAATAGATTG	GTATTTTGT	CCAGGAACCTG	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGGATGTGCA	GACACTAAAC	TCATCTGGGC	CACCGTTTGG	AAAGCTAGTG	1440
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	GTGAATCTAC	TTGGAGCCTG	CACCAATTGA	GGGCCCAACC	TGGTCATTAC	AGAATATTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTGAGA	AGAAAACGTG	ATTCAATTAT	TTGTTCAAAG	2100
35	CAGGAAGATC	ATGCGAAGC	TGCACCTTAT	AAGAACTTTC	TGCATTCAAA	GGAGTCTTCC	2160
	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGGCCG	ACAAAAGGAG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCCGCCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
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	ATGAACAGAA	AAACATTCTGA	TTTGGAAGAA	GAGAGGGAGG	TATGGACTGG	GGGCCAGAGT	3240
	CCTTTCCAA	GCTTCTCCAA	TTCTGCCCAA	AAATATGGTT	GATAGTTTAC	CTGAATAAAT	3300
	GGTAGTAATC	ACAGTTGGCC	TTCAGAACCA	TCCATAGTAG	TATGATGATA	CAAGATTAGA	3360
55	AGCTGAAAC	CTAAGTCTCT	TATGTGGA	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACCT	GGGCTTAAGA	AATCTAGTAT	TTCTATGCTG	GAATGAGACA	TAGGCCATGA	3480
	AAAAAATGAT	CCCCAAGTGT	GAACAAAAGA	TGCTCTTCTG	TGGACCACTG	CATGAGCTTT	3540
	TATACTACCG	ACCTGCTTTT	TAAATAGAGT	TTGCTATTAG	AGCAATTGAAT	TGGAGAGAAG	3600
	GCTCTCCCTAG	CCAGCACTTG	TATATACGCA	TCTATAAATT	GTCCGTGTTC	ATACATTGTA	3660
60	GGGGAAGACA	CCATAAGGTT	TCGTTTCTGT	ATACAAACCT	GGCATTATGT	CCAATGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAACAG	TTAATACCAT	TTTTTAAGGA	3780
	AAACAATATA	CCACAAAGCA	CAATTTGAAC	AAATCTCCT	CTTTTAGCTG	ATGAACCTAT	3840
	TCTGTAGATT	CTGTGGAACA	AGCCTATCAG	CTTCAGAAATG	GCATTGTACT	CAATGGATTT	3900
	GATGCTGTGT	GACAAAGTTA	CTGATTCACT	GCATGGCTCC	CACAGGAGTG	GGAAAAACCT	3960
65	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAATAAAGT	ATAGGTTTAG	CCTCCTTCGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTACGTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGGCCC	TGAGTCCAAG	AGGGTCTTTT	AGTACCTGAA	4140
	AAGTAACTTG	GCTTTTCAATTA	TTAGTACTGC	TCTTGTCTCT	TTTCACTAG	CTGTCTAGAG	4200
70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGACGTTT	ACCTGCACTT	AAGGCACCTT	GTTATTTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATAATGC	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTTAGACT	4380
	GTAGCCTGGA	TATTTATCTT	GTAGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
	AACCTCCCTT	CCTCAGTCC	CAATATAAAA	GGCAAAATGTG	TACATGGCAG	AGTTTGTGTG	4500
	TTGTCTTGAA	AGATTTCAGGT	ATGTTGCCTT	TATGGTTTCC	CCCTTCTACA	TTTCTTAGAC	4560
75	TACATTTAGA	GAACCTGTGGC	CGTTATCTGG	AAGTAACCAT	TTGCACTGGA	GTTCTATGCT	4620
	CTCGACCTT	TGAAAGTTTA	ACAGATTTTG	GGGTTGTGTT	GTACCCCAAG	AGATTGTTGT	4680
	TTGCCATACT	TTGTCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTTGT	TAGTTATAGA	TGTTCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTG	4800
	TTGCCATACT	TTGTCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
80	AAGTGGTTGT	TAGTTATAGA	TGTTCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTG	4920
	AATGCTTTT	GAAATTTCCC	AAGCCCATGA	GTCCCTGAAA	ATATTTTTTA	TATATACAGT	4980
	AACCTTATGT	GTAATATACAT	AAGCGGCGTA	AGTTTAAAGG	ATGTTGGTGT	TCCACGTGTT	5040
	TTATTCCTGT	ATGTTGTCCA	ATTGTTGACA	GTTCGAAGA	ATTC		

Seq ID NO: B74 protein sequence  
Protein Accession #: NP\_000213.1

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5 1      11      21      31      41      51
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MRGARGAMDF LCVLLLLLRV QTGSSQPSVS PGEPSPPSIH PGKSDILVRV GDEIRLLCTD 60
PGFVKWTFEI LDETENKQKQ EWITEKAEAT NTGKYTCTNK HGLSNSIYVF VRDPAKLFLV 120
DRSLYKEDN DTLVRCPLTD PEVTNYSLKG CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAFKA VPVSVSKAS YLLREGEFT VTCTIKDVSS 240
10 SVYSTNKREN SQTQLQEKYN SWHHGDFNYE RQATLTISSA RVNDSGVFMF YANNTFGSAN 300
VTITLEVVDK GFINIFPMIN TTVFVNDGEN VDLIVEYBAF PKPEHQWYI MNRTFTDKWE 360
DYPKSENESE IRYVSELHLT RLKGTGGTY TFLVNSDVN AAIANVYVN TKPEILTYDR 420
LVNGMLQCV AAGPEPTIDW YFCPGTEQRC SASVLEVDVO TLNSSGPPFG KLVVQSSIDS 480
SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG MNKEQIHPHT LFTPLLIGFV IVAGMMCIIIV 540
15 MILTYKYLQK PMYEVQWKVV EERINGNNYVY IDPTQLPYDH KWEFPPNRRLS FGKTLGAGAP 600
GKVVEATAYG LKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLVSLGNH MNIVNLLGAC 660
TIGGPTLVIT EYCCYGDLLN FLRRKRDSFI CSKQEDHAEA ALYKILLHSE ESSCSDSTNE 720
YNDMKPGVSV VVPTKADRRR SVRIGSYIER DVTFAIMEDD ELALDLEDLL SFSYQVAKGM 780
AFLASKNCIH RDLAARNILL THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAPEP 840
20 IFNCVYTFES DVNSYGFILW ELFSLGSSPY PGMFVDSKPY KMIKEGFRML SPEHAPAEY 900
DIMKTCNDAD PLKRTTFKQI VQLIEKQISE STNHIYSNLA NCSFNRQKPV VDHSVRINSV 960
GSTASSQPL LVHDDV

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Seq ID NO: B75 DNA sequence  
Nucleic Acid Accession #: NM\_004456  
Coding sequence: 58..2298

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30 1      11      21      31      41      51
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GAATTCGGGG CGACGCGCGG GAACAACGCG AGTCGGCGCG CGGACGGAAG AATAATCATG 60
GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTTGTT GGCGGAAGCG TGTAATAATCA 120
GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCA ATCGTCAGAA AATTTTGGAA AGAACGGAAG TCTTAAACCA AGAATGGAAA 240
CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG 300
35 GAGTGTTCGG TGACCAAGTA CTGTGGATTT CCAACACAAG TCATCCCATT AAAGACTCTG 360
AATGCAGTTG CTTCACTACC CATAATGTAT TCTTGTGCTC CCCTACAGCA GAATTTTATG 420
GTGGAAGATG AAACGTGTTT ACATAACATT CCTTATATGG GAGATGAAGT TTTAGATCAG 480
GATGTGACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAGATACA CGGGGATAGA 540
GAATGTGGGT TTATAAATGA TGAATTTTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
40 AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
GATCTGGAGG ATCACCAGAG TGATAAAGAA AGCCGCCAC CCGGAAATT TCCTTCGTAT 720
AAAAATTTGG AGGCCATTTT CTCATGTTT CCAGATAAGG GCACAGCAGA AGAATCAAG 780
GAAAAATATA AAGCACTCAC CGAACAGCAG CTCACAGGCG CACTTCCTCC TGAATGTACC 840
CCCAACATAG ATGGACCAAA TGCTAAATCT GTTCAGAGAG AGCAAAAGCTT ACATCTCTTT 900
45 CATACGCTCT TCTGTAGGCG ATGTTTTAAA TATGACTGCT TCCTACATCC TTTTCATGCA 960
ACACCCAACA CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTTGTGGA 1020
CCACAGTGTG ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
CGGATAAAGA CCCACCAAAA ACGTCCAGGA GCGCGCAGAA GAGGACGGCT TCCTCAATAAC 1140
50 AGTAGCAGGC CCGACACCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTATG 1200
AGGGAAGCAG GGAAGTAAAC GGGGCGAGAG AACATGATA AAGAAGAAGA AGAGAAGAAA 1260
GATGAAACTT CGAGCTCTCT TGAAGCAAAT TCTCGGTGTC AAACACCAAT AAAGATGAAG 1320
CCAAATATTG AAOCTCTCTG GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTAGA 1380
GTCTCATTTG GCACTTACTA TGACAATTTC TGTGCCATTG CTAGGTTAAT TGGGACCAAA 1440
55 ACATGTAGAC AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC 1500
GCTGAGGATG TGGATACTCC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA 1560
CACTGCAGAA AGATACAGCT GAAAAAGGAC GGCTCCTCTA ACCATGTTTA CAACTATCAA 1620
CCCTGTGATC ATCCAAGGCA GCCTTGTGAC AGTTCGTGCC CTGTGTGATC AGCACAATAA 1680
TTTGTGAAA AGTTTTGTCA ATGTAGTTCA GAGTGTCAAA ACGCTTTCC GGGATGCCGC 1740
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60 CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTGGG ACGTAAAAA TGTGTCTGTC 1860
AAGAACTGCA GTATTTCAGG GGGCTCCAAA AAGCATCTAT TGTGCGCAC ATCTGAOGTG 1920
GCAGGCTGGG GGATTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
TGTGGAGAGA TTATTCTCA AGATGAAGCT GACAGAAGAG GGAAGTGTA TGATAAATAC 2040
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AACAAAATTC GTTTTGCAAA TCATTCCGTA AATCCAACT GCTATGCAAA AGTTATGATG 2160
GTTAACGGTG ATCACAGGAT AGGTATTTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCGG CATCGAAAGA 2280
GAAATGGAAA TCCCTTGACA TCTGTACTCT CTTCCCTCTC CTCTGAAACA GCTGCCTTAG 2340
70 CTTCAGGAAC CTCAGTACT GTGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
AATTTCAGAA GTACTGTAAG AATAATTTAT AGTAATGAGT TTAATAATCA ACTTTTATTT 2460
GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CAGTGAATT TTTGCAATTA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAACCTTGA AAAAAA

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Seq ID NO: B76 Protein sequence  
Protein Accession #: NP\_004447

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80 1      11      21      31      41      51
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KQRRIQPVHI LTVSSSLRGT RECSVTSDDL PPTQVPIPLK LNAVASVPIM YSWSPLOQNF 120
MVEDSTVLHN IPYMGDEVLD QDGTFLIELI KNYDGKVVHD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DDPEEREKQ KDLEDRDDK BSRPPKPPS DKILEAISM FPDKGTAEEL 240
KEKYKELTEQ QLPALPPEC TPNIDGPNK SVQREQSLHS FHTLFCRRCP KYDCFLHPFH 300
ATPNTYKRKN TETALDNKFC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GRRRRGRPLN 360

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5  
 NSSRPSTPTI NVLESKDSTD DREAGTSTGG ENNDKEEEK KDETSSSSEA NSRCQTFIKM 420  
 KPNIEPPENV EWSGAEASMF RVLIGTYIDN FCAIARLIGT KTCRQVVEPR VKSSSIAPA 480  
 PAEDVDTPPR KKRKRHLWA AHCRKIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPCVIAQ 540  
 NFCEKFQCS SEQNRFPQC RCKAQCNTRQ CPCYLAVREC DFDLCLTCGA ADHWDSKNVS 600  
 CRKCSIQRS KKHLLAPSD VAGWGIPIKD PVOKNEFISE YGBIISQDE ADRRGKVYDK 660  
 YMCSEFLNIN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720  
 ELFVDYRYSQ ADALKYVGIE REMEIP

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 Seq ID NO: B77 DNA sequence  
 Nucleic Acid Accession #: NM\_007015  
 Coding sequence: 1..1005

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 AAGGTGGGAG CCGTGGTCTT CATTTGCGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180  
 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240  
 ATCAATGGGA AACTACAAGA TGGTCAATG GAAATAGACG CTGGGAACAA CTGGAGACC 300  
 20  
 TTTAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTCCA GAATGGCATC 360  
 ACAGGAATTC GTTTTGTCTG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420  
 ATTCTGAGG TGGGCGCGGT GACCAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC 480  
 ATGCCAGTCA AATATGAAGA AAATCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540  
 GACAACAGCT TCTTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTTCTGG 600  
 25  
 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660  
 GTTCCAACCT CCACAAAAGG ACCACACAGT GGACCAACGA GCAACCCAGG CGCTGGAAGA 720  
 CTGAATTAAT AAACACAGCC CAGTGTTCAG GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780  
 CCTATCATC ASCAGGAAGG GGAAGCATG ACATTGACCC CTAGACTGGA TCACGAAGGA 840  
 ATCTGTTGTA TAGAATGTAG GGGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900  
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 GGGGGCTATT ACCATGGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960  
 ATGCCATGTA GCTGGTGGGT GGGCGGTATC TTGGGCGATG TGTGAAATCA CTTCATATAT 1020  
 CAGGTGCTGT AAATAAGACA CTAGCTGAAG AGACAAACAA AGAAGCATTA AGGCAGGTTG 1080  
 ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCCTGA GCGGTATTTC TTGACACTCT 1140  
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 AGTTCAAGTC TAAATAGCCA TAAACCCGTT ATTTGTTATT TTTTATTTCG ATTGATTTCG 1260  
 CATAAGTCTT CCCTGTCTTG CATCTTCCAA AGCTATTTG AAATAAACAC GAAAAATTAC 1320  
 AGTTTGCC

40  
 Seq ID NO: B78 Protein sequence  
 Protein Accession #: NP\_008946

45  
 1 11 21 31 41 51  
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 MTENSDEVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KGVAVVLISG AVLLLFGAIG 60  
 AFYFWKGSDS HIYNVHYTMS INKQLQDGS EIDAGNNLET FKMGSAGEEA IAVNDFQNGI 120  
 TGIRFAGGEK CYIKAQVKAR IPEVGAUTKQ SISKLEKGI MPVKYEENSL IWVAVDQPVK 180  
 DNSFLSKVL ELQGLDPIFW LRPTYPKRIQ RRRREVVRKI VPTTTKRPHS GPRSNPGAGR 240  
 LNNETRPSVQ EDSQAFNPDN PYHQEGESM TFDPRLDHEG ICCIECRSY THCQKICEPL 300  
 50  
 GGYYPWFYNY QGCRSACRVI MPCSWWVARI LGMV

55  
 Seq ID NO: B79 DNA sequence  
 Nucleic Acid Accession #: NM\_012449.1  
 Coding sequence: 66..1085

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 AATTATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA 120  
 GGAGAAATTT AGAAGAAGAC GATTATTTGC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180  
 65  
 AAAGACCTGT GCTTTTGCAT TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240  
 CAGAACTTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTTGCCAAAT AAAATAGCTG 300  
 CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTTCTGAG GGAAGTAATT CACCCCTTAG 360  
 CAACCTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420  
 CAATGGTTTC CATCACTCTC TTGGCATTGG TTACCTGCC AGGTGTGATA GCAGCAATTG 480  
 70  
 TCCAACCTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540  
 TAACAGAGAA GCAAGTTTGGG CTCTCTAGTT TCTTTTTCG TGTACTGCAT GCAATTTATA 600  
 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAATT GCTAAACTGG GCATATCAAC 660  
 AGGTCCAACA AATAAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATT 720  
 75  
 ATGTGCTCT GGAATTTGTG GGAATGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780  
 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACCTA TATTCAGAGC AAGCTAGGAA 840  
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCTGGAAAT AAGTGGATAG 900  
 ATATAAAACA ATTTGTATGG TATACACCTC CAACCTTTAT GATAGCTGTT TTCCTTCCAA 960  
 TGTGTGTCCT GATATTAAAG AGCATACTAT TOCTGCCATG CTTGAGGAAG AAGATACTGA 1020  
 AGATTAGACA TGGTTGGGAA GACGTACCCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080  
 TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140  
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA

80  
 Seq ID NO: B80 Protein sequence  
 Protein Accession #: NP\_036581.1

1 11 21 31 41 51  
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 MBSRKDITNQ EELWQMKPRR NLEEDDYLRK DTGETSMLKR FVLLHLEQTA HADEFDCPSE 60  
 LQHTQELFPQ WHLPKIKAAI IASLTPLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLP 120

VSITLLALVY LPGVIAAIQV LHNGTKYKFP PHWLDKMLT RKQFGLLSFF FAVLEAIYSL 180  
 SYPMRRSRY KLINWAYQQV QONKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240  
 VSDSLTWREF HYIQSKLIV SLLGLTIHAL IFANWKWIDI KQFVWYTPPT FMAVFLPIV 300  
 VLIFKSILFL PCLRKKILKI RHGWEDVTIKI NRTBICSQL

5

Seq ID NO: B81 DNA sequence  
 Nucleic Acid Accession #: NM\_000684  
 Coding sequence: 87..1520

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 TGCTACCCGC GCCCGGGCTT CTGGGGTGT CCCTAACAC GGCAGAGCC TGCCACACC 60  
 CCGCCCCCG GCCTCCGAG CTCGGCATGG GCGGGGGGT GCTCGTCTG GCGCCTCCG 120  
 AGCCCCGTAA CCTGTCTGT GCGGCACCG TCCCGACGG CCGGCCACC GCGGCGGGC 180  
 15 TGCTGTGTGC CCGTCTGTG CCGGCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCCGAGC 240  
 CGCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGTGAT GCGCTCATC GTGCTGTCTA 300  
 TCGTGTGGCG CAATGTGCTG GTGATCGTGG CCATGCCCAA GACGCGCGG CTGCAGACGC 360  
 TCACCAACCT CTTTCATATG TCCCTGGCCA GCGCGACCT GGTATGGGG CTGCTGTGG 420  
 TGCGGTCTGG GGCACCATC GTGGTGTGG GCGCTGGGA GTACGGCTCC TTCTTCTGG 480  
 20 AGCTGTGGAC CTCAGTGGAC GTGCTGTGG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540  
 TTGCCCTGGA CCGCTACCT GCCATCACT CCGCTTCCG CTACAGAGC CTGTGAGCG 600  
 GCGGCGGGC GCGGGGCTC GTGTGCACCG TGTGGCCAT CTGCGCCCTG GTGTCTTCC 660  
 TGCCCATCTT CATGCACTGG TGGCGGGCG AGAGCGACGA GCGCGCGCG TGCTACACG 720  
 ACCCAAGTG CTGCGACTTC GTCAACCAAC GGCCTACGC CATCGCCTG TCCGTAGTCT 780  
 25 CCTTCTACGT GCCCTGTGC ATCATGGCTT TCGTGTACT GCGGGTGTTC CGGAGGGCC 840  
 AGAAGCAGT GAAGAAGAT GACAGCTGG AGCGCGCTT CCGCGCGCG CAGCGCGCG 900  
 CGCCTCGCC CTGCGCTCG CCGTCCCG CCGCGCGCG GCGCGCGGA CCGCGCGCG 960  
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 CGCGCTCTG GCGCTACG GAGCAGAGG CGCTCAAGAC GCTGGGCATC ATCATGGCG 1080  
 30 TCTTCACTG CTGCTGTGG CCTTCTTCC TGGCCAAGT GGTGAAGCC TTCCACGCG 1140  
 AGCTGTGGC CGACCGCTC TTGCTTCTT TCACTGGCT GGGCTACGC AACTCGGCT 1200  
 TCAACCCAT CATCTACTG CGCAGCCCG ACTTCGCAA GGCCTTCAG GACTGTCTT 1260  
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 CGGCTGTCT GCGCGCGCG GAGCCCGCG CATCGCCCG GCGCGCTCG GAGCAGAGC 1380  
 35 ACGACGATG GTGCGGGCG ACGCGCGCG CCGCGCTGCT GGAGCCCTG CCGCGCTGA 1440  
 ACGCGGGCG GCGCGCGCG AGCGACTCG GCCTGAGCA GCGTGGCGC CCGCGCTCG 1500  
 CCTCGGAAT CAAGGTGTAG GCGCGCGCG GCGCGCGCG CTCGCGCAC GGTTCOCAG 1560  
 GGGAAACGAG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAATCGA AGCCCAAT 1620  
 40 CCTGTCTGA ATCATCCAG GCAAGAGAA AAGCCACGA CCGTTCACA AAAAGGAAAG 1680  
 TTTGGGAAG GATGGAGAG TGGCTGTCTG ATGTTCTTG TTG

Seq ID NO: B82 Protein sequence  
 Protein Accession #: NP\_000675.1

45 1 11 21 31 41 51  
 MGAGVLVLA SEPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASEP EPLSQQWTAG 60  
 MGLLMALIVL LIVAGNLVLI VAIKTPRLQ TLNLFIMSL ASADLVMLGL VVPFGATIVV 120  
 WGRWYGGFF CELWTSVDVL CVTASITLC VIALDRYLAI TSPFRYQSL TRARARGLVC 180  
 50 TWHAISALVS FLPILMHWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240  
 AFVYLVRFE AQKQVKIDS CERRFLGGA RPPSPSPSPV PAPAPPGBP RPAATAATP 300  
 LANGRAGRR PSRLVALREK KALKTLGIM GVFTLCWLP FLANVVKAFH RELVPDLFV 360  
 FPNWLYANS AFNPILYCRS PDKRAEQGL LCARRAARR RHATHGRPR ASGCLARPG 420  
 PPSGAASDD DDDVVGATP PARLLEPWAG CNGGAAASD SSLDEPCRPG FASESKV

55

Seq ID NO: B83 DNA sequence  
 Nucleic Acid Accession #: NM\_000729.2  
 Coding sequence: 2..421

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 AGCCATGAAC AGCGGGTGT GCCTGTGCGT GCTGATGGG GACTGGCGG CTGGCGCCT 120  
 GACGACGCG GTGCTCCCG CAGATCCCG GGGCTCCGG CTGACGCGG CAGAGGAGGC 180  
 65 GCGCCGTAGG CAGCTGAGG TATCGCAGG AACGATGGC GAGTCCCGG CGCACTGGG 240  
 CGCCCTGCTG GCAAGATACA TCCAGCAGC CCGGAAAGT CCTCTGGAC GAATGTCCAT 300  
 CGTTAAGAAC CTGCGAAGC TGGACCCAG CCACAGGATA AGTGACGGG ACTACATGG 360  
 CTGGATGGAT TTTGGCGTC GCAGTGGGA GGAGTATGAG TACCCCTCT AGAGGACCA 420  
 70 GCGCCATCA GCGCAACGA AGCAACCTCC CAACCCAGG GAGGAGAAAT AAGACAACAA 480  
 TCACACTCAT AACTCATTGT CTGTGGAGT TGACATTGAA TGTATCTATT TATTAGTTC 540  
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACAGCT CACGAGAAT 600  
 TGTGAAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTCTG AAAATGTTG 660  
 TATGCTATTA AAGTGATTTC ATTCTGCC

75

Seq ID NO: B84 Protein sequence  
 Protein Accession #: NP\_000720.1

80 1 11 21 31 41 51  
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEAP RRQLRVSRQ DGESEHLAG 60  
 LLARYIQAR KAPSGRMSIV KNLQNDPSH RISDRYMGW MDPGRSAEB YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5	<b>A1 DNA SEQUENCE</b>	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
10	Nucleic Acid Accession #:	M31210
	Coding sequence:	251-1396
15	TCTAAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG 60 AAGCAACTCT CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAGGA 120 AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCAACC CTGAAGCCAG TGAAGGCTCT 180 CTCGCTCGCG CCTCTAGCGT TCGTCTGGAG TAGCGCCACC CCGGCTTCTT GGGGACACAG 240 GGTTCGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCCACCGCA GCTCGGTCTC 300 TGACTACGTC AACTATGATA TCATCGTCCG GCATTACAAC TACACGGGAA AGCTGAATAT 360 CAGCGCGGAC AAGGAGAACA GCATTAAACT GACCTCGGTG GTGTTCAATC TCATCTGCTG 420 CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCCA 480 CCGACCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTTGG CAGGAGTAGC 540 CTACACAGCT AACCTGCTCT TGTCTGGGGC CACCACCTAC AAGCTCACTC CCGCCAGTG 600 GTTTCGTGGG GAAGGGAGTA TGTTTGTGGC CCTGTGAGCC TCCGTGTTCA GTCTCTCGC 660 CATCGCCATT GAGGCTATA TCACAATGCT GAAATGAAA CTCACAACG GGAGCAATAA 720 CTTGCGCTC TTCTGCTAA TCAGCGCTCG CTGGGTCTAT TCCCTCATCC TGGGTGGCCT 780 GCCTATCATG GGCTGGAACG GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCGGCT 840 CTACCAACAG CACTATATCC TCTTCTGCAC CACGGTCTTC ACTCTGCTTC TGCTCTCCAT 900 CGTCATTCTC TACTGAGATA TCTACTCCTT GGTGAGGACT CGAGCGCGCC GCGTGAAGTT 960 CCGCAAGAAC ATTTCCAAGG CCAGCGCGAG CTCTGAGAAT GTGGCGCTGC TCAAGACCGT 1020 AATTATGCTC CTGAGCGTCT TCATGCGCTG CTGGGCACCG CTCTTCATCC TGCTCCTGCT 1080 GGATGTGGGC TGCAAGGTGA AGACCTGTGA CATCCTCTTC AGAGCGGAGT ACTTCTCGT 1140 GTTAGCTGTG CTCAACTCGG GCACCAACCC CATCATTTAC ACTCTGACCA ACAAGGAGAT 1200 GCGTCSGGCC TTTCATCGGA TCATGTCTGT CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG 1260 CAAATTCAAG CGACCCATCA TCGCGGCGAT GGAATTGAGC CGCAGCAAT CGGACAAATC 1320 CTCGCCACCC CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTATGTCTT CTGGAACCGT 1380 CAACCTCTCT TCCTAGAAGT GGAAGCTGTC CACCCACCGG AAGCGCTCTT TACTTGGTGG 1440 CTGGCCACCC CAGTGTGTTG AAAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT 1500 GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGGTGGTGT CGGTGTTGG 1560 TGGGTAGAGT TAGTTCTCTG GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGCGCT 1620 GGAAATATATA TTCTACCCCC CTGAGCTTTT GATTTTGCAC TGAGCCAAAG GTCTAGCATT 1680 GTCAAGCTCC TAAAGGGTTC ATTTGGCCCC TCCTCAAGA CAATATGCCC CATGTGAAG 1740 CGTCTCTTTG TCTGAGCTTT TGAGGAGATG TTTTCTTCA CTTTAGTTTC AAACCCAAAT 1800 GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCGCTGTACA TCCACACCC CACCCTCCCT 1860 TCCTTTCATA CCCCTCCTCA ACGTTCCTTT ACTTTTACT TTAACCTACCT GAGAGTTATC 1920 AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAT AGGCTATGTT GAGTACGTAG 1980 GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAACAAT GTCCTTCGCT GAGGCCAAAG 2040 TTTCCATGTA AGCGGGATCC GTTTTTTGA ATTTGGTTGA AGTCACTTTC ATTTCTTTAA 2100 AAAACATCTT TTCAATGAAA TGTGTTACCA TTTTCATATC ATTGAAGCCG AAATCTGCAT 2160 AAGGAAGCCC ACTTTATCTA AATGATATTA GCCAGGATCC TTGGTGTCTT AGGAGAAACA 2220 GACAAGCAAA ACTAAGTGAA AACCGAATGG ATTAACCTTT GCAAAACCAAG GGAGATTCTT 2280 TAGCAAAATGA GTCTAACAAA TATGACATCC GTCCTTCCCA CTTTGTGTTA TGTTTATTTT 2340 AGAATCTTGT GTGATTCAIT TCAAGCAACA ACATGTGTGA TTTTGTGTG TTAAGATAC 2400 TTTTCTTGAT TTTTGAATGT ATTTGTTTCA GGAAGAGTGC ATTTTATGGA TTTTCTAAC 2460 CCGTGTAAAC TTTTCTAGAA TCCACCTCTT TGTGCCCTTA AGCATTACTT TAACGTGTAG 2520 GGAACGCCAG AACTTTTAAG TCCAGCTATT CATTAGATAG TAATGAAGA TATGTATAAA 2580 TATTACAAAG AATAAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAAAC 2640 CGAGAGATGT CTTGTTTTTT TAAAAAAGAT AGTATTTAAT AGGTTTCTGA CTTTGTGGGA 2700 TCAATTTTGA CATAGCTTTA TCAACTTTTA AACATTAAAT AACTGATTTT TTAAAG	
60	<b>A2 Protein sequence:</b>	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
65	Protein Accession #:	AA52336
	Signal sequence:	none found
	Transmembrane domains:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Cellular Localization:	plasma membrane
70	1 11 21 31 41 51           MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSTV VFILICCFII 60 LENIPVLLTI WTKTKFHERPM YYPIGNLALS DLLAGVAYTA NLLSGATTY KLTFAQWFLR 120 EGSMFVALSA SVFSLLAIAI ERYITMLKKK LHNGSNPNRL PLLISACWVI SLILGGLPIM 180 GWNCSIALSS CSTVLPVLYK HYILPCTTVF TLLLLSIVIL YCRIYSLVRT RSRRLTFREN 240 ISKASRSSEN VALLKTVIIV LSVFIACWAP LPILLLLDVG CKVKTCDILF RAEYFLVLAV 300 LNSGTNPPIY TITNKEMRRA FIRIMSCCKC PSGDSAGKFK RPIIAGMEFS RSKSDNSSHP 360 QKDEGNFET IMSSGNVNSS S	
80	<b>A3 DNA SEQUENCE</b>	
	Gene name:	G protein-coupled receptor 51
	Unigene number:	Hs.198612
	Probeset Accession #:	AA452928
	Nucleic Acid Accession #:	NM_004624.1

Coding sequence: 1-2826 (underlined sequences correspond to start and stop codons)

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5 1 11 21 31 41 51
| | | | | |
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GGCGCGCTGC TACTGCTACT GCTGCTGCGG CTGCTGCTGC CTCTGGCGCC CGGGGCTTGG 120
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CTCATGCGCG TCACCAAGGA GGTGGCCAAG GGCAGCATCG GGCGCGGTGT GCTCCCGGCC 240
10 GTGGAAGTGG CCATCGAGCA GATCCGCAAC GAGTCACTCC TGCGCCCTTA CTCTCTGAC 300
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ATAAAATACG GCGCGAACCA CTGTATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC 420
ATCATTTGCA AGTCCCTCCA AGGCTGGAAT CTGGTGCAAG TTTCTTTTGC TGCAACCAAG 480
CCTGTTCTAG CGGATAAGAA AAAATACCTT TATTTCTTTC GGACCGTCCC ATCAGACAAT 540
15 GCGGTGAATC CAGCCATTCT GAAGTTGCTC AAGCACTACC AGTGAAGCG CGTGGGCAAG 600
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GGCGAGTACA TTGAGATTTC AGACACCGAG AGCTTCTCCA ACGATCCCTG TACCAATGTC 720
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20 GCAAAAGTGT TCTGTTGTGC ATACGAGGAG AACATGTATG TAGTAAATA TCAGTGGATC 840
ATTCGCGGCT GGTACGAGCC TTCTTGGTGG GAGCAGGTGC ACACGGAAGC CAACTCATCC 900
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CCCTGAGCT CAAGCAGAT CAAGACCATC TCAGGAAGA TCCACAGCA GTATGAGAGA 1020
GAGTACAACA ACAAGCGGTC AGGCGTGGG OCCAGCAAGT TCCACGGGTA CGCTACGAT 1080
25 GGCATCTGGG TCATCGCCAA GACACTGCAG AGGCGCATGG AGACACTGCA TGCGAGCAGC 1140
CGGCACGAGC GGATCCAGGA CTTCAACTAC ACGGACCACA CGCTGGGCGG GATCATCTTC 1200
AATGCCATGA ACGAGACCAA CTTCTTGGG GTACCGGTC AAGTTGTATT CCGGAATGGG 1260
GAGAGAATGG GGACCATTA ATTACTCAA TTCAAGACA GCAGGAGGT GAAGGTGGGA 1320
GAGTACAAGC CTGTGGCGGA CACACTGGAG ATCATCAATG ACACCATCAG GTTCCAAGGA 1380
30 TCCGAACAC CAAAGAGCAA GACCATCATC CTGGAGCAGC TGCGGAAGAT CTCCTACCT 1440
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TTCTTCAACA TCAAGAACCG GAATCAGAAG CTCATAAAGA TGTCGAGTCC ATACATGAAC 1560
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35 ACCGTGGGCT ACACGACCGC TTTTGGGGCC ATGTTTGCAA AGACCTGGAG AGTCCAAGCC 1740
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40 ATCCGCGCTC TCCTGGAGCA CTGTGAGAAC ACCCATATGA CCATCTGGCT TGGCATGCTC 1980
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45 GTGCGGAAGC TCATCAOCCT GAGAACAAC CCAGATGCAG CAACGCAGAA CAGGCGATT 2280
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CAOCCCTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTGAGCCC CTGCGTCAGC 2760
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CTGTAA

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55 **A4 Protein sequence:**  
 Gene name: G protein-coupled receptor 51  
 Unigene number: Hs.198612  
 Probeset Accession #: AA452928  
 Protein Accession #: NP\_005449.1  
 60 Signal sequence: 1-42  
 Pfam domains: 7tm\_3 [481-754], ANF\_receptor [130-204]  
 Transmembrane domains: 22-44, 477-499, 517-539, 552-574, 595-617, 653-675, 692-713, 722-744  
 Cellular Localization: plasma membrane

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65 1 11 21 31 41 51
| | | | | |
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IMPLTKEVAK GSGRGLVLP VELAIEQIRN ESLLRPVFLD LRLYDTECDN AKGLKAFYDA 120
IKYGNHLMV FGGVCPVST IIAESLQGN LVQLSPAATT PVLADKKRYP YPFRVPSDN 180
AVNPAILKLL KHYQWKRVT LTQDVQRFSE VRNDLTGVLY GEDIEISDT SPENDPCTSV 240
KKLKGNDVRI ILQFPDQMA AKVFCAYEE NMYGSKYQWI IPGWYEPSWV EQVTEANSS 300
RCLRNKLLAA MBGYIGVDFE PLSSKQIKTI SGKTPOQYER EYNNKRSVG PSKPHGYAYD 360
GIWVIKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIL NAMNETNFFG VTQGVVFRNG 420
ERMGTIKFTQ PQDSREVKVG EYNAVADTLE IINDTIRPQG SEPPKDKTII LEQLRKISLP 480
LYSILSALT LQMINASAPL PFNIKRNQK LKIMSSPYMN NLIIILGMLS YASIFLFLGD 540
GSFVSEKTFE TLCTVRTWIL TVGYTTFAGA MPAKTWRVHA IFKNVRMKKK IIKDQKLVI 600
VGMMLLIDL ILICQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN TMTIWLIV 660
70 YAYKGLMLP CFPLAWETRN VSIPALNSK YIGMSVYNVG IMCIIGAASV FLTRDQPNVQ 720
PCIVALVIIF CSTITLCIVF VPKLITLRTN PDAATQNRFF QFTQNKQKED SKTSTSVTSV 780
NQASTSRLEG LQSEHRLRM KITELDKDLE EVTMLQDTP EKTYYIKQNH YQELNDILNL 840
GNFTBSTDGG KAILKHLDO NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLFILR 900
HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L

```

A5 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120
GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCTCGGCA 180
GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
15 GTCAAAATGT GGCCTCAACT TCTTCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTGG 300
CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
AAACCCCTCTG CTTTGTCTCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420
GAGCTTCATC TGGATGGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
20 TTACCCGAGC ATCACTCTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
CCTGCTGGCA CTGCTCTGTC ACCACCGAGG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
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CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
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GGGCACTGCT GAGCCAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
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35 CGCTGAGACC AATCTCTCT GCTGGGTAGT TACCTTATAG CATTGGGGGA TTTGGGTTAG 1500
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GGAAACCGCA GAGTGTGCG TAAACCAAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
80 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

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A6 Protein sequence:

Gene name: ESTs



Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 5 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51  
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNNG RCIPGANQCD GLPDCFDKSD 60  
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 15 RWGLCIDKSP ICDGQNNQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPW YDLPPPPYSS DTESLNQADL PPRSRSSGSA 300  
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTREV

20 A7 DNA SEQUENCE  
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Nucleic Acid Accession #: NM\_002205  
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

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 50 CTTACCTTCA CTGGCCTAGA TGAGTTTGGC CGATTGGCA GCTCCTTGAC CCGCTGGG 1200  
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 CAGGTTCCTG AGCCCTCTGT GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380  
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 CAGGGCTCA GGCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920  
 ATCTTGCTGG ACTGTGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGT 1980  
 GGGGAGCAGA ACCATGTGTA CTTGGGTGAC AAGAATGCC TGAACTCAC TTTCCATGCC 2040  
 65 CAGAAATGCG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCTCCAGAG 2100  
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTCT CCAGCTGAG CTGTGACTAC 2160  
 TTTGCCGTGA ACCAGAGCGG CTGCTGTGTG TGTGACTGG GCAACCCAT GAAGGCAGGA 2220  
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGACAC TAAGAAAACC 2280  
 70 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2340  
 TCCTTTGGGC TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAGCCT 2400  
 GAGGCAGTGC TATTCCAGT AAGCGACTGG CATCCCGAG ACCAGCCTCA GAAGGAGGAG 2460  
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520  
 AGCCAGGGTG TGCTGGAACT CAGCTGTCCC CAGGCTCTGG AAGGTGAGCA GCTCCTATAT 2580  
 75 GTGACCAGAG TTAACGGACT CAACTGCACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640  
 GAGTTGGATC CCGAGGGTTC CCTGCACCC CAGCAAAAAC GGAAGCTCC AAGCGCAGC 2700  
 TCTGCTTCTC CGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2760  
 TGTGAGCTCG GGCCTCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTGCA TTTCCAGTCT 2820  
 TGGGCCAAGA CTTTCTTGA GCGGAGCAC CAGCCATTTA GCTGCAAGTG TGAGGCTGTG 2880  
 80 TACAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCA AAAAGAGCGT 2940  
 CAGGTGGCCA CAGCTGTGCA ATGGAACCA GCAAGAGGCA GCTATGGCGT CCACTGTGG 3000  
 ATCATCATCC TAGCCATCCT GTTGGCCTC CTGCTCTAG GTCTACTCAT CTACATCTC 3060  
 TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCATGGA AAAAGCTCAG 3120  
 CTCAAGCCTC CAGCCACCTC TGATGCTCGA

**A8 Protein sequence:**

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Protein Accession #: NP\_002196  
 Signal sequence: 1-42  
 Transmembrane domains: 998-1020  
 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036  
 Cellular Localization: plasma membrane

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15      1      11      21      31      41      51
      |      |      |      |      |      |
      MGSRTFESFL HAVQLRWGFR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
      GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCV WGASPTQCTP IEFDSKGSRL 120
      LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVTCYLST 180
      DNFTRILEYA PCRSDFSNAA GQGYCQGGFS AEPTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
      IAESYYPEYL INLVQGQLQT RQASSIYDDS YLGYSVAVGE PSGDDTEDFV AGVPKGNLTY 300
      GYVTILNGSD IRSLYNFSGE QMASYFCYAV AATDVNGDGL DDLVLVGAPLL MDRTPDGRPQ 360
      EVGRVYVYLQ HPAGIEPTPT LTLTGHDGEG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
      QQGVVVFVPG GPGLGSKSPS QVLQPLWAAS HTTPDFGSAI RGGRLDGNQ YPDLIVGSFG 480
      VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNFV ACINLSFCLN ASGKHVADSI 540
      GFTVELQLDW QKQKGGVRRR LFLASRQATL TQTLLIQNGA REDCREMKIY LRNESEFRDR 600
      LSPIHIALNF SLDPQAFVDS EGLRPAHYQ SKSRIEDKQA ILDDCGEDNI CVPDLQLEVP 660
      GEQNHVYLGQ KNALNLTFAH QNVGEGGAYE AKLRVTAPPE AEYSGLVREP GNPSSLSQDY 720
      FAVNQSRLLV CDLGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFDQILSK NLNNSQSDVV 780
      SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
      SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPGSLHSH QQKREAPSR 900
      SASSGPQLIK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLOREH QPFSLQCEAV 960
      YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020
      YKLGFPRKSL PYGTAMEKAQ LKPPATSDA
  
```

**A9 DNA SEQUENCE**

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Nucleic Acid Accession #: NM\_002211.1  
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

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45      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGAATTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTTGCT 60
      CAACACAGATG AAAATAGATG TTTAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA 120
      GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180
      TCTGCACGAT GTGATGATTT AGAAGCCTTA AAAAAGAAAG GTTGCCCTCC AGATGACATA 240
      GAAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAAACCA CCGTAGCAAA 300
      GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCA CAAGTTGGTT 360
      TTGCGATTAA GATCAGGGGA GCCACAGACA TTACATTAA AATTCAAGAG AGCTGAAGAC 420
      TATCCCATTT ACCCTCTACT CTTTATGGAC CTGCTTACT CAATGAAAGA CGATTGGAG 480
      AATGTAAAAA GTCTTGGAA CAGATCTGATG AATGAAATGA GGAGGATTAC TTCGGACTTC 540
      AGAATTGGAT TTGCTCTCAT TGTGGAAGA ACTGTGATGC CTTACATTAG CACAACACCA 600
      GCTAAGCTCA GGAACCCCTG CACAAGTGAA CAGAAGTCA CCAGCCCAT TAGCTACAAA 660
      AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGCG AAAACAGGCG 720
      ATATCTGGAA ATTTGGATTC TCCAGAAGGT GGTTCGATG CCATCATGCA AGTTGCAGTT 780
      TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTGTTT CACAGATGCC 840
      GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAAA TGATGGACAA 900
      TGTCACCTG AATAATATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
      CACCTTGTCC AGAAACTGAG TGAATAAAT ATTACAGCAA TTTTTCAGT TACTGAAGAA 1020
      TTTAGCCCTG TTTACAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
      TCTGCAAAAT CTAGCAATGT AATTCAAGTT ATCATTGATG CATACAATTC CCTTTCCTCA 1140
      GAAATCATTT TGGAAAACGG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
      TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCCATT 1260
      GGAGATGAGG TTCAATTTGA AATTAGCATA ACTTCAATA AGTGTCACAA AAAGGATTCT 1320
      GACAGCTTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC 1380
      ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
      AATGGGACAT TTGAGTGTGG CGCGTGCAGG TGCAATGAAG GCGGTGTGG TAGACATTGT 1500
      GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
      AGTTCAGAAA TCTGCAGTAA CAATGGAGAG TGGGTCTGCG GACAGTGTGT TTGTAGGAAG 1620
      AGGATAATA CAATGAAAT TTATTCTGGC AAATTCTGCG AGTGATGATA TTCAACTGT 1680
      GATAGATCCA ATGGCTTAAT TTGTGGAGGA AATGGTGTGT GCAAGTGTG TGTGTGTGAG 1740
      TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTTT TGGATACTAG TACTTGTGAA 1800
      GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT 1860
      ACAGATCCGA AGTTTCAAGG GCAAACTGTG GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
      GCTGAGCATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
      TGCAACAGG AATGTTCTTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
      CAGCCGTCCT AACCTGATCC TGTGTCCCAT TGTAAAGAGA AGGATGTTGA CGACTGTTGG 2100
      TTCTATTTTA CGTATTTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAA 2160
      CCAGAGTGTC CCACCTGGTC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220
  
```

GTCTCTATTG GCCTTGCACT ACTGCTGATA TGGAGCTTT TAATGATAAT TCATGACAGA 2280  
 AGGGAGTTTG CTAATTTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAAT 2340  
 CCTATTATA AGAGTGCCGT AACAACTGTG GTCATCCGA AGTATGAGGG AAAATGA

5 **A10 Protein sequence:**  
 Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Protein Accession #: NP\_002202.1  
 10 Signal sequence: 1-21  
 Transmembrane domains: 732-754  
 INB domain: 34-464  
 PSI domain: 26-76  
 15 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 20 MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60  
 SARCDLLEAL KKKGCPDDI ENPRGSKDIK KNKNVTNRSK GTAEKLPED ITQIQPQQLV 120  
 LRLRSGEPQT FTLLKPKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180  
 RIGFGSFVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKG VFNELVGKQR 240  
 25 ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVVFSTDA GFHPAGDGKL GGIVLPNDGQ 300  
 CHLENNMYTM SHYDYPSIA HLVOQLSENN IQTIFAVTBE FQPVYKELKN LIPKSAVGTL 360  
 SANSSNVIIQL IIDAYNSLSS EVILENGKLS EGVTSISKSY CRNGVNGTGE NGRKCSNISI 420  
 GDEVQFEISI TSNKCPKPKDS DPFKIRPLGF TEEVEVILQY ICECECQSEG IPESPCKHEG 480  
 NGTFECGACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVCRK 540  
 RDNTNBIYSG KFCECNFNC DRSNGLIOGG NGVCKCRVCE CNPNYTGSA CDSLDTSTCE 600  
 30 ASKQIQCNGR GICECGVCKC TDPKFQQTTC EMCQTCLGVC AEHKECVQCR AFNKGKKDOT 660  
 CTQECSYFNI TKVESRDKLP QVQPDVPVSH CKEKDVEDCW FYFTYSVNGN NBVMVHVVEN 720  
 PECPTGPDI PIVAGVVAGI VLIGLAILLI WKLLMIHDR REFAPKEKEK MNAKWDGTEN 780  
 PIYKSAVTTV VNPKYEGK

35 **A11 DNA SEQUENCE**  
 Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 40 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 45 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTA AGAGAGTGA 60  
 GCTGTGCTT ACACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120  
 CAGCAAAGGT ACACACACCT GGTTCGAATT CAAACACAAAG AAGAGATTGA GTACCTAAAC 180  
 TCATATTGA GCTATTACAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAAATGTG 240  
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300  
 50 GAACCAACA ATAGGCAAAA AGATGAGGAC TGGCTGGAGA TCTACATCAA GAGAGAAAAA 360  
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420  
 GCTGCCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAAT GTGAGCAAAT TGTGAACGTG 540  
 ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGTTTGCA GTCAACCACT GGGAAACTTC 600  
 55 AGCTACAAAT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 ACCATGCACT GATGTCTCTC TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720  
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCCCTGA 780  
 AGCTTCCCAT GSAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840  
 GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 60 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960  
 CCTGTGGAG AGTTCACTCT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020  
 TTGCAGGGAC CAGCCACGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCA 1080  
 GTTTGTGAAG CTTTCAGTGT CACAGCCTTG TOCAACCCCG AGCGAGGCTA CATGAATTGT 1140  
 CTTCCTAGTG CTTCCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200  
 65 GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260  
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320  
 GTGAGGTGTG CTCAATCCCC TATTGGAGAA TTCACTACA AGTCCTCTTG TGCTTCAGC 1380  
 TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA 1440  
 TGGACAGAAG AGGTTCCCTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCCGGGA 1500  
 70 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCTCTG 1560  
 CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620  
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680  
 CTTTCTGCTG CTGGAATCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTGGGAAA 1740  
 TGCTTACGGA AAGCAAAGAA ATTGTGTCCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800  
 75 GGAAGCTACC AAAAGCCTTC TTATATCCTT TAA

80 **A12 Protein sequence:**  
 Gene name: Selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Protein Accession #: NP\_000441  
 Signal sequence: 1-22  
 Transmembrane domains: 555-573  
 C-lectin domain: 23-139

Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
 MIAQSFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKEEIEYLN 60  
 SILSYSPSYW WIGIRKVVNV WVVVGTQKPL TEEARWAPG EPNRQKDED CVEIYIKREK 120  
 DVGWMDERC SKKLLALCYT AACTNTSCSG HGEVETINN YTCKCDPGFS GLKCEQIVNC 180  
 10 TALESPHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
 ECDAVTNPAN GFVECPQNPQ SFPWNTTCTF DCEEGFBLMG AQSLOCTSSG NWDNEKPTCK 300  
 AVTCRAVRQP QNGSVRCSSH PAGEPTFKSS CNFTCEEGFM LQGPQVBECT TQGWTOQIP 360  
 VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEPSCQEQ GFVLKGSXRL QCGPTGENDN 420  
 EKPTCEAVRC DAVHQPPKGL VRCASHPIGE PTYKSSCAPS CEEGFELYGS TQLECTSQGQ 480  
 15 WTEEVPSQCV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPPLWLWRK CLRKAKKFVP ASSCQSLESD 600  
 GSYQKPSYIL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Nucleic Acid Accession #: NM\_001508  
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60  
 CCGAGATTG AGGTGGCCAC CTGGATCAAA ATCACCCCTA TTCTGGTGTA CCTGATCATC 120  
 TTCTGATGG GCCTTCTGGG GAACAGCGCC ACCATTGGG TCACCCAGGT GCTGCAGAAG 180  
 30 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240  
 TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTTGACC 300  
 ACGTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTCC TCTTCGAGGC CTGCAGTAC 360  
 GCTACGCTGC TGCAGTGTCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC 420  
 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTGCTCTGG 480  
 35 GTCACTCCG CTCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTG 540  
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCGG CCAACACGAG 600  
 CAGCCGAGGA CTTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660  
 CAGTCCAGCA TCTTGGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCCTC 720  
 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780  
 40 ACGCGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840  
 ACCATCATCT TCTCAGGCTG GATTGTGTG ACATTGGCGG TATGCTGGAT GCCCAACCGG 900  
 ATTGGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCGGG 960  
 GCGTACATGA TCCTCTCCCT CTTCCTGGAG ACGTTTCTCT ACCTCAGCTC GGTTCATCAAC 1020  
 CCGCTCCTGT ACACGGTGTCT CTGCAGCAGG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC 1080  
 45 TGCCGCTGT CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140  
 ACCACCGACA GCGCCCGCTT TGTGCAGCGC CGGTGTCTCT TCGCGTCCCG GCGCCAGTCC 1200  
 TCTGAAGGA GAACGTGAGG GATTTTCTTA AGCACCTTTC AGAGCGAGGC CGAGCCCGAG 1260  
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC 1320  
 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Protein Accession #: NM\_001508, NP\_001409  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [72-172, 224-344]  
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
 60 Cellular Localization: plasma membrane

65 1 11 21 31 41 51  
 MASPSLPSSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK 60  
 KGYLQKEVTD HNVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLCKL HTPLFEACSY 120  
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVN VTSALVALPL LPAMGTETPL 180  
 VNVPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTVF QSSIFGAFVV YLVVLLSVAF 240  
 70 MCWNMQVLM KSQKSLAGG TRPPQLRKSE SEESRTARRQ TIIIFLRILVV TLAVCWMPNQ 300  
 IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLIYTVSSQQ FRRVFVQVLC 360  
 CRLSLQHANH ERRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTKIFL STPQSEAEPO 420  
 SKSQSLSLES LEPNSGAKPA NSAAENGFOE REV

A1 ProstateA15 DNA sequence

80 Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	GGGGTCCGCG	CACACCTCCC	CGGCGCGCGG	CGGCCACCGC	CGGCACTCCG	CGGCCTCTGC	60
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	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCCGC	CACCTGCTGT	GCTGGCGGGG	GCGCTCCGCG	180
5	CGGGTCGGGG	CCGTGCGCGG	GGGCGCGCAG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCGAGCGCC	CTGTGTGAGA	ACACACCCAC	CTCCTACAAG	TGCTCCTGCA	300
	AGCCTGGCTA	CCAAGGGGAA	GGCAGGCAGT	GTGAGGACAT	CGATGAATGT	GGAAATGAGC	360
	TCAATGGAGG	CTGTGTCCAT	GACTGTTTGA	ATATTCCAGG	CAATTATCGT	TGCACCTGTT	420
10	TTGATGGCTT	CAITGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGGAC	GAGTGCCTGG	480
	AGAACAATGG	CGGCTGCCAG	CATACCTGTG	TCAACGTCTT	GGGGAGCTAT	GAGTGTCTGT	540
	GCAAGGAGGG	GTTTTTCCTG	AGTGACAATC	AGCACACCTG	CATTCAACCG	TGGGAAGAGG	600
	GCCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCAAT	CTGCAAGGAG	GCCCCAAGGG	660
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15	TCTTGACCTG	TAACCATGGG	AAOOGTGGGT	GCCAGCACTC	CTGTGAOGAT	ACAGCOGATG	780
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	AGCGAGAGGA	CACCTGCTCG	GAGGTGACAG	AGAGCAACAG	CACATCAGTG	GTGGATGGGG	900
	ATAAACGGGT	GAAACGGGGG	CTGCTCATGG	AAACGTGTGC	TGTCAACAAT	GGAGGCTGTG	960
	ACCGCACCTG	TAAGGATACT	TGACAGGTG	TCCACTGCAG	TTGTCTGTT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGGAAGACA	TGTAAAGATA	TTGATGAGTG	CCAGACCCCG	AATGGAGGTT	1080
	GTGATCATTT	CTGCAAAAAC	ATCGTGGGCA	GTTTTGACTG	CGGCTGCAAG	AAAGGATTTA	1140
	AATTATTAA	AGATGAGAA	TCCTGCAAG	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACCACAG	CTGCATCAAC	CACCTGGGCA	CATTGTCTTG	TGCTTGCAAC	CGAGGGTACA	1260
	CCCTGTATGG	CTTCAACCC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
25	GTGACAGGTT	CTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGGCAC	CCTGGGTACA	1380
	AGCTCCACTG	GAATAAAAA	GACTGTGTGG	AAGTGAAGGG	GCTCCTGCCC	ACAAGTGTGT	1440
	CACCCCGTGT	GTCCCTGCAC	TGCGGTAAGA	GTGGTGGAGG	AGACGGGTGC	TTCTCAGAT	1500
	GTCACTCTGG	CATTCACTCT	TCTTCAGATG	TCACCACCAT	CAGGACAAGT	GTAACCTTTA	1560
	AGCTAAATGA	AGGCAAGTGT	AGTTTGAAAA	ATGCTGAGCT	GTTCCTCCGAG	GGTCTGCGAC	1620
30	CAGCATACCC	AGAGAAAGCA	AGCTCAGTAA	AAGAGAGCTT	CGCTAAGTGA	AACCTTACAT	1680
	GCAGCTCTGG	CAGCAAGTCT	CCAGGAGCCC	CTGGCCGACC	AAGCACCCCT	AAGGAAATGT	1740
	TTATCACTGT	TGAGTTTGAG	CTTGAACATA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGGGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
	AGGCGGTCCA	CAGGGAGCAG	TTTCACTCTC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
35	AAAGCCCTCC	CAGAAACATC	GAACGCCAGG	CAGAGTCTTG	TGGAGTGGGC	CAGGGTCATG	1980
	CAGAAAACCA	ATGTGTCTGT	TGCAGGGCTG	GGACCTATTA	TGATGGAGCA	CGAGAACGCT	2040
	GCATTTTATG	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATTC	GGGGCCCTGA	AGACCCGAGA	AGCTTGGAA	ATGCTGGAAT	2160
	GTGGAGGTCT	GTGTCAACCT	GGTGAATATT	CTGCAGATGG	CTTTGCACCT	TGCCAGCTCT	2220
40	GTGCCCTGGG	CAGTTCCAG	CCTGAAGCTG	GTGGAACCTC	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGCCAC	CAAAATCTAG	GGAGCTACTT	CCTTTCAGGA	CTGTGAACCC	AGAGTTCAT	2340
	GTTCACCTGG	ACATTTCTAC	AACACCAACA	CTCACCGATG	TATTGTTGTC	CCAGTGGGAA	2400
	CATACAGAGC	TGAATTTTGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAAT	ACTACGACTG	2460
	ACTTTGATGG	CTCCACAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	2520
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	AGTGTACGTG	GACCATCAAC	CCACCCCCCA	AGCGCCGCAT	CCTGATCGTG	GTCCCTGAGA	2640
	TCITCTCTGC	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
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	CCAGGTCAAA	GAGCTGTGG	ATTCAATTCA	AGTCCAATGA	AGGGAACAGC	GCTAGAGGGT	2820
50	TCCAGTCTCC	ATAGTGACA	TATGATGAGG	ACTACCAGGA	ACTCATTTGA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAAC	ATCAGGAAAT	ACTTAAGGAT	AAGAACTTAA	2940
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	AGTCCCGAGA	GATGTTTCCA	AGATCGTTCA	TCCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
	TTTTGAGACC	TTACAAATGA	CTCAGCCAC	GTGCCATCA	ATACAAATGT	TCTGTATAG	3120
55	GGTGTGTGGG	ACAGAGCTGT	CTTCTTCTG	CATGTCAGCA	CAGTCGGGTA	TTGCTGCCCT	3180
	CCGTATCAGT	GACTCATTAG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
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	AGTTCTAAGC	AGTGTCTGTG	AAAAAAGGAA	GCAGAAAGAA	TTAGAAATTA	ATAAAACTTA	3720
65	AGCACTTCTG	GAGACAT					

Al6 Protein sequence

Gene name: CEGP1  
 Unigene number: Hs.222399  
 ProbeSet Accession #: AA256485  
 Protein Accession #: CAB92285  
 Signal sequence: 1-31  
 Transmembrane domains: none  
 PFAM domains: EGF-like\_domains [49-84,132-167,177-213,286-321,407-442]  
 CUB\_domain [809-918]  
 Cellular Localization: may be secreted

	1	11	21	31	41	51	
80	MGVAGRNRP	AAAVLLLLL	LLPPLLLLAG	AVPPGRGAA	GPQEDVDECA	QGLDDCHADA	60
	LQNTPTSYK	CSCKPGYQGE	GRQCEIDEC	GNEINGGCVH	DCLNIPGNR	CTCFDGMFLA	120
	HDGHNCLD	ECLNNGGCG	HTCVNMGSY	ECCCKEGPFL	SDNQHTCIHR	SEEGLSQWAK	180
	DBGCSHLC	APRGSVACBC	RPGFELARNQ	RDCILTCHNG	NGGQHSDD	TADGPECSCH	240
	PQYKMTDGR	SCLEREDTVL	EVTSNTTSV	VDGDKRVKRR	LLMETCAVNN	GGCDRTCKDT	300

5 STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCRN IVGSFDCGCK KGFKLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGPTH CGDTNECSIN NGGQQQVCVN 420  
 TVGSYECQCH PGYKHLHNNKC DCVEVKQLLP TSVSPRVSLH CGKSGGSDGC FLRCHSGIHL 480  
 SSDVTTIRTS VTFKLNVEGKC SLKNAELPPE GLRPALPEKH SSVKBSFRYV NLTCSGKQV 540  
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCOLSCIVKR TEKRLRKAIR TLRKAVHREQ 600  
 FHLQLSGMNL DVAKKPPPTS ERQAESCQVQ QGHAENQCVS CRAGTYDGA RERCILCPNG 660  
 TFQNEEGQMT CBPCPPRGNS GALKTPAWN MSECGGLQCP GEYSADGPAP CQLCALGTTFQ 720  
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSGPHFY NTTTHRCIRC PVGTYPQPEFG 780  
 10 KNNCVSCPGN TTDFDGSSTN ITQCKNRRCG GELGDFGTGI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRILIV VPEIFLPIED DOGDYLVMRK TSSSNSVTYI ETCQTYERPI APTSRSKKLW 900  
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# 15 Al7 DNA sequence

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

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5 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACACG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCAAGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCCT AGGTGATGAA GACAGCCOGA 1620  
 10 TOCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAAOCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800  
 AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 TTGCCTCAGC TTCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACC CAACTAATT 1920  
 TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAATGA TGTGCTGCT TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC 2040  
 AGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 15 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTG 2160  
 ACGAGATAAG CAGTTATGTG ACCTCAOGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 GCACCAAGCC AGAAGTGAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCAAGAA 2280  
 CCAAAACCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCTAT TTTCTATGAT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400  
 20 TTGTCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAAA

**A20 Protein sequence:**

25 Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AIS38613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 30 Tryp\_SPC domain: 216-444  
 Cellular Localization: not determined

35 1 11 21 31 41 51  
 | | | | |  
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFFP IIVIGIIALI 60  
 LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF 120  
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQPREFV SIDHLLPDDK 180  
 VTALHSHVYV REGCASGHVY TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240  
 40 LCGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNESE NFPDGVKVCNT SGWGATEDGA GDASPVLNHA 360  
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQCQD SGGPLVCQER RLWKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

**A21 DNA SEQUENCE**

45 Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Nucleic Acid Accession #: AA428090  
 Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 | | | | |  
 ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAAT AGACCAAAGG 60  
 55 CAAGTTGTTG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC 120  
 TTTTCAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAACCGT 180  
 GATTCTGTTG GCGTTCTCTG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240  
 GGAAGAAACA CTAACCTCAG CCATTTGCCC AATTTCCACC TTGCTAGTTA TCAGAGTTCA 300  
 CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGGAAAT TATTCTGAGC 360  
 60 AAGTGTTTTG TTCAGCTTGC AGTATTAAAA CAAAAAAAC ATTGCCTCCA GCTGCAAGC 420  
 AAGGGCATTG CCATTATGAA AGCCCTCAA AGACTCTCTG CTATTTTCAA AACATGGAAA 480  
 GAAAAAGGGA AAAAAAGAAA AAAAAATAATA AITAGAAGGA TTTGTTCCCT AATTGGGCT 540  
 CCAAAAAATC AGAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAACCTCTC 600  
 CAAGCAATC TTTCTGAAGCA ATCAATTATT TATATACCTT ATGTTCTGTC TTTTGTATT 660  
 65 TTTCTCTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCTTTCTCT ATCTGGATCT 720  
 GTTCTGCTCT ATTTCTCTTT CAAAGTCATC TTTTCAGGGA CTTGCCCTGA TTAATTGAT 780  
 TTTAACCAAA CAAATAAGAT ATTTGATATA TTAATTTAAA CTTTTGTAGA TGATTGATTA 840  
 GGAATTGCAT CATGTTTACA TGAGTATACC GAATTCAAAG TTAACCTTCA TAAGCAGGAG 900  
 TTTTACACA TCGTAACATA ATCATTACCC AATACTCGAC ACTCAATATT TGATACTCAA 960  
 70 CTGAATGTTT TTGAATAAAA CACATTTTFA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020  
 CTTTTTACAC AAAATATATC AGTGAGAGAG TGTTTGTTTA AGAAAAAAA TCAAGCACA 1080  
 ACAAGTTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTGTAGA ATGGTGATT 1140  
 GATTTCACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200  
 TATATATATA TATATATATA TATATTACAA TGATCTGTAT TTCTATTGCT TAGAAGGATG 1260  
 75 AAAGTGAATC CATATAAACC ATACCAACGC CGTTATGTGT AACTGGTGGT AAAACTTTAT 1320  
 TATTCAAGTT TAGATGTAAAC AGACATCTTT GCTGCCTGAA GATTGTTTGC ATAAGAAATA 1380  
 CACCAAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAAAAAATA ATAAATAAAA 1440  
 ACGAAAAAAT TTCATGTGTT GTAAGAACAG AACTATTATA GCCAACATTC TAGTATTCAA 1500  
 ATCAGGACTA CAAATGTAAT TCTTTTCTCT AGCAACATGA AATCATTCCA TATGAAAGAC 1560  
 80 ATTTTCTGCT GGTGAATATT GCTGTAAGTT AAATTTTACA TTGGCATTTC GAGATGTTCC 1620  
 CCCCTCATGC CTCGCCCAAA GTTTTCCATG TGGTTGTCAA ATAGTCCGC

**A22 Protein sequence:**

Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 113-129  
 Cellular Localization: not determined

10 1 11 21 31 41 51  
 MKPSLKHWD IKMFSEIDQR QVVGEEIHLQ VVSYSYLVEN FSDTDDLSI VEESDSCYNR 60  
 DSVGLPGRAG DRLQPKTKPR GKTINLSHLP NFHLASYQSS LLFLKQSY YGNLIVEPILS 120  
 15 KCFVQLAVLK QKKHCLQLQS KGIAIMKAPQ RLSAIPKTNK EKGKKEKII IRRICSLIWA 180  
 PKNEK

## A23 DNA SEQUENCE

20 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Nucleic Acid Accession #: AL133619  
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCGAC CCCGGGCTCT 60  
 CGGCGCCGCG GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCGCA GAGCCGCGAG 120  
 30 CTCAGGCGAGA GCGACCGCA GAAACGGAAC CTGGAACCTG AGAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAA GCTCCATGAG AGATCGAGCA TCTGAAGCGG 240  
 GAAACAAAGG GTAGCGCGG GCGGGGCCCT AGGCGGGCCC TGCCCTCCCA GGCACACTCA 300  
 ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360  
 GGGGAACAC AGGACGGGGA GCCCCTCCAG ACTGTCTTGG CCCACCTGGC TGCACTGGCC 420  
 CCTGTATGCC AAGCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480  
 35 AGCCGTGGCT GACGATGTT ATGCAGCCAA GCACAGCAGG TGCTGCTCTC GGGAGGCCCA 540  
 GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGCT GCTCCCCAGA CCTCCCTCCT 600  
 CCAAGTAGAG CTGAATGGG AAGGAACCCC TGGGACAGCC CTGCGCCTGC TAGATCTTTG 660  
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCCCTAC 720  
 40 ATGCTGGGGG CCCAGGGGAT ATGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACCA TGGGACAAA GGGAGGAAGC AGAGTCTGT TCCCTTGCCA CTGTCCAG 840  
 GCACCTCCCC ATCTGCAGC CGGCCCCAC CCAGCCCAGG ATCTGGGCT GTGGTCTCAA 900  
 GCTCACTCC CATTATCTTT GGGGCTGGG CTGACATCAG GAGGACATCT GACTGGTGA 960  
 TGGAGCCAGC CTGGGAACAT GCGAGCTGGG GCAGTGCTA GGGCTCTCCC TTCCAGGGA 1020  
 45 GACATGGAGA AGGGGGTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080  
 CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCACTGC TGGGAGCGCT 1140  
 GACAGACAC GGAAGAGGC CATGCTTTCC CTCGGGACCT GCTGTTCAT GTGTCCCAAG 1200  
 CCCTCTGTCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCCTC TGCTCCCTTG 1260  
 GCGCTCGCT SGGCTGTGAT CAACGAGTG TGGGTAGAGC CGGAGGAGCC CAGCCCTGCC 1320  
 50 AGGCTGAAGG AGGGCTCCTC ACAGCACAC AGGCCAGGAG GCAAGCGTGG GGGTCTTGG 1380  
 GCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440  
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGCC 1500  
 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCAGGA AGGCGGACCT GGAAGAGGAG 1560  
 55 CCCTACTTTC ACACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGCCA GGCCAGAAAG 1620  
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680  
 AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCTTGC CCCTTCCCTC GCGAAAGCCC 1740  
 ACCACTTA GGCAGTGCGA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCTGCGAG 1800  
 ACCCAAGAGC TGCGGCACTT CAACTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCGACC 1860  
 CCGGAGGAG CTAGCTTTCC CAGGGACCAA GAAGCCAGC ATTTCCCAA GGTCTCCACC 1920  
 60 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980  
 CTGAAGCAGA CCCGGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCA 2040  
 AAACGGCGCC TGCACTGCTC AGTGCTTTGA

## A24 Protein sequence:

65 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Protein Accession #: T43457  
 Signal sequence: none found  
 Transmembrane domains: 303-322  
 Cellular Localization: not determined

75 1 11 21 31 41 51  
 MSGAGVAAGT RPPSSPTPGS RRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60  
 QQQHEMLAK LHEEIEHLKR ENKGEFARGP RPALPFQAH S TLPLQHRNT AINSSTRIGS 120  
 GGTQDGEPLQ TVLAHLAALA FVQPSGYRF WGTWTDAA S SRGWTMLCSQ AQHVLLSGSP 180  
 GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSPPCARSL PQIAAVARPR ISSPMALSPH 240  
 80 MLGAQGIWTH SIQGSPLAIW AATMGTGKGS RVLFPCHLSK ALPHFDSGPH PAQDPGLWSQ 300  
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGGP PPSRCGNSS 360  
 LFWAKGSPR QPOPCSAGDA DRTREBAMLS LGTCCSMCPK PSCFPDGPSP NHLRASAPL 420  
 GARWVCINGV WVEPGGPSPA RLKEGSSRTH RPPGKRGRLA GGSADTVRSP ADSLSMSSFQ 480  
 SVKSIGNSAN SQGRARPQPG SPFNKQDSKAD VSQKADLEES PLLHNSKLDK VPGVQQQARK 540



EKAESNAGA ACMGNSQHQG ROMGAGARPP MILPLPLRKP TTLROCEVLI RELWNTNLLQ 600  
 TQELHRLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660  
 LKQTPKNNFA ERQKRLQAMQ KRRLHRSVL

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A25 DNA SEQUENCE

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Nucleic Acid Accession #: NM\_000949  
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

10

1 11 21 31 41 51  
 15 GGAGGCTGAA ATCCCCAGAC GCGGGTTTTC TGGGCTGGGC TTCTGCTTA CTCACCTCTT 60  
 CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTTCACACA ATGGAGCTTC 120  
 ATGTCTCTGT GCAGGAAGTA CTCATGACTT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180  
 TAAAGAACTC TCCTATTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAAACCTGAA 240  
 20 GTGAACTTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300  
 CATCTGCAAC CGTTTCTACT CTGCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT 360  
 TACCTCCTGG AAAACCTGAG ATCTTTAAAT GTGTTCTCC CAATAAGGAA ACATTACCTT 420  
 GCTGGTGGAG GCGCTGGGACA GATGGAGGAC TTCTACCAA TTATTCACTG ACTTACCACA 480  
 GGGAAAGGAG GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCAATCTCT 540  
 25 GCCACTTTGG CAGACAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600  
 CTAACACAGT GGAAGACAGT TTCTGGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660  
 AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAACAA GCCAGAGAGC AGAAAACCTT 720  
 ACCTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAAGTGGT TGGTTACCGC 780  
 TCCTGTATGA AATTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTGCTG 840  
 30 GGCAGCAAAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTGTGCCAGG 900  
 TTGCTGCAAC ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTCAGA 960  
 TACCTAGTGA CTTACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCCTTCTG 1020  
 CTGTCTCTG TTTGATTATT GTCTGGGCAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080  
 GCATCTTTCC GCCAGTTCTT GGGCCAAAAA TAAAGGATG TGATGCTCAT CTGTGGGAGA 1140  
 35 AGGGCAAGTC TGAAGAACTA CTGAGTGCCT TGGGATGCCA AGACTTTCTT CCCACTTCTG 1200  
 ACTATGAGGA CTGTCTGGTG GAGTATTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260  
 TGTCAGTCCA TTCAAAGAA CACCCAGTC AAGGTATGAA ACCCAATAC CTGGATCCTG 1320  
 ACACTGCATC AGGCGGGGGG AGCTGTGACA GCGCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380  
 AACCCAGGCG CAATCCCTCC ACATTCATAT ATCTGAGGT CATTGAGAAG CCAGAGAATC 1440  
 40 CTGAAACAAAC CCACACCTGG GACCCCACTG GCATAAGCAT GGAAGGCCAA ATCCCTTATT 1500  
 TTCATGCTGG TGGATCCAAA TGTTCAACAT GGCCCTTACC ACAGCCGAGC CAGCACAAAC 1560  
 CCAGATCTCT TACACCAAT ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG 1620  
 CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA 1680  
 AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAGCTTC CATTTCTGAGA 1740  
 45 CTGACCAGGA TAGCCCTCTG CTGCTGCCCC AGGAGAAAC CCCCTTTGGC TCCGCTAAAC 1800  
 CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAGATGG TGCATTATCA TTGCTACCAA 1860  
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920  
 ATGCCAAGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGGTGCCA GATCCACATG 1980  
 CTAATAAGCT GGCTTCTTT GAAGAATCAG CCAAGAGGC CCCACCATCA CTTGAACAGA 2040  
 50 ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100  
 TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCTTTTAC TGATAGCTTG 2160  
 ACTAATGAAA TGATTGGTTA AAATGTGATT TTTCTTCAGS TAACACTACA GAGTACGTGA 2220  
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAGCTC CCAGCTCCTT TCATGCTCCA 2280  
 TTTTAAACCA CTGCGCTCTT TCTCCAGCAG CTGATTCAG AACAAATCAT TATGTTTCTT 2340  
 55 AACTGTGATT TGTAGATTTA CTTTGTCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400  
 AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAG 2460  
 GCTTTTCATG TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATGTG TTACCATAGA 2520  
 AAGATGACAA AAGAAAATT TCCACATAGG AAAATGCCAT GAAAATGTCT TTTGAAAAC 2580  
 AACTGCATAA CCTTACACT CCTGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT 2640  
 60 AAAGAAAGAA TGCAATCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700  
 TTGCTGATAT GCAAGTAAGA AAT

A26 Protein sequence:

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Protein Accession #: NP\_000940  
 Signal sequence: 1-23  
 Transmembrane domains: 237-253  
 FN3 domains: 28-112, 127-215  
 Cellular Localization: plasma membrane

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1 11 21 31 41 51  
 MKENVASATV FTLLPLPNTC LLNGQLPPGK PEIPKCRSPN KETFTCWWRP GTDGGGLPTNY 60  
 SLTYHREGT LMHECPDYIT GGFNSCHFGR QYTSWRTYI MMVNATQMG SSFSDLYVD 120  
 VTIIVQDPFP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYBI RLKPEKAAEW 180  
 EIHFAQQOTE FKILSLHPGQ KYLVQVRCKP DRGVWSANSP ATFIQIPSDP TMNDTTVWIS 240  
 VAVLSAVICL IIVVAVALKG YSMVTCIFPP VPGPKIKGPD AHLLEKKGSE ELLSALGQCD 300  
 FPPTSDYEDL LVEYLEVDDS EDQHLMSVHS KEHPSQGMKP TYLDPDSTDG RGSCDSPSL 360  
 SEKCEEPQAN PSTPYDPEVI EKPENPETH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420

PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQOREVE 480  
 SFHSETDQDT PWLLPQEKTP FGSAPLDYV BIHKVNDGA LSLLPKQREN SGKPKKPGTP 540  
 ENNKEYARVS GVMDNNILVL VPDPHAKNVA CFESAKEAP PSLEQNQAEK ALANFTATSS 600  
 KCRLQLGLD YLDPACFTHS FH

**A27 DNA SEQUENCE**

Gene name: Human neurotrophin Y receptor Y1 (NPYY1)  
 Unigene number: Hs.169266  
 Probeset Accession #: L07615  
 Nucleic Acid Accession #: NM\_000909.1  
 Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAA GACAAATTCC AAAGAGGATT 60  
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATTC CAATATCGGG 120  
 AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTTAAA 180  
 ATAATCTATA ACAACCAAC CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTTGAAAA 240  
 TCATTGATC CACTCTAATT TCTCAGAGAA GAATGCCGAG CTTCCTGGCT TTGAAAATGA 300  
 TGATTGTCT CATGCCCTTGG CCATGATATT TACCTTAGCT CTTCCTTATG GAGCTGTGAT 360  
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420  
 GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480  
 CATGTGTCTC CCCTTTACAT TTGCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540  
 GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTTCAATC ACTGTGTCCA TTTTCTCTCT 600  
 GGTCTCTCAT GCTGTGGAA GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660  
 TAATAGACAT GCATTATGAT GTATTGCTGT GATTGGGTC CTTCCTGTGG CTTCCTCTTT 720  
 GCCTTTCTCT ATCTACCAAG TAATGACTGA TGAGCCGCTC CAAATGTAA CACTTGTATG 780  
 GTACAAAGAC AATATCGTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTTAA 840  
 TACCACTCTC CTCTTGGTGC TGCAGTATT TGGTCCACTT TGTTTTATAT TTATTGTCTA 900  
 CTTCAGATA TATATACGCC TAAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960  
 TAAGTACAGG TCAGTGAAG CAAAAGAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020  
 ATTTGCACTG TGCTGGCTCC CTCTTACCAT CTTTAACACT GTGTTTGATT GGAATCATCA 1080  
 GATCATTTGT ACCCTGCAAC ACAATCTGTT ATTCTGCTC TGCCCACTCA CAGCAATGAT 1140  
 ATCCACTTGT GTCAACCCCA TATTTATGG GTTCCTGAAC AAAAAGTCC AGAGAGACTT 1200  
 GCAGTTCTTC TTCAACTTTT GTGATTTCGG GTCTCGGGAT GATGATTATG AAACAATAGC 1260  
 CATGTCCACG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC 1320  
 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT 1380  
 GTGCCCGAT ACCTGCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440  
 TCTCCCAAGG AATGGGGTGT AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500  
 TTACTGCTTT TGTGTAGTT GTCATTAATA CATTTGGAAC AAAAGGTGTG GGCCTTGGGG 1560  
 TCTTCTGGAA ATAGTTTGA CCAGACATCT TTGAAGTGCT TTTTGTGAAT TTATGCATAT 1620  
 AATATAAAGA CTTTATATCT GTACTTATG GAATGAAATT TCTTTAAAGT ATTACGATGC 1680  
 GCTGACTTGT GAAGTACCTG CCATCCAATA CGGTCTTATG ATTGGGTCTT CTGATTAGA 1740  
 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800  
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTG AGGAGCGGAA AGATAGTCTT 1860  
 GAAGTCATC AGAAGTGGTT TGAGGTTTCT GTTTTGTGGT GGTTTTGTGT TGTTTTGT 1920  
 TTTTTCACG TTAAGGGAGG CTTTCATTTC CTCCGACTG ATTGTCACTT AAATCAAAAT 1980  
 TTAATAATGA ATAAAGAGC ATACTTCTCA GCTGCAATA TTATGGAGAA TTGGGCACCC 2040  
 ACAGGAATGA AGAGAGAAAG CAGCTCCCA ACTTCAAAAC CATTTTGGTA CCTGACAACA 2100  
 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160  
 TATATTATT TGAATTGATG GTCAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAAGTG 2220  
 TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280  
 ACAAAATGCG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAAC TTTCAATGTC 2340  
 CATCTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTAC TTTACCTAGC 2400  
 AGGAAAAAT ACACAAAAC TGCAGTACT TCATATAGCC CATTTTAACT TGTATAAAT 2460  
 GTGTGACTTG TGGCGTCTA TAAATAATGC ACTGTAAAGA TTACTGAATA GTTGTGTCAT 2520  
 GTTAATGTGC CTAATTTCAT GTATCTTGT ATCATGATTG AGCCTCAGAA TCATTGGAG 2580  
 AAATATATT TAAAGAACCA AGACATACTT CAATGTATTA TACAGATAAA GTATTGATG 2640  
 TGTTTGATT TAAAGGGCG GACATTTTAT TAAATCAAT ATTGTTTGT CTTTCTCTGA 2700  
 GGAGTCTCT TCAATTTCT TTTTCTCAT CCTTGACTT CCTCCGATG GT

**A28 Protein sequence:**

Gene name: Human neurotrophin Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds  
 Unigene number: Hs.169266  
 Probeset Accession #: L07615  
 Protein Accession #: NP\_000909.1  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [57-91]  
 Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286, 300-322  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MNSTLFSQVE NHSVSNPSE KNAQLLAFEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA 60  
 LIIIIILKQRE MRNVNIIIV NLSFSDLLVA IMCLPFTFVY TLMDEWVFE AMCKLATPPVQ 120  
 CVSITVSIPS LVLIIVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180  
 DEPFQNVITLD AYKDKYVCFD QPFSDSHRLS YTTLLLVLYQ FGPLCFIFIC YFKIYIRLKR 240  
 RNNMMDKMDR NKYSRSETKR INIMLLSIVV APAVCWLPIT IFNTVFDNNH QIIATCNHNL 300  
 LFLCHLTLAM ISTCVNPIFY GFLNKNFQRD LQFFNFCDP RSRDDDYETI AMSTMTDVS 360

KTSLLKQASPV AFKKINNND NEKI

5 A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM\_032551.1

10 Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCACACCG TGCTACGTC CGGACCCCAAC GGTCTCTGGG GGGCACCGGC CAAAGCCTCC 60
GGCTGCCCGG GCTGTGGGCG CAACGCTCG GACGGCCAG TCCCTTCGCC GGGGGCCGTG 120
15 GAGGCTGGC TCGTGCCGCT CTTCTTCGCG GCGCTGATGC TGCTGGGCTT GGTGGGGAAC 180
TCGCTGGTCA TCTACGTCAT CTGCCGCCAC AAGCGATGC GGACCGTGAC CAACTTCTAC 240
ATGCCCAACC TGGCGGCCAC GGAAGTGACC TTCTCTCTGT GCTGCGTCCC CTTACGGGCC 300
CTGCTGTACC CGTGCCTCCG CTGGGTGCTG GCGACTTCA TGTGCAAGTT CGTCAACTAC 360
20 ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CGCCATGAG TGTGGACCGC 420
TGTAAGCTGA CGGTGTTCCT GTTGCCTGCC CTGACCGGCC GCACGCCCGC CCGTGGCGCTG 480
GCTGTGAGCC TCAGCATCTG GTTAGGCTCT GCGCGGCTGT CTGCGCCGGT GCTCGCCCTG 540
CACCGCCTGT CACCGGGGCC GCGCGCTTAC TGCACTGAGG CCTTCCCGAG CCGCGCCCTG 600
GAGCGCGCCT TCGACTGTGA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC 660
25 TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGGTGCG CCGCGCGCCC 720
GCCGATAGCG CCGTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCGGT GGGGGCCAAAG 780
GTCTCGCGCG TGTGTGGCGC GGTGGTCTCT CTCTTCGCGC CTGCTGGGG CCGCATCCAG 840
CTGTTCTCTG TGTGTGAGCG GCTGGGCCCC GCGGCTCTCT GGCACCCAGC CAGCTACGCC 900
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCGC GCTGAACCCG 960
30 CTGCTCTAGC CCTTCTCTGG CTCGCACTTC CGACAGGCGT TCCGCGCGGT CTGCCCCCTG 1020
GCGCGCGCGC CCGCGCGCGC CCGCGAGCCT CGGACCCCGC AGCCCCACAC 1080
GCGGAGCTGC ACCGCTGCG GTCCCAACCG GCGCGCGCA GGGCGCAGAA GCCAGGGAGC 1140
AGTGGGCTGG CCGCGCGCGG GCTGTGCTG CTGGGGGAGG ACAAGCCCC TCTCTGA

```

35 A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

40 Pfam domains: 7tm\_1 [59-323]

Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization: plasma membrane

```

45 1      11      21      31      41      51
|      |      |      |      |      |
MHTVATSGPN ASWGAPANAS GCPGCGANAS DGFVPSRAV DAWLVPLFFA ALMLLGLVGN 60
SLVIYVICRH KPMRTVINFY IANLAATDVT FLLCCVPFTA LLYPLPGWVL GDFMCKPFVNY 120
50 IQQVSVQATC ATLTAMSVDR WYVTVPPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
HRLSPGPRAY CSEAPPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
ADSALQGQVL AERAGAVRAK VSRLVAAVVL LFAACWGPIQ LFLVLQALGP AGSWHPRSVA 300
AYALKTWAEC MSYSNSALNP LLYAFLGSHF RQAFRRVPCP APRRRPRPRR PGPSDPAAPH 360
AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL

```

55 A31 DNA SEQUENCE

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM\_014246

60 Nucleic Acid Accession #: NM\_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

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65 1      11      21      31      41      51
|      |      |      |      |      |
ATGGCGCGCG CGCGCGCGCC CGTGTCTGCC GTGCTGCTGC TCCTGGCCGC CGCGCGCGCC 60
CTGCGCGCGA TGGGGCTGCG AGCGGCGCGC TGGGAGCGCG GCGTACCGCG CGGGAACCGC 120
GCCTTCGCCC TCCGGCCCGG CTGTACCTAC GCGGTGGGCG CCGCTTGACG GCCCGGGCGC 180
CGCGGGGAGC TGCTGGAAGT GGGCCGCGAT GGGCGGCTGG CAGGACGTGG GCGGTCTCTG 240
70 GCGCGGGGCG GCCCGCTGCC GCTGCAAGTC CGCTTGGTGG CCGGAGTGGC CCGGAGCGCG 300
CTGAGCGCGC GCTTGGGGGC GCGCACGAC CTTCCCGGCT GCGGAGCCCG TGCCCGGCTC 360
TGCGGAACCG GTGCGCGGCT CTGCGGGGCG CTCTGCTTCC CCGTCCCGCG CGGCTGCGCG 420
GCGCGCGAGC ATTGCGGCT GCGAGCTCCG ACCACCTTAC CGGCTGCGCG CCGCGCGCGC 480
CGCCCCAGGC CCGCGTGTCC CGGCGTTCCT ATCTGCTTCC CGCGGCGCG CTGCGTCCGC 540
75 CTGCGTCTGC TGTGCGCCCT GCGGCGCGCG GCTGGGCGCG TCGGGTGGG ACTGGGCTG 600
GAGGCGCGCA CCGGGGGGAC GCCCTCCGCG TCGCATCCC CATCGCCGCC CCGCGCGCG 660
AACTTGCCCG AAGCCCGGCG GGGGCGGCG GCGCGGCGCC GCGGCGGCG GAGCGGCGA 720
GGGAGCTCTG AGTTTCCGAT GCCCACTAC CAGGTGGGTT TGTTTGAGAA CGAACCGCG 780
80 GGCACCTTCA TCCTCCAGCT GCACGCGCAC TACACCATG AGGGCGAGGA GAGCGCGTG 840
AGCTATTACA TGGAGGGGCT GTTCGACGAG CGTCCCGGG GCTACTTCCG AATCGACTCT 900
GCCACGGCG GCGGAGCGTA GGACAGCGTA CTGGACCGCG AGACCAAGGA GAGCACGTC 960
CTCAGGGTGA AAGCGGTGGA CTACAGTACG CCGCGCGCT CGGCCACCA CTACATCACT 1020
GTCTTGTGTA AAGACACCAA CGACCAAGC CGGTCTTCC AGCAGTGGGA GTACCGCGAG 1080
CGCGTGCGGG AGAACCTGGA GGTGGGCTAC GAGGTGCTGA CCATCGCGCG CAGCGACCGC 1140

```

	GACTGCCCCA	TCAAAGCCAA	CTTGCGTTAC	CGCGTGTGG	GGGGCGCGTG	GGACGTCTTC	1200
	CAGCTCAACG	AGAGCTCTGG	CGTGGTGAGC	ACACGGGGCG	TGCTGGACCG	GGAGGAGGCG	1260
	GCGAGTACC	AGCTCCTGTT	GGAGGCCAAC	GACCAAGGGC	GCAATCCGGG	CCCGCTCAGT	1320
5	GCCACGGCCA	CCGTGTACAT	CGAGGTGGAG	GACGAGAACG	ACAACCTACC	CCAGTTTCAG	1380
	GAGCAGAACT	ACGTGTTCCA	GGTGCCCGAG	GACGTGGGGC	TCAACACGGC	TGTGCTGCGA	1440
	GTGCAGGCCA	CGGACCCGGA	CCAGGGGCCAG	AACCGGGCCA	TTACTACAG	CATCCTCAGC	1500
	GGGAACGTGG	CCGGCCAGTT	CTACCTGCAC	TGCTGAGCG	GGATCCTGGA	TGTGATCAAC	1560
	CCCTTGGAAT	TGAGGATGT	CCAGAAATAC	TGCTGAGCA	TTAAGGCCCA	GGATGGGGGC	1620
10	CGGCCCCCGC	TCATCAATTC	TTCAGGGGTG	GTGTCTGTGC	AGGTGCTGGA	TGTCAACGAC	1680
	AACGAGCCTA	TCITTTGTAG	CAGCCCCCTC	CAGGCCACGG	TGCTGGAGAA	TGTGCCCTCG	1740
	GGCTACCCCG	TGTTGACAT	TCAGGCGGTG	GACGCGGACT	CTGGAGAGAA	CGCCCGGCTG	1800
	CACATATCGC	TGGTGGACAC	GGCCTCCACC	TTTCTGGGGG	GCGGCAGCGC	TGGGCTTAAG	1860
	AATCCTGCCC	CCACCCCTGA	CTTCCCTTTC	CAGATCCACA	ACAGCTCCGG	TTGGATCACA	1920
15	GTGTGTGCGG	AGCTGGACCG	CGAGGAGGTG	GAGCACTACA	GCTTCGGGGT	GGAGGCGGTG	1980
	GACCACGGCT	CGCCCCCAT	GAGCTCCTCC	ACCAAGCGTT	CCATCACGGT	GCTGGAGCTG	2040
	AATGACAAAG	ACCGGCTGTT	CACGACGCCC	ACCTACGAGC	TTGCTGTGAA	TGAGGATGCG	2100
	GCGGTGGGGA	GCAGCGTGCT	GACCTGCAG	GCCCGCGACC	GTGACGCCAA	CAGTGTGATT	2160
	ACCTACCAAG	TCACAGGCGG	CAACACCCGG	AACCGCTTTG	CACCTCAGCAG	CCAGAGAGGG	2220
20	GGGGGCTCTA	TCACCTTGGC	GCTACCTCTG	GACTACAAGC	AGGAGCAGCA	GTACGTGCTG	2280
	GCGGTGACAG	CATCCGACGG	CACACGGTCG	CACACTGCGC	ATGTCCTAAT	CAACGTCACT	2340
	GATGCCAACCA	CCCAACAGGC	TGCTTTTCAG	AGCTCCCAAT	ACACAGTGAG	TGTCACTGAG	2400
	GACAGGCTCG	TGGGCACCTC	CATTGCTACC	CTCAGTGCCA	ACGATGAGGA	CACAGAGAG	2460
	AATGCCCGCA	TCACCTAAGT	GATTCAAGAC	CCCGTGCCCG	AGTTCCCGCAT	TGACCCCGAC	2520
25	AGTGGCACCA	TGTACACCAT	GATGGAGCTG	GACTATGAGA	ACCAGGTGCG	CTACACGCTG	2580
	ACCATCATGG	CCAGGACCAA	CGGCATCCCG	CAGAAATCAG	ACACCAACCAC	CCTAGAGATC	2640
	CTCATCTCGG	ATGCCAATGA	CAATGCACCC	CAGTTCCCTG	GGGATTCTTA	CCAGGGTTCC	2700
	ATCTTTGAGG	ATGCTCCACC	CTGACCCAGC	ATCTCCAGG	TCTCTGCCAC	GGACCGGGAC	2760
	TCAGGTCCCA	ATGGGCGTCT	GCTGTACACC	TTCCAGGGTG	GGGACGACGG	CGATGGGGAC	2820
30	TTCTACATCG	AGCCCCAGTC	CGTGTGTGAT	CGCACCCAGC	GCCGCTGGA	CCGGGAGAA	2880
	GTGGCCCGTG	ACAAACCTTT	GGCTCTGGCT	GTGGATCGGG	GCAGTCCAC	TCCCTTAGC	2940
	GCCTCGGTAG	AAATCCAGGT	GACCATCTTG	GACATTAATG	ACAATGCCCC	CATGTTTGAG	3000
	AAGGACGAAC	TGGAGCTGTT	TGTTGAGGAG	AACAACCCAG	TGGGTTCGGT	GGTGCAAAAG	3060
	ATTGCTGCTA	ACGACCCCTG	TGAAGGCCCT	AATGCCCCAGA	TCATGTATCA	GATTGTGGAA	3120
35	GGGACATGCG	GGCATTTCTT	CCAGCTGGAC	CTGCTCAACG	GGGACCTGCG	TGCCATGGTG	3180
	GAGCTGGACT	TTGAGGTCCG	GCGGGAGTAT	GTGCTGTGGG	TGCAGGCCAC	GTGCGCTCCG	3240
	CTGGTGAGCC	GAGCCACGGT	GCACATCCTT	CTGTGGGACC	AGAATGACAA	CCCGCTGTG	3300
	CTGCCGACT	TCCAGATCCT	CTTCAACAA	TATGTACCCA	ACAAGTCCAA	CAGTTTCCCC	3360
	ACCGGCGTGA	TCGGCTGCAT	CCCGGCCCAT	GACCCGACCG	TGTGAGACAG	CCTCAACTAC	3420
40	ACCTTGTGTC	AGGGCAACGA	GCTGCGCCTG	TTGCTGTGCG	ACCCCGCCAC	GGGGAACTG	3480
	CAGCTCAGCC	GCGACCTGGA	CAACAAACCG	CGCTGGAGGG	CGCTCATGGA	GGTGTCTGTG	3540
	TCTGATGGCA	TCCACAGCGT	CAOCCCTTTC	TGCACCTTGC	GTGTACCAT	CATCACGGAC	3600
	GACATGCTGA	CCAACAGCAT	CACGTGTCGC	CTGGAGAACCA	TGTCCACGGA	GAAGTTCTCT	3660
	TCOCCGCTGC	TGCGCCTCTT	CGTGGAGGGG	GTGGCCCGCG	TGCTGTCCAC	CACCAAGGAC	3720
45	GAGCTCTTCG	CTCTCAACGT	CCAGAACGAC	ACCGACGTCA	GCTTCAACAT	CTGAAACGTG	3780
	ACCTTCTCGG	CGCTGCTGCG	TGGCGCGTCC	CGCGGCCAGT	TCTTCCGCTC	GGAGGACCTG	3840
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	CCCTTCGACG	ACAACTCTG	CCTGCGCGAG	CCCTGCGAGA	ACTACATGAA	GTGCGTGTCC	3960
	GTCTGTGCGT	TGAGCAGCTC	CGCGCCTTTC	CTCAGCTCCA	CCACCGTGCT	TTTCCGCGCC	4020
50	ATCCACCCCA	TCACAGGCGT	GCGCTGCGCG	TGCGCGCCCG	GCTTCAACGG	CGACTACTGC	4080
	GAGACGGAGA	TGCACTCTG	CTACTCCGAC	CGGTGCGCGG	CCAACGGCCG	CTGCCCGAGC	4140
	CGCGAGGGCG	GCTACACCTG	CGAGTGCTTC	GAGGACTTCA	CTGGAGAGCA	CTGTGAGGTG	4200
	GATGCCCGCT	CAGGCGCGCT	TGCCAACGGG	GTGTGCAAGA	ACGGGGGAC	CTGCGTGAAC	4260
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55	GAGGTGACCA	CCAGGAGCTT	CCCGCCCCAG	TCTTCTGTCA	CCTTCCGGGG	CCTGAGACAG	4380
	CGCTTCCACT	TCACCATCTC	CCTCACGTTT	GCCACTCAGG	AAAGGAACGG	CTTGCTTCTC	4440
	TACAAACGCC	GCTTCAATGA	GAAGCAGCAG	TTTATCGCCC	TGGAGATCGT	GGAGGAGCAG	4500
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	GGTGTGAGTG	ACGGGGCGGT	GCACTCTGTG	CAGGTGCACT	ACTACAAACA	GCCCAATATT	4620
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	GAITGTGACA	CAACCATGGC	TGTGCGCTTT	GGAAAGGACA	TGSGGAACCTA	CAGCTGCGCT	4740
	GCCCAAGGCA	CTCAGACCGG	CTCCAAGAAG	TCCCTGGATC	TGACCGGCCC	TCTACTCCTG	4800
	GGGGTGTGCC	CCAACCTGCG	AGAAGACTTC	CCAGTGACCA	ACCGGCACTT	CGTGGGCTGC	4860
	ATGCGGAACC	TGTCACTGGA	CGGCAAAAAT	GTGGACATGG	CCGATTTCAT	CGCCAACAAT	4920
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	GGAGGCACCT	GTGTCAACAG	GTGGAATATG	TATCTGTGTG	AGTGTCCACT	CGATTTCGGC	5040
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	TCCTGGAGTG	ACCTGAACAT	CATCATCTCT	GTGCGCTGGT	ACCTGGGGCT	CATGTTCCGG	5160
	ACCGGAAGGG	AGGACAGCGT	TCTGATGGAG	GCCACCACTG	GTGGGCCAC	CAGCTTTGCG	5220
70	CTCCAGATCC	TGAACAACTA	CCTCCAGTTT	GAGGTGTCCC	ACGGCCCTTC	CGATGTGGAG	5280
	TCOCTGATGC	TGTCGGGGTT	GCGGGTGACC	GACGGGGAGT	GGCACCACTC	GCTGATCGAG	5340
	CTGAAGAAAT	TTAAGGAGGA	CAGTGAGATG	AAGCACCTGG	TCACCATGAC	CTTGAGCTAT	5400
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	GTGGTGGTGC	GAGGCGCTTC	TGAAGACAAG	GTCTCCGTGC	GCGTGGGATT	CCGAGGCTGC	5520
75	ATGCAGGGAG	TGAGGATGGG	GGGACCGCCC	ACCAACGTGG	CCACCTGAA	CATGAACAA	5580
	GCACTCAAGG	TCAGGGTGAA	GGACGGCTGT	GATGTGGAGC	ACCCCTGTAC	CTCGAGCCCC	5640
	TGTCCCCCGA	AGTCCGCTG	CCAAGAGGCT	TGGGAGGACT	ACAGCTGGGT	CTGTGACAAA	5700
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	GCTGCGTGC	GCTCCCGCG	CTCCCGCGAG	GGCTACGTGT	GCGAGTGTGG	GCCCAGTCA	5820
80	TAOGGGCGGT	ACTGTGAGAA	CAAACTCGAC	CTTCOGTGCC	CCAGAGGCTG	GTGGGGGAAC	5880
	CCOCTCTGTG	GACCTTGCCA	CTGTGCGGTC	AGCAAAAGCT	TTGATCCCGA	CTGTAAATAG	5940
	ACCAAGGCGC	AGTGGCAATG	CAAGGAGAAT	TACTACAAGC	TCCTAGCCCA	GGACACCTGT	6000
	CTGCCCTGCG	ACTGCTTCCC	CCATGGCTCC	CACAGCGCGA	CTTGGACAT	GGCCACCGGG	6060
	CAGTGTGCTC	GCAAGCCCGG	CGTCATGGGC	CGCCAGTGCA	ACCGCTGGGA	CAACCGGTTT	6120
	GCCGAGGTCA	CCAGCTTCGG	CTGTGAAGTG	ATCTACAATG	GCTGTCCCAA	AGCATTGAG	6180

	GCCGGCATCT	GGTGGCCACA	GACCAAGTTC	GGGCAGCCGG	CTGGGGTGCC	ATGCCCTAAG	6240
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	CTCTTTAACT	GTACCAACCA	CTCCTTCGTG	GACCTCAGGG	CCATGAATGA	GAAGCTGAGC	6360
5	CGCAATGAGA	CGCAGGTGGA	CGGCGCCAGG	GCCCTGCAGC	TGGTGAGGGC	GCTGCGCAGT	6420
	GCTACACAGC	ACACGGGCAC	GCTCTTTGGC	AATGACGTGC	GCACGGGCTA	CCAGCTGCTG	6480
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10	GAGGGCTACT	TCAGCAACGT	GGCAACGCAAC	GTGCGGCGGA	CGTACCTGCG	GCCCTTGGTC	6720
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	AGCCTCOGTT	TGCTTCACCG	GCCCATCAT	AATACCCCGA	TGGTGAGCAC	GCTGGTGTAC	7140
	AGCGAGGGGG	CTCGCTCC	GAGACCCCTG	GAGAGGCCCG	TCCTGGTGGG	GTTCGCCCTG	7200
	CTGGAGGTGG	AGGAGCGAAC	CAAGCCTGTC	TGCGTGTCT	GGAAACCACTC	CCTGGCCGTT	7260
20	GGTGGGACGG	GAGGGTGGTC	TGCCCGGGG	TGCGAGCTCC	TGTCCAGGAA	CCGGACACAT	7320
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	GAGAAAGGGG	AGGTCTCTGC	TCTGAAGATT	GTCACTATG	CGCTGTGTCT	CTTGCTACTG	7440
	GCAGCCCTGC	TGGTGGCTTT	GGTCTCTCTG	AGCCTGGTCC	GCATGCTGCG	CTCCAACTCTG	7500
	CACAGCATTC	ACAAGCACCT	CGCGTGGCG	CTCTCTCTCT	CTCAGCTGGT	GTTCGTGATT	7560
25	GGGATCAACC	AGACGGAAAA	CCCGTTTCTG	TGCACAGTGG	TGCGCATCCT	CCTCCACTAC	7620
	ATCTACATGA	GCACCTTTGC	CTGGACCCCT	GTGGAGAGCC	TGCATGTCTA	CGCATGCTG	7680
	ACCGAGGTGC	GCACATTCGA	CACGGGGCCC	ATGCGTTCT	ACTACGCTGT	GGGCTGGGGC	7740
	ATCCCGGCCA	TTGTACACAG	ACTGGCGTCC	GGCCTGGACC	CCCAGGGCTA	CGGGAACCCC	7800
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30	GCTGTTATTA	TCACTAACAC	AGTCACTTCT	GTCTATCTCT	CAAGGTTTTC	CTGCCAAGA	7920
	AAGCACATT	ATTATGGGAA	AAAAGGGATC	GTCTCCCTCT	TGAGGACCGC	ATTCTCTCTG	7980
	CTGCTGCTCA	TCAGCGCCAC	CTGGCTGCTG	GGGCTGCTGG	CTGTGAACCG	CGATGCATCTG	8040
	AGCTTTCACT	ACCTCTTCGC	CATCTTCAGC	GGCTTACAGG	GCCCCCTCTG	CCTCCTTTTC	8100
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35	CTGCACCTGG	AGGACTCCCG	CACCAACAGG	GCCACCTTGC	TGACGCGCTC	CCTCAACTGC	8220
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	TCGCTGGACA	GCATGCTCAG	GGATGAAGGG	ATCCAGAAAG	TCGCGTGTCT	CTCTGGGCTG	8340
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40	CCTGGGCCAG	ATTCCGACTC	AGATAGCGAG	CTGTCCCTGG	ATGAGCAGAG	CAGCTCTTAC	8460
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	CGCGCCAGGG	GCGCCGTCCA	CAGCACCCCC	AAAGGGGACG	CTGTGGCCAA	CCACGTTCCG	8580
	GCCGCTGGGC	CCGACACAGG	CCTGGCTGAG	AGTGACAGTG	AGGACCCAG	CGGCAAGCCC	8640
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	CCACACAGGC	TGCGGCTCA	CCCTCAGACC	TTGGAGCCCA	AGGGGCCACT	GCCCTTGAAG	9120
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55	CAGTCAAGGC	CAGAACTGAG	AGGGGACCCC	AGACTGGGCC	CAGAGGCTGG	CCAGAGTTCA	9360
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	CTCCCCCGCG	GCCCCCTGGG	TCCCCAGTGT	TGCGTGTGTG	TGCGTTTGTG	CTCTGCTGCC	9840
	ATCTGCCCCG	GCTGTGTGAA	TTCAAGACAG	GGCAGTGCAG	CAGTAGGCAG	GTGTGAGGAG	9900
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65	TCTGTGACCA	CCACCCCTCT	CCCTCACCGC	CTCCAGGTG	GCCCCGGAGC	TGCAGTGGG	10020
	GATGGCTTTG	TCCCTTGTCT	CTGCTCCCGG	TGGGACCTGG	GACCTTAAAG	CGTTGCAGGT	10080
	TCCTGATTTC	GACAGAGGTG	TGGGGCCCTC	CAGGCGGTTA	CATACCTCCT	GCCAAATCTC	10140
	TAACCTCTCT	AGACTGCGAG	GATCTCCAGG	CAGGGTCTCT	CCCTCTGGAG	TCTGACCAAT	10200
	TACTTCAATT	TGCTTCAAAT	GGCCAAATGT	GCAGAGGAC	AAAGCCACAG	CCACACTCTT	10260
70	CAACGGTTAC	CAAACCTGTT	TTGGAAATTC	ACACCAAGGT	CGGGCCACT	GCAGGCAGCT	10320
	GGCACAGGCT	GGCCCGAGGG	GCTGTGGAAC	GGGTCCCGGA	ACTGTACAGC	ATGTTTGATT	10380
	TTAGCGTTTC	CTTTGTTCTT	CAAAACAGGT	GCCCAATAAA	GTGATCAGCA	CAGCTGCTTC	10440
	CAAAATAGGAG	AAACCATAAA	ATAGGATGAA	AATCAAGTAA	AATGCAAGAA	TGTCCACACT	10500
	GTTTTAAACT	TGACCCCTGAT	GAAAATGTGA	GCACTGTTAG	CAGATGCCTA	TGGGAGAGGA	10560
75	AAAGCGTATC	TGAAAATGGT	CCAGGACAGG	AGGATGAAAT	GAGATCCGAG	AGTCTCTACA	10620
	CCTGAAATGAA	TTATACATGT	GCCCTACAGG	GTGAGTGGTC	TTTGGAGGAT	AAAAAACTCT	10680
	AGTCCCTTTA	AAAGTTTGCC	CCTGGCGTTT	CCTAAGTACG	AAAAGGTTTT	TAAGTCTTGG	10740
	AACAGTCTCC	TTTCTAGACT	TTAACAGGAT	TCTGCCCTCT	GAGGTGTAA	TTTTTTGTTT	10800
	TATTTTTTTC	CACGTACTCC	ACAGCAACCA	TCAAGAGGTG	TAATTTTTAA	TTTGATCAGA	10860
80	ACTGTATACCA	AAAAACAACT	GTCACTTTTA	TTGAGATGGG	AAAAATGTAA	ACCTATTTTT	10920
	ATTACTTAAG	ACTTTATGGG	AGAGATTAGA	CAGTGGAGGT	TTTTAACAGA	ACGTGTATTT	10980
	ATTAAATGTT	AAAAACATGG	AATTACAAAT	GAGAAGAGTC	TACAAATAAT	TAAATTTTTT	11040
	GAATTTGTAC	TTCTGCGGTG	CTGGTTTCTT	TCCACAAACA	CCCCCGCCCC	TCCCCATGCC	11100
	CAGGGTGGCC	GTGGAGAGGA	CGGTTTACGG	ACGTGCAGCT	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGGAACGT	GCCGGAACCT	TTTGTCCATT	CCCTAGTAGG	CCTGCCACAG	11220

CCTAGATGGG CAGTITTTGT CTTTCACCAA ATTTGAGGAC TTTTITTTTT TGCCATTATT 11280  
 TCTTCAGTTT TCITTTCTTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340  
 AGACGTTAGA CCTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTC

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**A32 Protein Sequence**

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo  
 (Drosophila) homolog (CELSR1),  
 Hs.252387  
 Unigene number:  
 Protein Accession #: NP\_055061  
 Signal sequence: 1-20  
 Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092,  
 1110-1199  
 Pfam domains: Laminin\_EGF [2003-2048], 7tm\_2 [2465-2708]  
 Latrophilin/GPS domains: 2407-2460  
 Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704  
 Cellular Localization: plasma membrane

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1	11	21	31	41	51	
MAPP PPPVLP	VLLLLAAAA	LPAMGLRAAA	WEPRVPGGTR	APALRPGCTY	AVGAACTFPA	60
PRELADVGRD	GRLAGRRRV	GAGRPLPLQV	RLVARSAPTA	LSRRLRARTH	LPGCGARARL	120
CGTGARLCOA	LCFVPGGCA	AAQHSALAAP	TTLPACRCPP	RPRPRCPGRP	ICLPGGGSVR	180
LRLLCALRRA	AGAVRVGLAL	EAATAGTPSA	SPSPSPPLPP	NLPEARAGPA	RRARRGTSGR	240
GSLLKFPMPNY	QVALFENEP	GTLLQLLHAH	YTIAGEEERV	SYMEGLFDE	RSRGYFRIDS	300
ATGAVSTDSV	LDRETKETHV	LRVKAVDYST	PPRSATTYIT	VLVKTNDHS	VFVEQSEYRE	360
RVRENLEVG	EVLITRASDR	DSPINANLRY	RVLGANDV	QINSSSGVVS	TRAVLDREEA	420
AEYQLLVEAN	DQGRNPGPLS	ATATVYIEVE	DENDNYQPFS	EQNYVVQVPE	DVGLATAVLR	480
VQATDRDQGG	NAIHYSIILS	GNVAGQFYLE	SLSGILDVIN	PLDFEDVQKY	SLSIKAQDGG	540
RPLINSSGV	VSVQVLVDND	NEPIFVSSPF	QATVLENVPL	GYPVHHQAV	DADSGENARL	600
HYRLVDAST	FLGGGSAGPK	NPAPTDFPP	QIHNSSGWIT	VCALRDREBV	EHSYFGVEAV	660
DHGSPPMSSS	TSVSIITVLDV	NDNDFVFTQP	TYELRLNEDA	AVGSSVLTLQ	ARDRDANSVI	720
TYQLTGGNTR	NRFALSSQRG	GGLITLALPL	DYKQEQYVVL	AVTASDGRS	HTAHVLINVT	780
DANTHRPFVQ	SSHYTVSVSE	DRPVGTSIAT	LSANDEDTGE	NARITYVIQD	PVPQFRIDPD	840
SGTMYTMEL	DYENQVAYTL	TIMAQDNIGP	QKSDTTTLEI	LILDANDNAP	QFLMDFYQGS	900
IFEDAPPSTS	ILQVSATDRD	SGPNGRLLYT	FQGGDDGDGD	FYIEPTSGVI	RTQRRLDREN	960
VAVYNLWALA	VDRGSPTPLS	ASVEIQVTIL	DINDNAPMPE	KDELELFVEE	NNPVGSVVAK	1020
IRANDPDEGP	NAQIMYQIVE	GDMRHFQQLD	LLNGDLRAMV	ELDFEVRRREY	VLVVQATSAP	1080
LVSRAVTHIL	LVQNDNPFV	LPDFQILFNN	YVTNKSNSFP	TGVIGCIPAH	DFDVSDSLNY	1140
TFVQGNELRL	LLDLPATGEL	QLSRDLNNR	PLEALMEVS	SDGIHVSATP	CTLRVTITD	1200
DMLTNSITVR	LENMSQEKPL	SPLLALFVEG	VAVLSTTKD	DVFVFNQND	TDVSSNILAV	1260
TFSALLPGGV	RQGFPSSEDL	QEYIYLNRTL	LTITSTQVRL	PFDDNICLRE	PCENYMKCVS	1320
VLRFDSAPP	LSSTTVLFRP	IHPINGLRRC	CPFGFTGDYC	ETEIDLCSYD	PCOANGRCRS	1380
REGGYTCBCF	EDPTGEHCEV	DARSGRCANG	VCKNGGTCVN	LLIGGFHCVC	PPGEYERFPC	1440
EVTTSPFPQ	SFVTFRGLRQ	RFHFTISLTP	ATQERNGLLL	YNGRFNEKHD	PIALEIVDEQ	1500
VQLTFSAGET	TTTVAPKVPS	GVSDGRWHSV	QVQYNNKPN	GHLGLPHGPS	GEKMAVTVTD	1560
DCDTTMAVRP	GKDIGNYSCA	AQGTQTGSKK	SLDLTGPLLL	GGVNPMPEDF	PVHNRQFVGC	1620
MRLSVVDGKN	VRMAGFIANN	GTREGCAARR	NFCDGRRCON	GGTCVNRWNN	YLCECLRFGR	1680
GKNCQAMPH	PQLFSGESV	SWSDLIHIIIS	VFWVLGLMFR	TRKEDSVLME	ATSGGPTSF	1740
LQILNNYLQF	EVSHGPSDE	SVMLSGLRVT	DGEWHLLIE	LGNVKEDSEM	KHLVTMTLDY	1800
GMDQNKADIG	GMFGPLTVRS	VVGGAASEDK	VSVRRGRFCG	MQGVRMGGTP	TNVATLNMNN	1860
ALKVRVKGDC	DVDDPCTSSP	CFPNRSRCHDA	WEDYSCVCDK	GYLGINCUDA	CHLNPCENMG	1920
ACVRSPGSPQ	GYVCEGSPSH	YGPYCENKLD	LPCPRGWMGN	PVCGPCHCAV	SKGFPDPCNK	1980
TNGCQCKEN	YYKLLAQDTC	LPDCDFPHGS	HSRTCDMATG	QCACKPGVIG	RQCNRCDNPF	2040
AEVTTLGCEV	IYNGCPKAF	AGIWWPQTKF	GQPAAVPCPK	GSVGNVAVRH	SGEKGWLPPE	2100
LFNCTIISFV	DLRAMNEKLS	RNETQVDGAR	ALQLVRLARS	ATQHTGTLP	NDVRTAYQLL	2160
GHVLQHSWQ	QGFDLAATQD	ADPHEDVIHS	GSALLAPATR	AAWEQIQORSE	GGTAQLLERL	2220
EGYVSNVAV	VRRTYLRPPV	IVTANMILAV	DIFDKFNFTG	ARVPRFTDTH	EEFPRELESS	2280
VSPADFFRP	PEKEGFPILL	PAGRRITPQT	TRPGPGTERE	APISRRRRHP	DDAGQFAVAL	2340
VIIYRTLQGL	LPERYDPRR	SLRLPHRPII	NTPMVSTLVY	SEGAPLPRPL	ERFVLVEFAL	2400
LEVEERTKPV	CVFWNHSLAV	GGTGGWSARG	CELLSRNRTH	VACQCSHTAS	PAVLMDISRR	2460
ENGEVLPKLI	VTYAAVLSL	AALLVAFVLL	SLVRMLRSNL	HSIHKLAVA	LPLSQLVEVI	2520
GINQTNPFPL	CTVVAILLHY	IYMSTFAWTL	VESLHVYRML	TEVRNIDTGP	MRFYVVGWVG	2580
IPAIVTGLAV	GLDPQGYGNP	DFCNLSLQDT	LIWSFAGPIG	AVIIINTVTS	VLSAKVSCQR	2640
KHHYKGGKI	VSLRLTAFL	LLLSATWLL	GLLAVNRDAL	SPHYLFAIPS	GLQGPVLLF	2700
HCVLNQEVRL	HLKGLVGRK	LHLEDSATR	ATLLTRSLNC	NTTFDGDGDM	LRTDLGESTA	2760
SLDSIVRDEG	IQKLVSSGL	VRGSHGEFDA	SLMPRSCKDP	PGHSDSDSBS	LSLDEQSSSY	2820
ASSHSSDSDE	DGVGAEEKWD	PARGAVHSTP	KGDVAVNHVP	AGWPDQSLAB	SDSEDPGSKP	2880
RLKVETKVS	ELHREBQGS	RGEYPPDQES	GGAARLASSQ	PPEQRKGILK	NKVYTPPPLT	2940
LTEQTLKGR	REKLADCEQS	PTSSRTSSLG	SGGPDCAITV	KSPGREPRGR	HLNGVAMNVR	3000
TGSAQADGSD	SEKP					

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**A33 DNA SEQUENCE**

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Probeset Accession #: X95876  
 Nucleic Acid Accession #: X95876  
 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

80

1	11	21	31	41	51	
CCAACCAAA	GCACCAAGC	AGAGGGGCG	GCAGCACACC	ACCCAGCAGC	CAGAGCACCA	60
GCACAGCAT	GGTCTTGAG	GTGAGTGACC	ACCAAGTGCT	AAATGAGGCC	GAGGTGCGG	120

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CCCTCCTGGA GAACTTCAGC TCTTCCTATG ACTATGGAGA AAACGAGAGT GACTCGTGCT 180
GTACCTTCCC GCCTTGCCCA CAGGACTTCA GCCTGAACCT CGACCGGGCC TTCTTGCCAG 240
CCCTCTACAG CCTCTCTTTT CTGCTGGGGC TGCTGGGCAA CGGCGCGGTG GCAGCCGTGC 300
TGCTGAGCCG GCGGACAGCC CTGAGCAGCA CCGACACCTT CCTGCTCCAC CTAGCTGTAG 360
CAGACAAGCT GCTGGTGTCT ACAGTGCCTC TCTGGGCAGT GGAGCGTGCC GTCCAGTGGG 420
TCTTTGGCTC TGGCCTCTGC AAAGTGGCAG GTGCCCTCTT CAACATCAAC TTCTACGCAG 480
GAGCCCTCCT GCTGGGCTGC ATCAGCTTTG ACCGCTACCT GAACATAGTT CATGCCACCC 540
AGCTCTACCG CCGGGGGGCC CCGGGCCGCG TGACCTCTAC CTGCTGGCT GTCTGGGGGC 600
TCTGCTGCTT TTTGCTGCTT CCAGACTTCA TCTTCTGTCT GGCCACCACC GACGAGCGCC 660
TCAACGCCAC CCACTGCCAA TACAACCTCC CACAGGTGGG CGCACCGGCT CTGCGGGTGC 720
TGCACTGTGT GGTCTGGCTT CTGCTGCCCC TGCTGGTTCAT GGCCCTACTGC TATGCCACCA 780
TCTTGGCCGA GGTGCTGGTT TCCAGGGGCC AGCGGCGCCT GCGGGCCATG CGGCTGGTGG 840
TGGTGGTCTG GGTGGCTTTT GCCCTCTGCT GGACCCCTTA TCACCTGGTG GTGCTGGTGG 900
ACATCCTCAT GGACCTGGGC GCTTTGGCCC GCAACTGTGG CCGAGAAAGC AGGGTAGACG 960
TGGCCAACTG GGTCACTCTA GGCTTGGGCT ACATGCACTG CTGCCTCAAC CGCTGTCTCT 1020
ATGCTTTTGT AGGGGTCAAG TTCCGGGAGC GATGTGTGAT GCTGCTCTTG CGCCTGGGCT 1080
GCCCAACCCA GAGAGGGCTC CAGAGGCAGC CATGCTCTTC CCGCGCGGAT TCATCTGTGT 1140
CTGAGACCTC AGAGGCTCTC TACTCGGGCT TGTGAGGCGC GAATCCGGGC TCCCTTTTCG 1200
CCCACAGTCT GACTTCCCGG CATTCACAGC TCCTCCCTCC CTCTGCCGGC TCTGGCTCTC 1260
CCCAATATCC TCGCTCCCGG GACTCACTGG CAGCCCCAGC ACCACCAAGT CTCCCGGGAA 1320
GCCACCTCTC CAGCTCTGAG GACTGCACCA TTGCTGCTCC TTAGCTGCCA AGCCCATCC 1380
TGCCGCCCGA GGTGGCTGCC TGGAGCCCCA CTGCCCTTCT CATTTGGAAC CTAAGAACTC 1440
ATCTTCCCCA AGTGGGGGGA GTACAAGGCA TGGCGTAGAG GGTGTGCCCC CATGAAGCCA 1500
CAGCCAGGCG CTCAGCTCTA GCAGTGAAGT TGGCCATGGT CCCCAGAGCC TCTATATTTC 1560
CTCTTTTATT TTTATGTCTA AAATCCTGCT TAAAACTTTT CAATAAACAA GATCGTCAGG 1620
ACCAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA BHCLITERAT 1680
UREBHCBLAS TPBHCORTHO LOGUESMOUS ECKCRMVLEV SERQVLDASD PAFLENSTST 1740
PYDYGENESD FSDSPPCPDQ FSLNFDRTFL PALYSLFLFL GLLNGAVAA VLLSQRTALS 1800
STDFTLLHLA VADVLLVLTFL FLNVAADAAVQ WVFGPGLCKV AGALFNINFY AGAPLLACIS 1860
FDRYLSIVHA TDYLRDPRV RVALTCIVVW GLCLLFLALPD FIYLSANYDQ RLNATHCQYN 1920
FPQVGRALR VLQVLVAGFL PLVLMAYCYA HILAVLLVSR GQRFRFRMR L VVVVAAFAV 1980
CWTPYHLVVL VDLMDVGV L ARNCGRESHV DVAKSVTSQM GYMHCCLNPL LYAPVGVKFR 2040
EQMMMLFTRL GRSDQRGPQR QPSSSRRESS WSETTEASYL GL

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**A34 Protein sequence**

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Protein Accession #: P49682  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [70-318]  
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323  
 DRY box: 148-149  
 Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | |
MVLEVSDEQV LNDAEVAALL ENFSSSYDYG ENESDSCTCS PPCPDPSLN PDRAFLPALY 60
SLLFLGLLGG NGAAVAALLS RRTALSTDT FLHLAVADT LLVLTPLWA VDAAVQWVFG 120
SGLCKVAGAL FNINFYAGAL LLACISFDYR LNTVHATQLY RRGPPARVTL TCLAVWGLCL 180
LFALPDPFIL SAHNDERLVA THCQYNFPQV GRTALRLVLQ VAGFLLPLLV MAYCYAHILA 240
VLLVSRGQRR LRAMRLVVVV VVAFALCWT P YHLVVLVDIL MDLGALARNC GRESRVDAK 300
SVTSGLYNMH CCLNPLLYAF VGVKFRERMW MLLRLGCPN QRGLQRQPS SRRDSSWSET 360
SEASYSGL

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**A35 DNA SEQUENCE**

Gene name: Differentially expressed CO16 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 Probeset Accession #: AA447522  
 Nucleic Acid Accession #: BC001291  
 Coding sequence: 44-541 (start and stop codons are underlined)

65  
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1 11 21 31 41 51
| | | | |
GGGGGGCGCG CGCGCTGACC CTCCTGGGCG ACCGCTGGGG ACGATGGGCG TGCTGCGCTT 60
GCTGCTGGTC GTGGCCCTAC CGGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120
AGATCCAGAG GACTCCCGAGC GAACGGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180
TGAGAGAGAA AACACTTTGG AGTGCCAGAA CCCAAGGAGG TGCAATGGA CAGAGCCATA 240
CTGCGTTATA GCGGCGGTGA AAATATTTC ACCTTTTTC ATGGTTTGGG AGCAGTGTCT 300
CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360
GCCATGCCC TTTCTTTTACC TCAAGTGTG TAAATTOGC TACTGCAATT TAGAGGGGCC 420
ACCTATCAAC TCATCAGTGT TCAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
GCTGTGGCTG GCCATCTCC TGCTGCTGGC CTCCATTGCA GCGGCGCTCA GCCTGTCTTG 540
AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTGTCT 600
ACCTGTGCA TTAACCTTGT TTTCTGTGA TTACCTCTTG GTTTGACTTC CCAAGGTCTT 660
GGGATGGGAG AGTGGGGATC AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC 720
ACATTGAGAG GAAGTCCAGA TCTCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTGG 780
AAATCAAAACC TTGTAACCTA TTTATTGCTG ATGGCCACTC TTTTCTTGA CTCCCTCTTG 840
CCTCTGAGGG CTCTGAGTAT GATGGGGAGG GAGGCCTAAG TACCACTCAT GGAGAGTATG 900
TGCTGAGATG CTTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG 960
GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCACTGG GGCACACGTT 1020
AGGGCTGCCC CCATTCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTT 1080

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5 CTACCAAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140  
 ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200  
 ACTTAGGGCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260  
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCACCC AAAAACAAAT ACAAGGGGAC 1320  
 TTCAAAGTT CACGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

10 A36 Protein sequence:  
 Gene name: Differentially expressed C016 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 Probeset Accession #: AA447522  
 Protein Accession #: AAH01291  
 Signal sequence: 1-17 (first underlined sequence)  
 Transmembrane domain: 146 - 162  
 Cellular localization: plasma membrane

20 1 11 21 31 41 51  
 MALLALLLVV ALPRVMTDAN LTARQRDPED SQRTEGDNR VVCHVCEREN TFECQNPERRC 60  
 KWTEPYCVIA AVKIFPRPFM VAKQCSAGCA AMERPKPEEK RFLLEEFMPF FYLKCCCKIRY 120  
 CNLEGGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSL

25 A37 DNA SEQUENCE  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51  
 AGCAACGAGC CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG 60  
 CCTGCTGCTG AGCAGGCGCG CGGAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120  
 GTGCAACATA CCGAGCAACT TCATGTGCAG CAATGGAACG TGCACTCCCG GCGCCTGGCA 180  
 GTGTGACGGG CTGCGTGAAT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 GTCGAATATG GGCCCAACCT TCTTCCCTCG TGCCAGCGCG ATCCATTGCA TCATTGGTCC 300  
 CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCCCTCG CTTTGTCTCA CCGCCCGCTA CCACTGCAAG AACCGCCTCT GTATTGACAA 420  
 GAGCTTCATC TCGATGGAGC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 AAGTTCTCAA GAACCCGCGA GTGGGCGAGT GTTTGTGACT TCAGAGAACC AACCTGTGTA 540  
 TTACCCGAGC ATCACTATG CCACTCATCG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 CCGCTGGGCA AATGGCTTTC ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660  
 GCACCGGCTG CAGCACCCTG TGCTGTCTGC CCGCCTGGTG GTCCCTGGAC ACCCCACCA 720  
 CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 GAATGCGCTG GAAGTAGGCT CCCACCCCTC CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840  
 TGCGTGGTAT GAOCCTCCTC CACCGCCCTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900  
 CGACCTGGCC CACTCTCCCT CCGGCTCCCG GAGTGCCAAC AGTGCCAGCT CCGAGGCGAG 960  
 50 CAGCAGCCTC CTGAGCGTGG AAGACACCA CCAACGCCCC GGGCAGCCTG GCCCCAGGA 1020  
 GGGCACTGCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTCCCATTC TAACAATTG 1140  
 TGCTCATGGG AAGCTCTTTA AGCACTGTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 AACTATCTCT GCATTCCCTC CCTCCCCCAG ACTTCAGAGA TGTTTTCTG GGTCTCAGT 1260  
 55 TGACATGATC TGTGTGCGCT CTTTCTGTCT AGGTCACTCT TCCCTTGGGA CCGAGATCA 1320  
 CACCCCTATT TTTCACATTA TTCTGTTTCT GTTGAGAGAG CAGCATATAA AACAGTATTG 1380  
 AATAGGCTG GAGAGAGAGA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTATAGC CATTTGGGGA TTGGGTTAG 1500  
 60 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTACCCCCC CAAAAAATT CCAATTGAGC 1560  
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 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTG CCAAGAAATG 1740  
 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTAA AATAGGCAAG 1800  
 65 GAGCCCTCC CATGAGTTTA TCCAAGTCTC CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860  
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 ACCCTGCGCT AGCCAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAGATC TGACCTGGCT 1980  
 GTATGTCCCT GTGGCCCA CAACAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC 2040  
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 70 ACTGGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCAATAACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTCAAGGCT AGGCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
 AGACAATTG GAGTCAAGAT TTCCATTGG GATCTATTTT AAATCTTTTA GAAATGCATT 2340  
 TGAAACAGTG TGTGTGTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400  
 75 AGCTGTCTCT TTTTGTGTT TTCTTTTAA AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460  
 ACACCTGTC CCGCTGATAA CAGTCACTC CAGACTAACC TGTGTGCCAG 2520  
 ACATTGTGTC ATGTGTGCAC TTTGAGGTTA TTATTATCA AGTTCCTGAA GGAAGCAGAA 2580  
 AGAGGCACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGTAGTTT TTTCTTTT 2640  
 80 TTCTCTGTGT CCACTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700  
 AGGTGTGTGT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATAGGAA CCAGGTAGAG 2760  
 CCACTCCGGG CAGCTGTAC CCACTCAGAA CTTCTTTCC CAGCTGAAGA AATGTTCACT 2820  
 AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAG TGGCATTGAG 2880  
 TGATCTGTGT CTGTAGACTT TTTCTTCTTT TTTTAAACAA ATCCAAAGGA TGTTCAGAAA 2940  
 AAGCTAGCCA CTGTTATTTT GTTTTGTTTA AAAAAAAGA GAAAGAGAAA 3000



AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAGAA CTCTTGATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTCATCT CCTGTAGTTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180  
 TTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT 3300  
 AGATAAGGGA TGCTACTAA TGCTTTTTTA AAACAAACAG GCACATTTT ATTATAGATT 3360  
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CCACAACAG 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAT GAGATCCGTG TTTTATTTA GCATTAAATT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTGT GTGTCGTGTC TTTTGTGTT TTGGTTAGGC TTGTTTTGT TTTTAAATT 3780  
 TTATACTTTC TAATAAATT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840  
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAAC CCACTTCGGG 3900  
 TGGGGCGCG GGGCCACGCT AGGTACGCGC ACCACGCGGG CCCAAACGGG ACCCCAGAAG 3960  
 GAAACCCCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACAGCGCGGG 4020  
 GGAAACCGCA GAGTGTTCG TAAACCAAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

**A38 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MWLLGLPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60  
 EKECEPKAKSK CGPTFFPCAS GIHCCIIGFRF CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSF ICDGQNNQOD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHHRQRK NNLMTLHVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV

**A39 DNA sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGCTGCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCAGA 60  
 GGAAGAAAC TTCCGTGGGA GGCTTCCATC GTGCGGCACA CCTCCGAGG GCGAGGCAGC 120  
 GACCGGAGGA GGGAGAGCCG GCGGGAGGCT GCGGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGAGGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGAATCCGCG CCAGCAGCAG 240  
 CCGCGGCGCG CGCCAGCTGG GCAAGCTCCC GGGACTGCGG CTGGGGCGCG GCAGSACCT 300  
 CGCTGCGTCT CTGGACGTTT CCGGGGAGAG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360  
 TCGGAGCAGC AGCCCGCGGG GCCTTCTGAC TGCAATCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTCTCTGAC CTAGGGCCCG GGTCTGTCGC CTCTGGGCG TCGCGGAGCA GGGGAGTGGC 540  
 CCGCGCGGAA AGCGCGCGCG GACAGTCAGT GAGGAGGCCG GGGGTCGCC GGGGCCACGA 600  
 CTTCTCGGAG ACCGTCCCTG GCTCTCTGGA GAGCGCTGTG CGCGGCCAG GGTGGTGCCA 660  
 TGTGGGGCGC TCGCGCTCG TCGTCTCCT CATCTGGAA CGCGCTCTCG CTCTGCAGC 720  
 TGCTGCTGGC TCGCTGCTG GCGCGGGGGG CAGGGGCCCA GCGCGAGTA CTGCCACGGC 780  
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCCTCCAGT GTCCCGAGCG CTTGCAAGCG 840  
 GCGGAGCGCA CCATCTGCTG CGGAGCTGCG GCGTTGCGCT ACTGCTGCTC CAGCGCGCAG 900  
 GCGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960  
 CCGGCGGACA AAGAAGGGCC CCGACGGCTC GGCAGGGCTT CATGCTTAG GGGTACCCAA 1020  
 GGAGACGGCG AGGGTGGCGC CCCACCGCTG AGGGCTTGGC AGCGGTGCTC CCTTGAAGGC 1080  
 TCCCGAAGAG GAAGGCGAGT CTTAGGGGCT TTCCCGGGGC TGCTGCCCGG TGCCAGACGC 1140  
 CGCGGATTCC CATCTTCTCC ACGGGCGGCG CCTCTCCGCC TGCAGCGGCC CGCCTTGCCC 1200  
 ATCTACGTGC CGTTCCTCAT TGTGGGCTCC GTGTTTGTGG CCTTTATCAT CTTGGGGTCC 1260  
 CTGGTGGCAG CCGTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCGCA 1320  
 GCGCCAGGGG GTAAACCGCTT GATGAGAGCC ATCCCATGTA TCCCATGTC CAGCACTCC 1380  
 CGGGGTGCTT CCTCAGGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACCTC 1440  
 GGGGCGCGGG CGCCCGCAAC AAGGTCACAG ACCAAGTGTG GCTTGGCGGA AGGGACCATG 1500  
 AACAACTGTG ATGTCAACAT GCGCAGCAAT TTCTCTGTGC TGAAGTGTCA GCGAGGCCAC 1560  
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCOCCAT ACGTGGGGTA CAGGTGCGAG 1620  
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA CGCTGGCTAC 1680  
 AGGCAGATTG AGTCCOCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGGAAGTCC GCACATGTGG GTGGTATTTA TGGCAGGATT CTTTGGATGG 1860  
 GCTTCATTGG CCCCAGACT GTATGAAAC ATCTCOGAAT TAGCATTTC GGAATATGTT 1920  
 CATCCAGGGT ATCATTGATT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100

5 TGTGTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160  
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCG 2220  
 TGGTGGGATC TGGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCCTGCCTC 2280  
 AGCTCCACAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT 2340  
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGGTGGTCTC ACTCTCTGTA CCTCAAGCAA 2400  
 TCTGCTCTGC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC 2460  
 TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520  
 ATTCTAAAGG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580  
 10 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640  
 GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700  
 TTAATAAGAG ACTGAAATAA ATTGTATAGT TACTTAACCTA ATGAAGACAT TTCAGAACTC 2760  
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCTTTC 2820  
 TTGATTGTAT CTTAATTTTC TGGCTTAAAG GTGACATCTG AGAGGTAATG CATTCTTTTT 2880  
 TATATTGAAA TCATAAACTA TCACCCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940  
 15 TGGTTATGGT TTGGCGTTTC CTCTGTTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000  
 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTCTGCTTA GATCTGATAA 3060  
 AAAAAATTTT TTGTCTTAGT TATAAAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTTACTTT 3180  
 20 GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTATTTTTTC AGGCACTAAG 3240  
 GATTGTTAAG AGAAAGCTT TTCAACGAAG GATTGCTTTT CTCTCCAC ACTGTTCTTG 3300  
 ATTTCTCTC TCCTTCAGGC CTCACAGGC ACTGTATCA TTGCCAATGT TCCAAATAT 3360  
 CAAATCAAG TGAATTTAT TGTGTGTTCT TACTTATAT AAAAAAAGT AACTTTAAG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480  
 25 GTATGTTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATT 3540  
 TGTTCATGTA CTGAAATAAT TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600  
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660  
 TGAATAAATA AAAAAAATA AAAAAAATA

30 **A40 Protein sequence**  
 Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 35 Transmembrane domains: 402-424  
 Cellular localization: not determined

40 1 11 21 31 41 51  
 | | | | |  
 MLSGFLMSPS TOHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLMDRAAA 60  
 GEAEKGNRGE PPAWIRAQQQ KRPPPPAGQAP GTAAGGADQP RLPRGRSRGR VRLPVKPPPEA 120  
 SGRQPPRPSD CIPRPPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180  
 45 PRGKRRTGVS DEARGSPGPR LLGDRPALSG DALSAFVVPV CGALAARPSF HPGTPLRSCS 240  
 CCLNRCWRRG RPSGSEYCHG WLDAQGVNRI GFQCFERFDG GDATICCGSC ALRYCCSSAR 300  
 ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPPV RAWQRCSPEG 360  
 SPKGRQLLRA PPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAPIILGS 420  
 LVAAACRCRL RPKQDPQQR SR AFGGNRLMET IPMIPASST RGSSSRQSST AASSSSSANS 480  
 50 GARAPPTRSQ TNCCLEPGTM NNVVNMPTN FSVLNCQQAT QIVPQGGYLL HPPYVGYTVQ 540  
 HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQRMYPV TV

**A41 DNA SEQUENCE:**  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 55 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51  
 | | | | |  
 OGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTTTGGGTCT CTGCTCTTA CTGCTCACAG TTTCTTCCA CCTTGCCATT 120  
 65 GCAATAAAAA AGGAAAAGAG GCTCCTCAG ACACCTCAA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATT 240  
 ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCC 300  
 CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420  
 70 GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTTAACAG ATTGTACACA 480  
 TATGAGCCTC GGGATTTACC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540  
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAAGT CAAATTTTAT 600  
 GAGAAAAACC TCTGGCCATC TGACAAATCA TAAATGTGCA AGTATATAGA TTTTGTAAATA 660  
 75 TTACTATTTA GTTTTCTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTCTTAA 720  
 TCTGAAAAAA AAAAAAATA AAAAAAATA

**A42 Protein sequence:**  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 80 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

1 11 21 31 41 51  
5 MMLHSALGLC LLLVTSSNL AIAIKKEKRP POTLSRGWGD DITWVQTYEE GLFYAQKSKK 60  
PLMVIHLED CQYSQALKKV PAQNEEIQEM AQNKPIMLNL MHETDKNLS PDGQYVPRIM 120  
FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

10 A43 DNA SEQUENCE  
Gene name: ATPase, Ca++ transporting, type 2C, member 1  
Unigene number: Hs.106778  
Probeset Accession #: N51919  
Nucleic Acid Accession #: AF189723  
15 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
20 ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGA GAAGTATATT 180  
TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCCTGGCTT CTGCAGTCAT CAGTGTTTTA 240  
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
25 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTGAAG AATTGAGTAA ACTTGTGCCA 360  
CCAGAATGCC ATTTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGGCCG AGACTTGGTT 420  
CCAGGTGATA CAGTTTGCCT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTT 480  
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540  
AAGGTGACAG CTCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600  
30 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTGTTCAT TGGAAACAGGA 660  
GAAAAATCTG AATTGGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780  
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840  
ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTGT GGTCAAGTGT 900  
35 AGCTAGCTC TTGGTGTAT GAGAATGGTG AAGAAAGGG CCATTGTGAA AAAGCTGCCT 960  
ATGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTCG AACACTGACG 1020  
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCGTCATGC TGAGGTTACT 1080  
GGAGTTGCT ATAAATCAAT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTC 1140  
40 TATAACCCAG CTCTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200  
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260  
ATGGGCTCTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320  
GAGCAAAAGT GGATGGCTGT TAAGTGTTGA CACGAAACAC AGCAGGACAG ACCAGAGATT 1380  
TGTTTATGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
45 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAAG GAAGGCACGC 1500  
ATGGGCTCAG CGGACTCAG AGTTCCTGCT TTGGCTTCTG GTCCTGAAT GGGACAGCTG 1560  
ACATTCTCTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620  
ACAACACTCA TTGCTCAGG AGTATCAATA AAAATGATTA CTGAGATTAC ACAGGAGACT 1680  
CGAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCCAAAA CTCCAGTC AGTCTCAGGA 1740  
50 GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTTCAAAA TAGTACCAA GGTTCAGTA 1800  
TTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGTACA GAAGAACGGT 1860  
TCAGTTGTAG CCAATGACAG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920  
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGA AAGAGGCAGC AGACATGATC 1980  
CTATGGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040  
55 AATAACATTA AAAATTTCGT TAGATTCCAG CTGAGCAOGA GTATAGCAGC ATTAACCTTA 2100  
ATCTCATGG CTACATTAAT GAATCTTCTT AATCTCTCA ATGCCATGCA GATTTGTGG 2160  
ATCAATATTA TTATGGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAAC AGTGGAATAA 2220  
GATGTCAATC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGTACTA AAACCTTGATA 2280  
CTTAAATATG TTTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340  
60 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400  
TTTTTTGACA TGTTCATGCT ACTAAGTCC AGATCCGAGA CCAAGTCTGT GTTTGAGATT 2460  
GGACTCTGCA GTAATAGAAT GTTTGTCTAT GCAGTCTCTG GATCCATCAT GGGACAATTA 2520  
CTAGTTATTT ACTTCTCTCC GCTTCAGAA GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580  
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAG 2640  
65 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700  
CTTGAAGTAT GA

A44 Protein sequence:  
Gene name: ATPase, Ca++ transporting, type 2C, member 1  
70 Unigene number: Hs.106778  
Probeset Accession #: N51919  
Protein Accession #: AAF27813  
Signal sequence: none found  
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
75 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
Cellular Localization: not determined

1 11 21 31 41 51  
80 MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FRGMNEFDIS EDEPLWKQYI 60  
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVOEYRSEK SLEELSKLVP 120  
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180  
KVTAPQPAAT NGDLASRSNI AFMGTILVRCG KAKGVVIGTG ENSEFGEVFK MMQABEAPKT 240  
PLQKSMDDLQ KQLSPYSFPI IGIIMLVGWL LGKIDLEMT ISVSLAVAAI PEGLPFIVTV 300

5 TLALGVMRMV KRAIVKILP IVETLGCCNV ICSDKTGTLT KNEMTVTHIP TSDGLHAEVT 360  
 GVGYNQFGEV IVDGTVVHGF YNPVAVSRIVE AGVCVNDABI RNNTLMGKPT EGALIALAMK 420  
 MGLDGLQQDY IRKAEYFPSS EQKMWAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480  
 10 GQTLTLTQQQ RDVYQEKAR MGSAGLRVLA LASGPELGQL TPLGLVGIID PPRTGVKEAV 540  
 TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG ESIDAMDVOQ LSQIVPKVAV 600  
 FYRASPRHFM KIISLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGQTGT DVCKEADMI 660  
 LVDDDFQTIM SAIEBGGIY NNINPFVRFO LSTSIALLTL ISLATLMNFP NPLNAMQILW 720  
 15 INIIMDGPFA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780  
 ELRDNVITPR DTTMTPTCFV FDFMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840  
 LVYIFPPLQK VFQTESLSIL DLLFLGLTS SVCIVABIIK KVERSREKIQ KHVSTSSSF 900  
 LEV

**A45 DNA sequence**

15 Gene name: ESTs  
 Unigene number: Hs.157601  
 Probeset Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60  
 25 TTTTATTGCG AGACCTGGGC CGATGCCGCT TTAACAAACG CGAGGGGCTC TATGCACCTC 120  
 CCTGCGCGTA GTTCTCCGGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180  
 ACAACACGGT GTCCACACGT GCAGCCGCGC CCGGGGCGCC CCTCCTGTGA TCCCGTAGCG 240  
 CCCCCTGGCC CGAGCCGCGC CCGGCTCTGT GAGTAGAGCC GCCCGGCGAC CGAGCGCTGG 300  
 TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCCTTTCC TGTGTCTGGA GGCCGCTCTG 360  
 30 GTTTTCCCTGT TTTCCAGAGT GCGCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAACCAA 420  
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGCG TGCACTGGAC 480  
 ATCATGTTCG TGTAGATGG GTCTAACAGC GTCCGGAAGG GGAGCTTTGA AAGGTCCAAG 540  
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600  
 GCATTCACGT TCAGTTCAC TCCTCATCTG GAATTCCTCT TGGATTCTAT TTCAACCCAA 660  
 35 CAGGAAGTGA AGGCAAGAAAT CAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720  
 CTGTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCC 780  
 CAGATCCCTCA TCATGTCAC TGATGGGAAG TCCACGGGGG ATGTGGCACT GCCATCCAG 840  
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTCCT CAGGTGGGAG 900  
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGC TGCTGTGGGC TGAGCAGGTG 960  
 40 GAGGATGCCA CCAACGGGCT CTTCAGCACC CTGAGCAGCT CGGCCATCTG CTCCAGCGCC 1020  
 ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGAAGCTGGA GATGGTCCGG 1080  
 GAGTTGCTCG GCAATGCCCC ATGCTGAGGA GGATCGCGGC GGACCTTCGC GGTGCTGGCT 1140  
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCCTAA CCCACCTGCG CACTGCTTAC 1200  
 AGGACCACCT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260  
 45 CCAGAGGAC TGGACGGCTA CCAAGTGCCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320  
 TGTGCGCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCTGCTT GGACAGCTCT 1380  
 GCGGGCACCA CTCTGGACGG CTCTGCTCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGGCG 1440  
 GCGGTGGCGG GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500  
 50 GGCATTCCCT TCGGTGTGGG CCCCACCTCG ACGGGCAGTG CCTTGGCGCA GGCGGACAG 1560  
 CTGGGCTTGG GGAGCGCCAC CAGGACAGGC CAGGACCGGC CAGCTAGAGT GGTGTTTTCG 1620  
 CTCACCTGAG CACACTCCGA GGATGAGGTT GCGGGCCCGC CGCTCACAGC AAGGGCGCGA 1680  
 GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1740  
 55 GGACGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1800  
 GAGCTGCGAG GGAAGCTGTG CAGCCGGCAG CGGCCAGGGT GCCGACACA AGCCCTGGAC 1860  
 CTGCTCTTCA TGTGGACAC CTCTGCCCTCA GTAGGGCCCG AGAATTTTCG TCAGATGCAG 1920  
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGC 2040  
 CTGCTGCTGT ATGCGAGCCA GGTGCAACT GCCTTCGGGC TGGACACCAA ACCCACCCTG 2100  
 60 GCTGCGATGC TCGCGGCCAT TAGCCAGGCC CCTACCTAG GTGGGTGGG CTCAGCCGGC 2160  
 ACCGCCCTGC TGCACATCTA TGAACAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTTGGT 2220  
 GTCGCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCTT 2280  
 GCCCAGAAAG TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGGTGGG GCCTGTCTTA 2340  
 AGTGAGGGTC TGCGGAGGCT TGCAAGTCCC CGGATTCCTG TGTATCCAGT GGCAGCTTAC 2400  
 65 GCGACCTGCG GGTACCAACA GGAAGTGTCT ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG 2460  
 CCAGTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGGGT CCTGCAGAA 2520  
 GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580  
 TGGAGCTCTT TGTGATGATG TGTGAGCCAG GGATGGATTG TTGAGACGCC CCTGAGGCAC 2640  
 ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCTCCCA GCACTACAG AGAAGGCTCT 2700  
 70 GGCACTGAAA TGGTGCTTAC CTTCTGGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760  
 TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820  
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACCAACA AACGATGTTG TTGAAAGTAT 2880  
 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGCTGTG CCTGTTGAG GCTATGCTT 2940  
 CTGCCACCTT TCCCTTGAGG ATAACAAGG GGTCTGAAG ACTTAAATTT AGCGGCTCTG 3000  
 75 OGTTCTTTTG CACACAATCA ATGCTGCCA GAATGTTGTT GACACAGTAA TGCCACAGCAG 3060  
 AGGCCCTTAC TAGAGCATCC TTTGGAGCGC GAAGGCCAAG GCCTTCAAG ATGGAAGACA 3120  
 GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATGAGTC TGAAGGGGGG 3180  
 CTTGAGGAC GTTTGTGACT TCTTGGGAC TGCCTTTTGT GTGTGGAGA GACTTGAAGA 3240  
 GGTCTCAGAC GAAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGA GGGGCTGAGT 3300  
 80 TGTGATGGG CCCAGTCTG GAGGGCCAG TAAATCGTT CTGAGTGTG AGCAGTGTCC 3360  
 ACCTTGAAGG TCTTC

**A45 Protein sequence**

Gene name: ESTs

Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGV domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

10 1 11 21 31 41 51  
 | | | | |  
 MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60  
 SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQPSSTPH LEPLDSFST QQEVKARIKR 120  
 MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180  
 15 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGBA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360  
 RAKVVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVPLDVNSL DGIPFRGGPT 420  
 20 LTGSAIRQAA ERGFGSATRT QDRPRRVVV LLETSHSEDE VAGPARHARA RELLLLGVS 480  
 EAVRAELEEI TGSPKHMVY SDPQDLFNQI PELQKLCSSR QRPQCRTQAL DLVFMLOTS 540  
 SVGPENFAQM QSFVRSICALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APVLGGVGSAT GTALLHIYDK VMTVQRGARP GVPKAVVVLIT GGRGAEDAAV PAQKLNNNGI 660  
 SVLVVGVGFPV LSEGLRRLAG PRDSLIVHAA YADLRVHQDV LIENLCGEAK QPVNLCCKPSP 720  
 25 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780  
 RTPPSNYREG LGTEMVPTFW NVCAPGP

#### COLON

30 A47 DNA SEQUENCE:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 35 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 | | | | |  
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCACAG TTTCTTCCAA CCTTGCCATT 120  
 GCAATAAATA AGGAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
 45 ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCC 300  
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAAACCACTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420  
 GACCCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
 TATGAGCCTC GGGATTATTACC CCTATTGATA GAAAACATGA AGAAAGCAIT AAGACTTATT 540  
 50 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAGAAGT CAAATTTCAT 600  
 GAAGAAAAAC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660  
 TTACTATTTA GTTTTITTA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTITTA 720  
 TCTGAAAAA AAAAAA AAAAAA

55 A48 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 60 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

65 1 11 21 31 41 51  
 | | | | |  
 MMLHSALGLC LLLVTSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60  
 PLMVIHLED CQYSQALKKV FAQNEBIEQM AQNKFIMLNL MHEFTDKNLS PDGQVPRIM 120  
 70 FVDPSLTVRA DIAGRYNRL YTYEPRDLPL LIENMKALR LIQSEL

A49 DNA SEQUENCE  
 Gene name: G protein-coupled receptor 56  
 75 Unigene number: Hs.6527  
 Probeset Accession #: AA478599  
 Nucleic Acid Accession #: NM\_005682  
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 | | | | |  
 CGGCAGCAGG GTCTCGCTCT GTACACAGG CTGGAGTGCA GTGGTGATG CTTGGCTCAT 60  
 CGTAACCTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG 120  
 ATTACAGGTG GTGACTTCCA AGAGTGACTC CGTCGGAGGA AAATGACTCC CCAGTCGCTG 180

	CTGCAGACGA	CACTGTTCTT	GCTGAGTCTG	CTCTTCTGG	TCCAAGGTGC	CCAAGGACAG	240
	GGCCACAGGG	AAGACTTTTG	CTTCTGCAGC	CAGCGGAACC	AGACACACAG	GAGCAGCCTC	300
	CACTACAAC	CCACACACGA	CCTGCGCATC	TCCATCGAGA	ACTCCGAAGA	GGCCCTCACA	360
5	GTCCATGCC	CTTTCCCTGC	AGCCCCACCT	GCTTCCCGAT	CCTTCCCTGA	CCCCAGGGGC	420
	CTCTACCACT	TCTGCTCTA	CTGGAACCGA	CATGCTGGGA	GATTACATCT	TCTCTATGGC	480
	AAGCGTACT	TCTTGCTGAG	TGACAAAGCC	TCTAGCTCC	TCTGCTTCCA	GCACAGGAG	540
	GAGAGCCTGG	CTCAGGGCCC	CCCGCTGTTA	GCCACTTCTG	TCACCTCCTG	GTGGAGCCCT	600
	CAGAACATCA	GCCTGCCAG	TGCGCCAGC	TTCACCTTCT	CCTTCCACAG	TCTTCCCCAC	660
10	ACGGCCGCTC	ACAATGCCCT	GGTGGACATG	TGCGAGCTCA	AAAGGGACCT	CCAGCTGCTC	720
	AGCCAGTTCC	TGAAGCATCC	CCAGAAGGCC	TCAAGGAGGC	CCTCGGCTGC	CCCCGCCAGC	780
	CAGCAGTTGC	AGAGCCTGGA	GTCGAAACTG	ACCTCTGTGA	GATTCAATGG	GGACATGGTG	840
	TCCTTOGAGG	AGGACCGGAT	CAACGCCACG	GTATGGAAGC	TCCAGCCAC	AGCCGGCCTC	900
	CAGGACCTGC	ACATCCACTC	CCGGCAGGAG	GAGGAGCAGA	GCGAGATCAT	GGAGTACTCG	960
	GTGCTGCTGC	CTCGAACACT	CTTCCAGAGG	ACGAAAGGCC	GGAGCGGGGA	GGCTGAGAAG	1020
15	AGACTCTCTC	TGGTGGACTT	CAGCAGCCAA	GCCCTGTTCC	AGGACAGAA	TTCAGCCAA	1080
	GTCTGGGTG	AGAAGGTTT	GGGATTTGTG	GTACAGAAAC	CCAAAGTAGC	CAACCTCAG	1140
	GAGCCCGTGG	TGCTCACTTT	CCAGCACCCG	CTACAGCCGA	AGAATGTGAC	TCTGCAATGT	1200
	GTGTCTCTGG	TTGAAGACCC	CACATTGAGC	AGCCCGGGGC	ATTGGAGCAG	TGCTGGGTGT	1260
20	GAGACCGTCA	GGAGAGAAAC	CCAAACATCC	TGCTTCTGCA	ACCACTTGAC	CTACTTTGCA	1320
	GTGCTGATGG	TCTCTCGGT	GGAGGTGGAC	GCCGTGCACA	AGCACTACCT	GAGCCTCCTC	1380
	TCTTACGTGG	GCTGTGTGCT	CTCTGCCCTG	GCCCTGCCTG	TCACCATTCG	GCCTACCTC	1440
	TGCTCCAGGG	TGCCCTGCCC	GTGCAGGAGG	AAACCTCGGG	ACTACACCAT	CAAGGTGCAC	1500
	ATGAACCTGC	TGCTGGCCGT	CTTCTGCTG	GACACGAGCT	TCCTGCTCAG	CGAGCCGGTG	1560
25	GCCTTGAGAC	GCTCTGAGGC	TGGCTGCCGA	GCCAGTGCCA	TCTTCCCTGA	CTTCTCCCTG	1620
	CTCACTCTCC	TTTCTCGGAT	GGGCTCGAG	GGGTACAACC	TCTACCGACT	GCTGGTGGAG	1680
	GTCTTTGGCA	CCTATGTCCC	TGGCTACCTA	CTCAAGCTGA	GCGCCATGGG	CTGGGGCTTC	1740
	CCCATCTTTC	TGCTGACGCT	GGTGGCCCTG	GTGGATGTGG	ACAATATG	CCCCATCATC	1800
	TTGGCTGTGC	ATAGGACTCC	AGAGGGCGTC	ATCTACCTTT	CCATGTGCTG	GATCCGGGAC	1860
30	TCCTTGCTCA	GCTACATCAC	CAACCTGGGC	CTCTTACGCC	TGGTGTCTCT	GTTCAACATG	1920
	GCATGCTAG	CCACCATGGT	GCTGCAGATC	CTGCGGCTGC	GCCCCACAC	CCAAAAGTGG	1980
	TCACATGTGC	TGACATGCT	GGGCTCAGC	CTGTCTCTTG	GCCCTGCCCTG	GGCCTTGATC	2040
	TTCTTCTCT	TTGCTTCTGG	CACCTTCCAG	CTTGTCTGCT	TCTACCTTTT	CAGCATCATC	2100
	ACCTCTTCT	AAGGCTTCT	CATCTTCTATC	TGGTACTGGT	CCATGCGGCT	CGAGGCCCGG	2160
35	GGTGGCCCTC	CCCTCTGAA	GAGCAACTCA	GACTGCGCCA	GGCTCCCAT	CAGCTCGGGC	2220
	AGCACCTGCT	CCAGCCGAT	CTAGGCTCCT	AGCCCACTG	CCCATGTGAT	GAAGCAGAGA	2280
	TGCGGCTCTG	TGCGACATG	CCTGTGGCCC	CCGAGCCAGG	CCCAGCCCA	GGCCAGTCAG	2340
	CCGACAGACT	TGGAAGCCCC	AACGACCATG	GAGAGATGGG	CCGTGCCAT	GGTGGACGGA	2400
	CTCCCGGGG	TGGGCTTTT	GAATTGGCCT	TGGGGACTAC	TGGGCTCTCA	CTCAGCTCCC	2460
40	ACGGGACTCA	GAAGTGCGCC	GCCATGTCTG	CTAGGGTACT	GTCCCCACAT	CTGTCCCAAC	2520
	CCAGCTGGAG	GCGTGTCTC	TCCTTACAAC	CCCTGGGCCC	AGCCTCATTG	CTGGGGCCCA	2580
	GGCCTTGGAT	CTTGAGGGTC	TGGCACATCC	TTAATCTCTG	GCCCCGCTG	GGGACAGAAA	2640
	TGTGGCTCCA	GTTGCTCTGT	CTCTCGTGGT	CACCTGAGG	GCACCTCTGCA	TCTCTGTCTA	2700
	TTTAACTCT	AGGTGGCACC	CAGGGCGAAT	GGGGCCGAGG	GCAGACCTCT	AGGGCCAGAG	2760
45	CCCTGGCGGA	GGAGAGGCC	TTTGCCAGGA	GCACAGCAGC	AGCTCGCTTA	CCTCTGAGCC	2820

**A50 Protein sequence**

50	Gene name:	G protein-coupled receptor 56
	Unigene number:	Hs.6527
	Protein Accession #:	NM_005682.1
	Signal sequence:	1-26
	GPS domain:	342-394
55	Pfam domain:	7tm_2[400-665]
	Transmembrane domains:	410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
	Cellular Localization:	plasma membrane

60	1	11	21	31	41	51	
	MTPQSLQTT	LPLLSLLFLV	QGAHGRGHRE	DFRFSQRNQ	THRSSLHYKP	TPDLRISIE	60
	SEALTVHAP	PAAHPASRS	FPDPRGLYHF	CLYWNHAGR	LHLLYGRDP	LLSDKASSLL	120
	CFQHEESLA	QGPPLLATSV	TSWNSPQNIS	LPSAASFTPS	FHSPFHTAAH	NASVDMCEKL	180
65	RDQLQLSQFL	KHPQKASRRP	SAAPASQQLQ	SLESKLTSVR	FMGDMVSFEE	DRINATVWKL	240
	QPTAGLQDLH	IHSRQEEQS	EIMEYSVLLP	RTLFRQTKGR	SGEAEKRLLL	VDFSSQALPQ	300
	DKNSSQVLGE	KVLGIUVQNT	KVANLTFPVV	LTFQHLQPK	NVTLCQVFWV	EDFTLSSPGH	360
	WSSAGCSTVR	RETQTSFCFN	HLTYFAVLNV	SSVEVDAVHK	HYLSLLSVYG	CVVSALACL	420
	TIAYLCSRVR	PLPCRKPRD	YTIKVMNLL	LAVFLDTSF	LLSEPVALTG	SEAGCRASAI	480
70	FLHFSLLTCL	SWMGLBSYNL	YRLVVEVFGT	YVPGYLLKLS	AMGWGFPIPL	VTILVALVDVD	540
	NYGPIILAVH	RTPEGVIYPS	MCWIRDSLVS	YITNLGLFSL	VFLPNMAMLA	TMVVQILRLR	600
	PHTQKWSRVL	TLGLSLVLG	LFWALIFFSP	ASGTFQLVVL	YLFSTITSFQ	GFLPIPIWTS	660
	MRLQARGGPS	PLKNSDCAR	LPISSGSTSS	SRI			

**A51 DNA SEQUENCE**

75	Gene name:	Hypothetical protein FLJ20063
	Unigene number:	Hs.5940
	Probeset Accession #:	AA053660
	Nucleic Acid Accession #:	AA053660
80	Coding sequence:	218-1360 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	CCCCATGAC	TTTGACAGC	TACTTCACTG	CTTCCCCCA	ATTAGTACAC	ATAGTCTCTC	60

5 CACAATTCCT ACACCTGCTC CCCCCATAAT CAGTACACAT AGTTCCTCCA CAATTCCTAT 120  
 ACCTACTGCT GCAGACAGTG AGTCAACCAC AAATGTAAT TCATTAGCTA CCTCTGACAT 180  
 AATCACCCTC TCATCTCCAA ATGATGGATT AATCACAATG GTTCTCTCTG AAACACAAAG 240  
 TAACAATGAA ATGTCCCCCA CCACAGAAGA CAATCAATCA TCAGGGCTC CCACCTGGCAC 300  
 CGCTTTATGG GAGACAGCA CCCTAAACAG CACAGGTCCC AGCAATCCTT GCCAAGATGA 360  
 TCCCTGTGCA GATAATTCGT TATGTGTAA GCTGCATAAT ACAAGTTTTT GCCTGTGTTT 420  
 AGAAGGGTAT TACTACAACT CTTCTACATG TAAGAAAGGA AAGGTATTCC CTGGGAAGAT 480  
 TTCAGTGACA GTATCAGAAA CATTTGACCC AGAAGAGAAA CATTCCATGG CCTATCAAGA 540  
 10 CTTGCTATAGT GAAATTACTA GCTTGTATA AGATGTATTT GGCACATCTG TTTATGGACA 600  
 GACTGTAAAT CTTACTGTAA GCACATCTCT GTCAACAGA TCTGAAATGC GTGCTGATGA 660  
 CAAGTTTGTG GATGTAACAA TAGTAACAAT TTTGGCAGAA ACCACAAGTG ACAATGAGAA 720  
 GACTGTGACT GAGAAAAATTA ATAAAGCAAT TAGAAGTAGC TCAAGCAACT TTCTAAACTA 780  
 TGATTTGACC CTTGGTGTGG ATTATTATGG CTGTAACAG ACTGCGGATG ACTGCCTCAA 840  
 15 TGGTTTAGCA TGGGATTGCA AATCTGACCT GCAAGGCCT AACCACAGA GCCCTTCTG 900  
 CGTGTCTCC AGTCTCAAGT GTCCTGATGC CTGCAACGCA CAGCACAAGC AATGCTTAAT 960  
 AAAGAAGAGT GGTGGGGCCC CTGAGTGTGC GTGCGTGCCC GGCTACCAGG AAGATGCTAA 1020  
 TGGGAAGCTC CAAAAGTGTG CATTGTGCTA CAGTGGACT GACTGTAAAG ACAAAATTCA 1080  
 GCTGATCCTC ACTATTGTGG GCACCATGCG TGGCATTGTC ATTCTCAGCA TGATAATTGC 1140  
 20 ATTGATTGTC ACAGCAAGAT CAAATAACAA AACGAAGCAT ATTGAAGAAG AGAACTTGAT 1200  
 TGACGAAGAC TTTCAAATTC TAAACTGCG GTGACAGGC TTCAACCAATC TTGGAGCAGA 1260  
 AGGGAGCGTC TTTCCTAAGG TCAGGATAAC GGCTCCAGA GACAGCCAGA TGCAAAATCC 1320  
 CTATTCAAGT CACAGCAGCA TGCCCCGCC TGAATTATG AATCATAAGA ATGTGGAAAC 1380  
 CGCCATGGCC CCCAACCAAT GTACAAGCTA TTAATTAGAG TGTTTAGAAA GACTGATGGA 1440  
 25 GAAGTGAGCA CCAATTAAGA TCTGGCCTCC GSGGTTTTTC TTCCATCTGA CATCTGCCAG 1500  
 CCTCTCTGAA TGGAAAGTGT GAATGTTTGC AACGAATCCA GCTCACTTGC TAAATAAGAA 1560  
 TCTATGACAT TAAATGTAGT AGATGCTATT AGCGCTTGTC AGAGAGGTGG TTTTCTTCAA 1620  
 TCAGTACAAA GTACTGAGAC AATGGTTAGG GTTGTTTTCT TAATCTTTT CCTGGTAGGG 1680  
 CAACAAGAAC CATTTCGAAT CTAGAGGAAA GCTCCCGAGC ATTGCTTGCT CCTGGGCAAA 1740  
 30 CATTGCTCTT GAGTTAAGTG ACCTAATTCC CTGGGAGAC ATACGCATCA ACTGTGGAGG 1800  
 TCCGAGGGGA TGAGAAGGGA TACCCACCAT CTTTCAAGGG TCACAAGCTC ACTCTCTGAC 1860  
 AAGTCAGAA AGGGACACTG CTTCTATCCC TCCAATGGAG AGATTCTGGC AACCTTTGAA 1920  
 CAGCCAGAG CTTGCACACT AGCCTCACCC AAGAAGACTG GAAAGAGACA TATCTCTCAG 1980  
 CTTTTCAGG AGGCGTGCTC GGGAAATCCAG GAACCTTTTG ATGCTAATTA GAAGGCCTGG 2040  
 35 ACTAAAAATG TCCACTATGG GGTGCACCTC ACAGTTTTTG AAATGCTAGG AGGCAGAAAG 2100  
 GGCAGAGAGT AAAAAACATG ACCTGGTAGA AGGAAGAGAG GCAAGGAAA CTGGGTGGGG 2160  
 AGGATCAATT AGAGAGGAGG CACCTGGGAT CCACCTTCTT CCTTAGGTCC CCTCTCCAT 2220  
 CAGCAAAAGGA GCACCTCTCT AATCATGCC TCCGAAGAC TGGCTGGGAG AAGGTTTAAA 2280  
 AACAAAAAT CCAGAGAGTA GAGCCTTAGG TCAGTTTGAA ATTGGAGACA AACTGTCTGG 2340  
 40 CAAAGGGTGC GAGAGGGAGC TTGTGCTCAG GAGTCCAGCC GTCCAGCCTC GGGGTGTAGG 2400  
 TTTCTGAGGT GTGCAATTGG GGCTCAGCC TTCTCTGGT ACAGAGGCTC AGCTGTGGCC 2460  
 ACCAACACAC AACCAACAC ACACAACCAC ACACAACAAT GGGGGCAACC ACATCCAGTA 2520  
 CAAGCTTTTA CAAATGTTAT TAGTGTCTT TTTTATTCT AATGCCTTGT CCTCTTAAAA 2580  
 45 GTTATTATTAT TTGTTATTAT TATTGTCTT TGACTGTTAA TTGTGAATGG TAATGCAATA 2640  
 AAGTGCCTTT GTTAGATGTT GAAAAAATA AAAAAAATA AAAAAAATA A

**A52 Protein sequence:**

Gene name: Hypothetical protein FLJ20063  
 50 Unigene number: Hs.5940  
 Probeset Accession #: AA053660  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 289-311  
 55 EGF domain: 45-74  
 SEA domain: 80-196  
 Cellular Localization: plasma membrane

60 1 11 21 31 41 51  
 | | | | |  
 MVPSETQSN EMSPITTEDNQ SSGPPTGTAL LETSTLANSTG PSNQCQDDPC ADNSLCVKLH 60  
 NTSFCLCLEG YYNSSTCEK GKVPFGKISV TVSETFDPEE KHSMAVQDLH SEITSLFKDV 120  
 FGTSVYGQTV ILTVSTSLSP RSEMRADDFK VDVITVITLA ETTSDEKTV TEKINKAIRS 180  
 65 SSSNPLNYDL TLRCDYGCN QTADDCLNGL ACDCSDLQR PNPQSPFCVA SSLKCPDACH 240  
 AQHKQCLIKK SGAPEACACV PGYQEDANGN CQKCAFYSG LDCKDKFOLI LTIVGTIAGI 300  
 VILSMIALI VTARSNNKTK HIEBENLIDE DFQNLKLRST GFTNLGAEGS VPPKVRITAS 360  
 RDSQMNPYS RHSSMRPDY

**A53 DNA SEQUENCE**

70 Gene name: TMFRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 75 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 | | | | |  
 ACCGGGCACC GGAAGGCTCG GGTACTTTCTG TTTCTTAATTA GGTATGCCCC GTGTGAGCCA 60  
 GGAAGGGCTG GTGTTTATGG GAAGCCAGTA AACTGTGTGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180  
 AGAGGTCTCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240

5 TCATCCGAT CGCTTTTGG CCTTGATGAT TTGAAATAA GTCTGTGTC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCAGCTGC 420  
 TCAGGGAAGT ACAGATGTGCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TOGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA OGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
 10 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCCCTCG GCCACGTGGT TACCTTGCAG TGACACAGCT GTGGTCATAG AAGGGCTAC 840  
 AGCTCAOGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900  
 CTTGAGTTCC AGGGCTACCA CCGTGTGCGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 15 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGGCC TTATGAAGCT GGCAGGCCCA 1140  
 CTCAGCTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GATGGAAGAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCCTGTCC TGAACCAAGC GGCGCTCCCT TTGATTTCCA ACAAGATCTG CAACCAACAGG 1320  
 20 GACGTGTACG GTGGCATCAT CTCCCCTCC ATGCTCTGCG OGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCGCTGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGGACACAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCG AGGTGATGAA GACAGCCCGA 1620  
 25 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCGGGCACC AGTAGCAGCG CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCGCTT CCTCGGTTCA AGCGATTCTC 1860  
 TTGCTCAGC TTCCCAGTA GCTGGGACCA CAGGTGCCCG CCACACACC CAACTAATTT 1920  
 30 TTGTATTTT AGTAGAGACA GGGTTTCACT ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAATGA TGTGCTGCT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040  
 ACGCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTGTGA 2100  
 AGGGCGGCTT TCCCACTGGT TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160  
 ACGAGATAAG CAGTTATGTG AOCTCACGTG CAAAGCCACC AACGCCACT CAGAAAGAC 2220  
 35 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAOGTT TTTCTCTCTA GGGACCAGAA 2280  
 CCAACCCAC CCTTCTTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCCTAT TTTTATGATT TCTTTGTAGC ATTTGGTGTG TGACGTATTA 2400  
 TTGTCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAA

**A54 Protein sequence:**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 55 MGENDPFAVE APFSFRSLFG LDDLKISFVA PDADAVAQI LSLPLKFFP IIVIGIILI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIBLIA RCGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120  
 TAASWTKMCS DDWKGHYANV ACAQLGPPSY VSSDNLRVSS LEGQFREBFV SIDHLLPDDK 180  
 VTALHSHSVV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240  
 LCGSVITPL WITTAARCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCMT SGWGATEDGA GDASPVLAHA 360  
 60 AVPLISNKC NHRDVYGGII SPSMLCAGYL TGGVDSQGD SGGPLVCQER RLWKLVGATS 420  
 FGIICAEVKN PGVYTRVTSF LDWIHEQMER DLKT

**A55 DNA SEQUENCE**

Gene name: Putative G protein-coupled receptor GPCR150  
 Unigene number: Hs.97101  
 Probeset Accession #: AA215333  
 Nucleic Acid Accession #: NM\_014373  
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 70 GTGGCTCGA GGTGGTGGCA GGGCGGCCCC CTGCAGTCCG GAGACGAACG CACGGACCGG 60  
 GCCTCCGGAG GCAGGTTCCG CTGGAAGGAA CCGCTCTCGC TTCGTCTTAC ACTTGCACAA 120  
 75 ATGTCTCGCA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180  
 AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240  
 GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATTT CAGCAGGTCT 300  
 TCTTGAATTT TAATAAAAA TAAGACTGCT CTCTCTTCAG AGAACTGCTC TTTTCAGTAC 360  
 CAGTTACGTC AAACAAACCA GCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420  
 80 GGGAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAT 480  
 TTTATGGAAT ATTTTGTGAT TTCCTAGCA TTCGTTGATC TTTTACTTTT GGTAAACATT 540  
 TCCATTATAT TGTATTTTCA GGAATTTGTA CTTTAAAGCA TTAGTTTCA TAAATACCAC 600  
 ATCTGCCTAT TTAATCAAT TATTTCCTTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC 660  
 CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCTAAAA CAACCAAGCT TTCAATTAG 720  
 TGTCAAAAT TATTTTATTT CTTTACAGTA ATTTTAATTT GGAATTCAGT CCTTGCTTAT 780



5 GTTTTGGGAG ACCCAGCCAT CTACCAAAGC CTGAAGGCAC AGAATGCTTA TTCTGTCAC 840  
 TGCTCTTTCT ATGTGAGCAT TCAGAGTTAC TGGCTGTCAT TTTTCATGGT GATGATTTTA 900  
 TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960  
 ACTTCCTATA TGAATGAAAC TATCTTATAT TTCTCTTTT CATCCACTC CAGTTATACT 1020  
 GTGAGATCTA AAAAATATTT CTTATCCAAG CTCATTGTCT GTTTTCTCAG TACCTGGTTA 1080  
 CCATTGTATC TACTTCAGGT AATCATTTGT TTACTTAAAG TTCAGATTCC AGCATATATT 1140  
 GAGATGAATA TTCCCTGGTT ATACTTTGTC AATAGTTTTT TCATTGCTAC AGTGTATTGG 1200  
 TTTAATTTGC ACAAGCTTAA TTTAAAGAC ATTGGATTAC CTTTGGATCC ATTGTCAAC 1260  
 10 TGGAGTGTCT GCTTCATTCC ACTTACAATT CCTAATCTTG AGCAAAATGA AAAGCCTATA 1320  
 TCAATAATGA TTTGTTAATA TTATTAATTA AAAGTTACAG CTGTCATAAG ATCATAATTT 1380  
 TATGAACAGA AAGAAGCTCAG GACATATTAA AAAATAAACT GAACATAAAC AACTTTTGCC 1440  
 CCCTGACTGA TAGCATTTC AATGTGTCT TTTGAAGGGC TATACCAATT ATTAAATAGT 1500  
 GTTTTATTTT AAAACAACAA TAAATCCAAG AAGTTTTTAT AGTTATTTCAG GGACACTATA 1560  
 15 TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACATT TGGCTATACT 1620  
 GATGTTTGTG TTAAGTCAAA AACTACTGG ATGCAAACTG TTATGTAAAT CTGAGATTTC 1680  
 ACTGACACTT TTAAGATATC AACCTAAACA TTTTATTAA ATGTTCAAA GTAAAGCAAGA 1740  
 AAAAAAAAA

#### 20 A56 Protein sequence

Gene name: Putative G protein-coupled receptor GPCR150  
 Unigene number: Hs.97101  
 Protein Accession #: NP\_055188  
 Signal sequence: none found  
 25 Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297  
 Cellular Localization: plasma membrane

30 1 11 21 31 41 51  
 | | | | |  
 MTALSSSENC FQYQLRLNQ PLDVNYLLPL IILGKILLNI LTLGMRKNT CQNFMEYFCI 60  
 SLAFVLLLL VNISILLYFR DFVLLSIRFT KYHICLPTQI ISFTYGLHY PVFLTACIDY 120  
 CLNFSKTLK SFKQCLFYF FTVILINISV LAYVLGDPAL YQSLKAQWAY SRHCPFYVSI 180  
 QSYWLSFFMV MILFVAFITC WEEVTLVQA IRTSYMNET ILYPPFSSHS SYTVRSKKIF 240  
 35 LSKLIVCFIS TWLPFVLLQV IIVLLKVQIP AYIEMNIPWL YPVNSFLIAT VYWFNCHKLN 300  
 LKDIGLEPLD FVNWKCCFIP LITPNLEQIE KPISIMIC

#### 40 A57 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 | | | | |  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAAGGTTT GGAGATGATG 120  
 50 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTTGG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGCCCC CCGTCCCTGC CCGTACGTCC 360  
 55 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAAACGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCAAGC AGCTGGAGCA GGAGAGTCG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCGCG GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTGTGTGGCC GGGTGGGCCC CCAGGGCCAG CTTGGCACTC 600  
 AGCCCTTCGA GGGTGGGCGC CCATCGCAC CCACTCTCTC TGGCTGGAGA CCGCCGCGAG 660  
 60 GCCCAGGCAC AGTCCCGGAG TGGGGGCTT CTGCGGCC TTGCCAGATG GGCTCCCGAG 720  
 GCGTGGCCCC GCGTGGTCCC CGCACCGAGC GCTTGACTCC GTTTGGGCTC CTGGTTGTGT 780  
 ACATGGGCTG GGGGCTCTCT TAGTCCGCA TAGTCCGAG CTAAGTCTGG CCGCTGTGAG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCG TTTCCAGCGG TGCCGCGCTG 900  
 GGTCCCATCT TCAGGGAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960  
 65 AGAGGGGCGG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGCGAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCTGGCC TGGCTGGGGA GCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140  
 CTGGCCAGG CTGAGGGACC CTGGCTGAGC CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200  
 GGCTGCAATG TGCCTCCAC AGACCTTGGG GTGATGGCTT TCCCTCTCTT GGCCGGGACG 1260  
 70 TTGCCCCAGG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCGAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCAAGTCA TAGGCAAGGC CTGTTTCCCC CGACTCAGGA TTTCCAGGCG 1380  
 CTGGGGTCTT GCTCACCCCC CTTTGCTCTC AGCCCCAGCC TGTCCCGAGG TTTTCTGCTG 1440  
 GAGAGGCCAC CTCCTCAGC CAAGGAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500  
 GGCAAGTCCC CTGGGTGTC ACTCCCTCAG CCCCCTGCCA GGCCCACTCC CGCTGGTGTCT 1560  
 75 GGAGTAGCCA CTGGTGGGGG GGCCCTGTCT AGCCCAACCT GGAGGGTCCC AGTGTCAACA 1620  
 GAACAGGGG CACCGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGCGCAG GGCTCCGAT GCGGGGTGAG TGGCTGGGGG GCGCAGGGCC 1740  
 CCGATGCGG GGTGAGTGGG TGGGGGGGCG AGGGCCCCCT CGTGTCCAGG GCACCTTGGT 1800  
 ACACCTGTCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860  
 80 CCTTCCGAGC CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920  
 TGCTGCACCT GGTCTGAGG GGTGTCCAG GACAGGCCCA AGTCAGGCCA GCATGCACTC 1980  
 GCGCTCTAC CCGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCTGGG 2040  
 ACCTCTGGG CAGGAAGGGG TGCAAGTCTT GAGGGGCTGT GCGCCACAGC CCCAGCACCC 2100  
 AGGTGGAAGT CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGTTCAGCA 2160  
 GGCTGGGGTC TGCCACCCAG GCCTTCCCCA CGTCTGCCCT TGAGGGTGGC TGCCATGCCC 2220

5	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGAGACC	GCCCACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCCTCG	GAAGAACTGC	CTTTACGCCT	TGGTGTTCGG	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAAGTG	CCCTGGAGAC	2460
	CACGAGGGGA	GAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GOTGGCTGGC	AGAGGCACAT	2520
	GCAGACCCTG	CCTGGAGCCT	GCCCTAGGAC	GCTGGGCGGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CCTGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAAGT	ACATACACGT	2640
	CGGTGCACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
10	CAGAAAGTGC	CCAGATTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GCCTCAGGA	2760
	TTTTGTGTGG	ATCAAGTTCC	AAGGAAAGG	AACATCTCAG	CCGGGCGTGG	TGGTTCACGC	2820
	CTGGAATCCC	AGCACTTGAG	GCCAGGAGTT	CCAGAGCAGC	CTGGGCAACG	CAGTGAGAGA	2880
	CCCCATCTCT	ACAAAGAAAA	AAAAAGAAAG	AAAGAAATG	AGAGATCCAG	GTTTAAAAAT	2940
	TCATAAACAC	CACAAGGAAA	CAATACACTA	TGAGACCCAG	CAGAAGCAAC	AGATTGACTC	3000
15	TAGACCCAGA	TACTAGAATT	ATCAGAGAGA	ATATAAAGTA	ACAGTGTTTT	ATATATCTAA	3060
	AGAAATAAAA	GAGATTTCTG	GAAACATGAA	AAAAAA			

A58 DNA sequence

	Gene name:	ESTs
	Unigene number:	Hs.157601
20	Probeset Accession #:	W07459
	Nucleic Acid Accession #:	AC005383
	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

25	1	11	21	31	41	51	
	GACAGTGTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
	TTTTATTTCG	AGACCTGGGC	CGATGCCGCT	TTAAAAACG	CGAGGGGCTC	TATGCACCTC	120
	CCTGCGCGTA	GTCTCTCCGA	CCTCAGCCGG	GTGCGGTGCT	GCGGCCCTCT	CCAGGAGAG	180
30	ACAAACAGGT	GTCCACAGTG	GCAGCCGCGC	CCCGGGCGCC	CCTCCTGTGA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TGCGCGCTCT	CCTTCCGTTA	TATCAACATG	CCCCCTTTCC	TGTGTCTGGA	GGCGGTCTGT	360
	GTTTTCTCTG	TTTCCAGAGT	GCCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAAA	420
	GAAACCATCG	GGAAGATTTC	AGCTGCCAGC	AAAATGATGT	GGTGCTCGGC	TGCAGTGGAC	480
35	ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTCCGGGAAAG	GGAGCTTTGA	AAGGTCCAAG	540
	CACCTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTTCCCT	TGGATTCAAT	TTCAACCCAA	660
	CAGGAAGTGA	AGGCAAGRAAT	CAAGAGGATG	GTTTTCAAG	GAGGGCGCAC	GGAGACGGAA	720
40	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCTGGAG	GCAGAAATGC	TTCTGTGCC	780
	CAGATCCCTCA	TCATCGTCAC	TGATGGGAAG	TCCACGGGGG	ATGTGGCACT	GCCATCCAAG	840
	CAGCTGAAGG	AAAGGGGTGT	CACGTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
	GAGCTGCATG	CACTGGCCAG	CGAGCCTAGA	GGGCAGCAGG	TGCTGTTGGC	TGAGCAGGTG	960
	GAGGATGCCA	CCAGCGGCCT	CTTCAGCACC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020
45	ACGCCAGACT	GCAAGGTGGA	GGCTCACCCC	TGTGAGCACA	GGACGCTGGA	GATGGTCCGG	1080
	GAGTTGCGTG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGACCCCTTG	GGTGTGGCT	1140
	GCACACTGTC	CTTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCACCTTGC	CACCTGTCTAC	1200
	AGGACCACCT	GCCCAGGCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
	CCAGAGGAGC	TGGAAGGCTA	CCAGTGCCCT	TGCCCGCTGG	CCTTTGGAGG	GGAGGCTAAC	1320
50	TGTGCCCTGA	AGCTGAGCCT	GGATGACAGG	GTGGAACCTC	TCTTCTGCTG	GGACAGCTCT	1380
	GCGGGCACCA	CTCTGGACGG	CTTCTGCGGG	GCCAAAGTCT	TCGTGAAGCG	GTGTTGTGGG	1440
	GCGGTGCTGA	GCGAGGACTC	TGCGGGCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
	CTGGTGGGCG	TGCTGTGGGG	GGAGTACCA	GATGTGCTGG	ACCTGGTCTG	GAGCCTCGAT	1560
	GGCATTCCCT	TCCGTGTGGG	CCCCACCCCT	ACGGGCACTG	CCTTGGCGCA	GGCGGCAGAG	1620
55	CCTGGCTTGG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAAT	GGTGGTTTGG	1680
	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCAG	GCGTCAACGC	AAGGGCGCGA	1740
	GAGCTGTCTC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
	GAGCTGCAGG	GGAAGCTGTG	CAGCGGCGAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
60	CTGCTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	1980
	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTCCGC	2040
	CTGGTGGTGT	ATGGCAGCCA	GGTGCAGACT	GCCTTGGGGC	TGGACACCAA	ACCCACCCCG	2100
	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	COCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
	ACCGCCCTCG	TGCACATCTA	TGACAAAGTG	ATGACCTCC	AGAGGGGTGC	CCGGCCTGGT	2220
65	GTCCCAAGAG	CTGTGGTGGT	GCTCACAGGC	GGGAGAGGGG	CAGAGGATGC	AGCGGTTCTC	2280
	GCCCAGAAGC	TGAGGAACAA	TGGCATCTCT	GTCTTGTGCG	TGGGCGTGGG	GCCTGTCTTA	2340
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGGATTCCC	TGATCCACGT	GGCAGCTTAC	2400
	GCGACCTGCG	GGTACCACCA	GGACGTGCTC	ATTGAGTGGC	TGTGTGGAGA	AGCCAAGCAG	2460
	CCAGTCAACC	TCTGCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAA	2520
70	GGGAGCTACC	GCTGCAAGTG	TGCGGATGGC	TGGGAGGGCC	CCCAGTGGGA	GAACCGTGG	2580
	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATTG	TTGAGAGGCC	CCTGAGGCAC	2640
	ATGGCTCCCG	TGCGAGAGGG	CAGCAGCGGT	ACCCCTCCCA	GCAACTACAG	AGAAAGGCGT	2700
	GTCAGCTGAA	TGGTGCCTAC	CTTCTGGAAT	GTCTGTGCC	CAGGTCTCTA	GAATGTCTGC	2760
	TTCCCGCGGT	GGCCAGGACC	ACTATTCTCA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC	2820
75	ATGCTGTCTA	GAGACAAGAA	AGCAGCTGAT	GTCAACCCCA	AACGATGTTG	TTGAAAGATT	2880
	TTGATGTGTA	AGTAAATACC	CATTTCTGT	ACCTGCTGTG	CCTTGTGAG	GCTATGTCT	2940
	CTGCCACCTT	TCCCTTGAGG	ATAAACAAGG	GGTCTGTAAG	ACTTAAATTT	AGCGGCTGTA	3000
	CGTTCTCTTG	CACACAATCA	ATGCTGCCCA	GAATGTGTT	GACACAGTAA	TGCCAGCAG	3060
	AGGCCCTTAC	TAGAGCATCC	TTTGGACGGC	GAAGGCCACG	GCCTTTCAAG	ATGGAAAGCA	3120
	GCAGCTTTTC	CATTTCCCCA	GAGACATTCT	GGATGCATTT	GCATTGAGTC	TGAAAGGGGG	3180
80	CTTGAGGGAC	GTTTTGTGAT	TCTTGGCGAC	TGCCTTTTGT	GTGTGGAAGA	GACTTGGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGGA	GGGGCTGAGT	3300
	TGTGCATGGG	CCAGGTCTG	GAGGGCCACG	TAAATCGTT	CTGAGTCGTG	AGCAGTGTCC	3360
	ACCTTGAAGG	TCTTC					

**A59 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 BGF domains: 298-333; 715-748  
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLLEAV CVFLPSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSGN 60
    SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQPSSTPH LEFPLDSFST QQEVKARIKR 120
    MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
    FAVGVPRPFR BEELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPPGCD 300
    SPPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
    RAKVFEVRFV RAVLSDSRA RVGVATYSRE LLVAVFVGEY QDVDPDLVWSL DGIPFRGGPT 420
    LTGSALRQAA ERGFGSATRT QQDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVGS 480
    EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSS RPPGCRQTAL DLVFMIDTSA 540
    SVGPENPAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
    APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLNRNGI 660
    SVLVVGVGPF LSEGLRRLAG PRDSLHVAA YADLRVHQDV LIEWLCEGAE QPVLNCKPSP 720
    CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
    RTPPSNVYREG LGTEMVPTFW NVCAPEGP
  
```

**A60 DNA SEQUENCE**

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTTCACAG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
    AAACCCCGTA TCCCATGGA GACCTTCAGA AAGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
    CTGGAAGTGC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
    45  GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCCACTGCG AGGTGCTGGA CTCGGCCACA 360
    GGGAACTGGT TCTCTGCTCTG TTTCGACAA TCCACAGAAG CTCTCGCTGA GACAGCCTGT 420
    AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCTG 480
    GATCTGGATG TTGTTGAAT CACAGAAAC AGCCAGGAGC TTGCTATGCG GAACTCAAGT 540
    50  GGGCCTGCTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGCG GAAGAGCCTG 600
    AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
    AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGAGCC CCACTGGGTC 720
    CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
    GGCTCAGACA AACTGGGCAG CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
    55  TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
    ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
    GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAAG AGAATGGAGG GAAGATGTCT 1020
    GACATACATG TCAGAGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAG TGCAGAGCAT 1080
    GCGTACCAAG GGAAGATCAC CAGAAAGATG ATGTGTGCAG GCATCCCGSA AGGGGGTGTG 1140
    60  GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
    GTGGGCTACG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
  
```

**A61 Protein sequence:**

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 70 LDL domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

```

1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSQPF LNSLDVKPLR KPRIPMTFR KVGIPITIAL LSLASIIIVV VLIKVILDKY 60
    YFLCGQLPHF IPRRLQCDGE LDCPLGEDEE HCVKSPPEGP AVAVRLSKDR STLQVLDSAT 120
    80  GWNFSACFDN FTEALAEATC RQMGYSSEKPT FRAVEIGFDQ DLDVVEITEN SQLEMRNNS 180
    GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWPHQV SIQYDKQHVC GGSILDPHWV 240
    LTAHCFRKH TDVFNKVRV GSDKLGSFSS LAVAKIIIE FNFMYPKDND IALMKLQFPL 300
    TFSGTVRPIC LPPFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
    AYQGEVTERK MCAGIPEGGV DTCQGDSSGP LMYQSDQHEV VGIWSWGYGC GGPSTPGVYT 420
    KVSAYLNWYI NVWKAEI
  
```

**A62 DNA SEQUENCE**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
CTGAGATCCT TGCATAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
AGACCCAGCT GTGCTCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCACT CTTACGAAA CGGAGCCCAC 300
CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCATGGCAG 420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTTGGAGCAG CAACGAATGC 540
AACAAAGGCC AACCTTCTCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
AACTCCTGCA CCAGCCCCGT CCTCTTCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTITA 720
GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG 780
CCCCGCCATC CTTTCCACA GTATCCTTCT TCCCTCCTCC CCTGTCTCTG GCTGTCTCGA 840
GCAGTCTAGA AGAGTGATC TCCAGCCTAT GAAACAGCTG GGTCTTGGC CATAAGAAGT 900
AAAGATTTGA AGACAGAAGG AAGAAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCTTCTT GCCTCTCTC CATTGCTGAC ACCCCACCCC AGCCACTCAA CTCTGCTGCT 1020
TTTTCTCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCGA 1080
TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

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**A63 Protein sequence:**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Protein Accession #: none found  
 Signal sequence: 1-22  
 Transmembrane domains: none found  
 C-type lectin domain: 47-156  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSG AFGWFYHKSN CYGYPRKLRL WSDAELECOQS 60
YNGNAHLASI LSLKEASTIA EYISGVQRSG PIWIGLEHDPQ KRQWQWIDG AMYLYRSWSG 120
KSMGGNKHCA EMSSNNNFLT WSSNECNKRO HFLCKYRP

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**A64 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

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1      11      21      31      41      51
|      |      |      |      |      |
GCGGAACACC GGCCCGCGGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCTCTGTGG ACCTCTCGCG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGAGGCGG 180
GGGAGCAGCA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCAATCCAAA CGTATCTTAC 360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
TCATCTGTAC CGACCAAGAT GACCAACAGC CCAAGTTTAC CAGGACACC TTCCGAGGGA 720
GTGTCTTAGA GGGAGTCCTA CCAGTACTTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
CCAGTGGGCT GGACCGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA GGGCTCCACC ACCAOCGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAATGCTCC CATGTTTGAC CCCCAGAAGT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAGCG CCCCACTCA CCAAGCTGGC 1140
GTGCCACCTA CCTATTGATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCAACC 1200
CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
CCTCCAAAGT GGTGAGGTC CAGGAGGGCA TCCCACCTGG GGAGCCTGTG TGTGTCTACA 1440
CTGCAGAAGA CCTTGACAAG GAGAACTAAA AGATCAGCTA CGCATCTCTG AGAGACCCAG 1500

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CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGAGTGA GCACTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCCACTACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
 ACCATGGGCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740  
 5 ACGTGTCTGA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCCAGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACTTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 10 ATGTGAAAC CTGCCCTGGA CCTGGAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCCTC CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAGGAGGCC CCTCTACTC CCAGAAGATG ACACCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGC TGGCGAAGAG GACCAAGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 15 AGSCGGCTAA CACAGACCCC ACAGCCCCG CCTACGACAC CCTCTTGGTG TTCGACTATG 2400  
 AGGCGACGG CTCCGACGCC GGTCCCTGA GCTCCCTCAC CTCTCGGCC TCCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACGGTGGCGG GGAGGACGAC TAGSCGGCCT GCCTGCAGGG CTGGGGACCA AACGTGAGGC 2580  
 CACAGAGCAT CTCCAAGGGG TCTCAGTTC CCCTTCAGCT GAGGACTTCG GAGCTTGTC 2640  
 20 GGAAGTGGCC CTGCAACTT GCGCGAGACA GGCTATGAG CTGACGTTAG AGTGGTTGCT 2700  
 TCCTTAGCCT TTCAAGATGG AGGAATGTGG GCACTTTGAC TTCAGCACTG AAAACCTCTC 2760  
 CACCTGGGCC AGGGTTGCC CTGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCTGAAAA 2820  
 TGCTCAACCC TGTGTCTCTG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 25 CTGGAATGGA ACCTCTTAG GCCTCTGCT GCACTTAAAT TTTTCTTTT AATGCTATCT 2940  
 TCAGAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCG 3000  
 TCTCTGATT TTGGTTTCCA GACCCCAATG CCTCCATTC GGATGGATCT TCGGTTTCT 3060  
 ATACTGAGTG TGCTAGGTT GCCCTTATT TTTTATTTT CTTGTGCGT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAATTTTT TATTAAAGAA A

#### A65 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 35 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)  
 Cellular localization: plasma membrane

1 11 21 31 41 51  
 MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTL EA GGAEQEPQQA LGKVFMGCPG 60  
 QEPALFSTDN DDPFVRNGET VQERRSLKER NFLKIPPSKR ILRRHRRDWV VAPISVPENG 120  
 45 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWL LN KPLDREEIAK 180  
 YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAIYTNV GVVAYSISHQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TMDMDGSGTT TAVAVVEILD ANDNAPMFDQ QKYBAHVPEV AVGHEVQRLT VTDLDAPNSP 360  
 50 AWRATYLING GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDK E NQKISYRILR 480  
 DPAGWLAMPD DSGQVTVAGT LDREDEQFVR NNIYEVMLVA MDNGSPPTTG TGTLLLLTID 540  
 VNDHGVPVPEP RQITICNQSF VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKPL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660  
 55 GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVYF YGEBGGGEED QDYDITQLHR 720  
 GLEARPEVLV RNDVAPTIIP TFMVPRPAN PDEIGNPIE NLKAANTDEPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

#### A66 DNA SEQUENCE

60 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Nucleic Acid Accession #: AF189723  
 65 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 70 TTTCTATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTTCCTGGCT CTGCACTCAT CAGTGTTTTA 240  
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTACAGTT 300  
 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360  
 75 CCAGATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420  
 CCAGGTGATA CAGTTTGCCT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTCT 480  
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCTC 540  
 AAGGTGACAG CTCTCAGCC AGCTGCAACT AATGGAGATC TTGATCGAG AAGTAACATT 600  
 80 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTGTTCAT TGGAACAGGA 660  
 GAAATTTCTG AATTGTGGGA GGTTTTAAAT ATGATGCAAG CAGAGAGGCC ACCAAAAACC 720  
 CCTCTGAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780  
 ATAGGAATCA TCATGTTGGT TGGCTGTGTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840

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ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTACAGTG 900
ACGCTAGCTC TTGGTGTAT GAGAAATGGT AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 950
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAAACTGG AACACTGACG 1020
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTG 1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAAAT 1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTAGCTCT 1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAAG GAAGGCACGC 1500
ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGAACT GGGACAGCTG 1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACAACACTCA TTGCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTG ACAGGAGACT 1680
GCAGTTGCAA TGGCCAGTCT TCTGGGATTG TATTCCAAAA CTTCACAGTC AGTCTCAGGA 1740
GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTCAGTA 1800
TTTTCAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTOGCTACA GAAGAACGGT 1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040
AATAACATTA AAAATTTGCT TAGATTCCAG CTGAGCAGCA GTATAGCAGC ATTAACCTTA 2100
ATCTCATTGG CTACATTAAT GAACCTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTTG CTTCGGCGGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCATGTC ACTAAGTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTCTCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTCTTTTGGG TCTCACTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA
  
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35  
 40  
 45

**A67 Protein sequence:**  
 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Protein Accession #: AAF27813  
 Signal sequence: none found  
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
 Cellular Localization: not determined

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 55  
 60

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1      11      21      31      41      51
|      |      |      |      |      |
MIPVLTSKKA SEFPVSEVAS ILQADLQNL NKCEVSHERRA FHGWNEFDIS EDEPLWKKYI 60
SQFKNFLIML LLASAVISVL MHQFDDAVSI TVAILIVTVV APVQBYRSEK SLEELSKLVP 120
PECHCVREK LEHTLARDLV PGDTVCLSVG DRVPADLRFP EAVDLSDIES SLTGETTFCPS 180
KVTAQPAAT NGDLASRSNI APMGTLVRCG KAKGVVIGTG ENSEFGEVFK MQQAEAPKT 240
PLQKSDLLG KQLSFYSPGI IGIIMLVGWL LKQDILEMPT ISVSLAVAAI PEGLPFIVTV 300
TLALGVMRMV KKRRAIVKLEP IVETLGCCNV ICSDKTGLTL KNEMTVTHIP TSDGLHAEVT 360
GVGYNQFGEV IVDGDVVHGP YNPVSRIVE AGCVNDNAVI RNTLMGKPT EGALIALAMK 420
MGLDGLQDQY IRKAEYFPSS EQKWMVAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RDVYQKQKAR MGSAGLRVLA LASGPELGQL TFLGLVGTID PPRTGVKEAV 540
TTLIASGVSI KMITGDSQBT AVAIASRLGL YSKTSQSVSG BEIDAMDQVQ LSQIVPKVAV 600
PYRASPRHM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQGT DVCKEADMI 660
LVDDPRTIM SAIEBGGIY NNIKNFVRFO LSTSIALTIL ISLATLMNFP NPLNAMQILW 720
INIIMDGPPA QSLGVEFVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
ELRDNVITPR DTTMTPTCFV PFDMPNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840
LVYFPPLQK VFQTESLSIL DLLFLGLTSS SVCIVAEIIE KVERSRREKIQ KHVSTSSSF 900
LEV
  
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65  
 70

**A68 DNA SEQUENCE**  
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719  
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

75  
 80

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1      11      21      31      41      51
|      |      |      |      |      |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CGGAGCGCCG GGTAGCGCGT AGAGCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCGCACAGC CTTCGTGCGG CTCTGGGCAC 180
CCCTGTTCTT GCTGCGCTCC GCGCTGGCGG ACTTCAGCCT GGACAAAGAG GTGCACTCGA 240
GCTTCATCCA CGGCGGCTCC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTCTT GCTGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
GCCAGGGCTT CTCCTACCCC TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGCGCA 480
GCCTGCAAGA TAGCCATTTC CTCACCGAGC CGACATGGT CATGAGCTTC GTCAACCTCG 540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCGCGGA ATTCCGGATC TACAAGGACT 660
  
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15  
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ACATCOGGGA ACGCTTOGAC AATGAGAGCT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCGCTCGG 780
AGGAGGGCTG GCTGTGTTT GACATCACAG CCACGAGCAA CCACTGGGTG GTCAATCCGC 840
GGCACAACCT GGGCGCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGTTGGCTT 960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGCTC CACGGGGAGC AACACAGCGCA 1020
GCCAGAACC CTCCAAGCG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTAGCGCGCC TACTACTGTG 1200
AGGGGGAGTG TGCCCTTCCCT CTGAACTCCT ACATGAACGC CACCAACCA GGCATCGTGC 1260
AGACGCTGGT CCACTTCATC AACCCGGAAG CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
AGCTCAATGC CATCTCCGTC CTCTACTTGG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCAGAA TTCAGACCTT 1440
TTGGGGCCAA GTTTTCTGG ATCCTCCATT GCTGCGCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCGCTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGTACAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCTTCAAGC TGTGACAGCA AACCTAGCA GGAAGAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCATTGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGCGT GGCAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAACG AATGAATG

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25

A69 Protein sequence:  
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195  
Probeset Accession #: BE616633  
Protein Accession #: NP\_001710.1  
Signal sequence: 1-30  
Pfam domains: TGFb\_propeptide [37-281]  
Transmembrane domains: none found  
Cellular Localization: secreted

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1 11 21 31 41 51
| | | | |
MHVRSRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE REMQREILS 60
ILGLPHRRP HLQCKKNSAP MFMLDLINAM AVBEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
LQDSHPLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
IRERFNETF RISVYVQLQE HLGRESDLFL LDSRTLWASE EGWLWFDITA TSNHWVNP 240
HNLGLQLSVE TLGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
QNRSKTPKQK EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAAYCE 360
GECAPFLNSY MNATNHAIQV TLVHFINPET VKRPCCAPTQ LNAISVLYFD DSSNVILKKY 420
RNMVVRACGC H

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50

Cervical

A70 DNA sequence  
Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.87223  
Probeset Accession #: AA250737  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

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60  
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1 11 21 31 41 51
| | | | |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGAACGCGGC AGTGGGAGA CCGCGGCGCT 60
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGTGGGAGTT CAGCCTACTC TTCTTAGAT 120
GTGAAGGAA AGAAGATCA TTTCATGCCT TGTGATAAA GGTTCAGACT TCTGCTGATT 180
CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300
AATGTGGGCA CCAAGAAAGA GATGGTGAG AGTACAGCCC CCAACCCCGG TCCAAAGGTC 360
TTGCGTGTGA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGACGACA 420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACATCCCAT TCCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
CTGCTCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACACAG GGCTTTACTT 660
ATATCTGTGA CTGCTGTAG TTTGCTCTTG GTCTTATCA TATTATTTTG TTACTTCGG 720
TATAAAAGAC AAGAAACCCG ACCTCGATAC AGCATTTGGT TAGAACAGGA TGAACCTTAC 780
ATTCCTCTG GAGATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
TCAGGCTTCC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTGAGT GGTGAAACAG 900
ATTGGAAAG GTGCTATGG GGAAGTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT 960
GTGAAGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGCATGTA AAACATTTTG GGTTCATCTG CTGCAGATAT CAAAGGGACA 1080
GGGTCTGGA GTGCTATGG CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCACACC AGCAATTGCC 1260
CATCGAGATC TGAAAAGTAA AAACATTTCT GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
ACTCGAGTTG GCACCAAGCG CTATATGCCT CCAGAAAGTG TGGACGAGAG CTTGAACAGA 1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560
CTAGTCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620

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10  
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CGCCCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
ACACTTGCCA AAATGTGAGA GTCCCAGGAC ATTAAGCTCT GATAGGAGAG GAAAAGTAAG 1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC 1920
CTTTCAGGGA GGCACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
TCTGTTTGTG GCGCGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT
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A71 Protein sequence  
Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.72472 / Hs.87223  
Probeset Accession #: AA250737 / U89326  
Protein Accession #: NP\_001194  
Signal sequence: 1-13  
Transmembrane domains: 128-144  
PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
MLLRSGAKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPPE DSVNNICSTD GYCFTMIEED 60  
DSGLPVVTSGL CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120  
GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
EQSQSSSGSGS GLPLLQRTI AKQIQMKVQI GKGRYGEVNM GKWRGEKVAV KVFFTTTEAS 240  
WFRTEIYQOT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNIVL KXNGTCCIAI LGLAVKFISS 360  
TNEVDIPFNT RVGTRKYMPP EVLDESLNRN HFQSYIMADM YSFGILLWEV ARRCVSGGIV 420  
EYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHPAS 480  
RLTALRVKKT LAKMSSESQDI KL

Bladder

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40

A72 DNA SEQUENCE  
Gene name: Homo sapiens type II membrane serine protease mRNA  
Unigene number: Hs.63325  
Probeset Accession #: AA411502  
Nucleic Acid Accession #: NM\_016425  
Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
ATGTTACAGG ATCCTGACAG TGATCAACT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60  
AAAACCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCTCAT CATAGCACTA 120  
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180  
TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240  
CTGGAAGTGC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC GGAAGGGCCT 300  
GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGGGCCACA 360  
GGGAAGTGGT TCTCTGCCCTG TTTGCAACAC TTCACAGAAG CTCTGCTGTA GACAGCCTGT 420  
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480  
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540  
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAAGAGCCTG 600  
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660  
AGCATCCAGT ACACAAACCA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACCTGGGT 720  
CTCAGCGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780  
GGCTCAGACA AACTGGGAGC CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840  
TTCAACCCCA TGATCCCAAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900  
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960  
GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020  
GACATACATG TCAGGCGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080  
GGTACCAAGG GGAAGATCAC CGAGAAGATG ATGTGTGTCG GCATCCCGGA AGGGGGTGTG 1140  
GACACCTGCC AGGGTACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200  
GTGGGCACTG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260  
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

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70  
75  
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A73 Protein sequence:  
Gene name: Homo sapiens type II membrane serine protease mRNA  
Unigene number: Hs.63325  
Probeset Accession #: AA411502  
Protein Accession #: NP\_057509  
Signal sequence: none found  
Transmembrane domains: 31-53  
LDLa domain: 54-94  
Tryp\_SPc domain: 204-429  
Cellular Localization: plasma membrane/ER

1 11 21 31 41 51  
MLQDPDSQDP LNSLDVKPLR KPRIPMETPR KVGIPITIAL LSLASIIIVV VLIKVILDKY 60  
YFLOGQPLHP IPRKQLCDGE LDCPLGEDEE HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120



5 GNPFSACFDN FTBALAETAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180  
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPMQV SIQYDKQHVC GGSILDPHWV 240  
 LTAACFRFKH TDVFNWVRA GSKLGSFSS LAVAKIIIE FNPMPKND IALMKLQPL 300  
 TFSGTVRPIC LPFFDEELTP ATPLWIIGW FTKQNGGKMS DILLQASVQV IDSTRQADD 360  
 AYQGEVTEKM MCAGIEGGV DTCQDSSGP LMYQSDQMHV VGIWSWGYC GGPSTPGVYT 420  
 KVSAYLWIIY NVWKAEL

## A74 DNA SEQUENCE

10 Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51  
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 20 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTCGG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGGCCC CCTGCCCTGC CTGACGTCC 360  
 25 ACCTCACCCC OGCTCTGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTGG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTGTGGGGCC GCGTGGGGCC CCAGGGCCAG CCTGGCACTC 600  
 AGCCCTTGA GGTGGGGCC CCGATCGCAC CCACCTCTC TGGCTGGAGA CCCCAGGAG 660  
 30 GCGGAGGAGC AGTCCCGGAG TGGGCGCCTT CTGCGCGCCC TTGCCAGATG GGCTCCCGAG 720  
 GCCTGCCCCC GCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGVTG 780  
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 TGGACAGTGG GTTACCCCTC CATGAGTTAG GGTCCCCCGG TTTCAGCGG TGCGGCCCTG 900  
 GGTCCCTGCT TCAGGGGAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960  
 35 AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGTG GGAACGGCTC 1080  
 GTAAGCGGGG GGTGCTCTGC TGGCTGGGGA GCGCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140  
 CTGGGCCAAGG CTGAGGGAGC CTGGCTGCAG CGGATCGGCA CGCGGGGTGG GCGAGAGCTT 1200  
 GGCTCTGATG TGCTCCCAAG AGACCTCTGG GTGATGGCCT TCCCCCTCTT GGCGGGGAGC 1260  
 40 TTGCCCCAGG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCACTCA TAGGCAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380  
 CTGGGGTCTC GCTCAACCCC CTTTGTCTC ACGCCGAGC TGTCCCCAGG TTTCAGCTGG 1440  
 GAGAGGCCAC CTCCCTCAGC CAAGGAAAAC GAGAAACCCC AGGGTACAGG AGGAGGCTGG 1500  
 45 GGCAAGTCCC CTGGGTGTC ACTCCCTCAG CCCCAGGCA GGGCCACTCC CGCTGGTGTG 1560  
 GAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620  
 GAACCGGGG CAGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTT TGGGGGCGAG GGCTCCGAT GCGGGGTGAG TGGTGGGGG GCGCAGGGCC 1740  
 CCGGATCGGG GGTGAGTGG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT 1800  
 50 ACAGTGTCCC ACAGGCAACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860  
 CCTTCGGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTOCC 1920  
 TGTCTGACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGGCCA GCATGCAGCT 1980  
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 ACCTCTCTGG CAGGAAGGG TGCAGGTCTT GAGGGCTGT GCCCACAGC CCCAGCACCC 2100  
 AGGTGACTG CAGCGCAGT GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGTCAGCA 2160  
 55 GGTGGGGTCT TGCCACCAG GGCCTCCCCA CGTCTGCTT TGAGGGTGGC TGCCATGCCC 2220  
 TGGGGGATCC TGGCATCTTT ACTGGAGTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280  
 GGTGATCTCA GCGGAGAGC GCCACATAG AGCTGGAACC CGCAGCTGAA GCGGAAATG 2340  
 GAGACAGGCT GGCACCTCG GAAAACTGC CTTTCAGCT TGGTGTCCG TGCAAGGTGA 2400  
 60 AAAGAAATAG GTCTCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCTTGAGAGC 2460  
 CAGAGGGGGA GAATTTAAAG GCGCGGCTG GCAGGGTCTA GGTGCTGGC AGAGGCACAT 2520  
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 GAGCAGCGTC CCGGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACAGT 2640  
 65 GGTGCAACAC TGTGATGACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700  
 CAGAAGTGT CCGAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCTCAGGA 2760  
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 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 70 CCCCATCTCT ACAAAAAA AAAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 TAGACCAGA TACTAGAAAT ATCAGAGAGA ATATAAAGTA ACAGTGTGTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

## A75 DNA SEQUENCE

75 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor  
 Unigene number: Hs.227948  
 Probeset Accession #: AB035089  
 Nucleic Acid Accession #: AB035089  
 Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 | | | | |  
 GGCATGCGAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60  
 CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAGAAGG 120  
 CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180  
 TTGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTTGG CAGAGTAGGA 240

	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACGTG	ACTTACATAT	300
	GAGACTATTT	CCCTCTCTGC	TTTTCAAACC	TACTGGAGT	TGTTTTCCCT	CATGAAAACC	360
	AAGAAAGTAA	AGCTAGTTAG	TCTTGTCTCG	AGGTTGTTC	ATGTATACAT	ATCTATATCT	420
5	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTTATTTG	ATGCTTGAAA	480
	AATCTCCCTC	ACTAACCGAT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACTTTA	CAGCCTTCAT	600
	AAGGAAGTGA	GGTCCAGGAA	AATCTAGGAG	ATATTTCTTA	ACCAATCTAT	AAAGGCATTA	660
	GTAATGACAG	GATATTTTCT	GAAAGTGTAA	TTTCCCATTG	AGGATTTGTT	TTTAAATTTCT	720
10	GGATTCCTGG	AGCCAAATGAA	GTTGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTC	TATGCAAAAA	CTTCTTGGAA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCTTTT	CTAGCCTGTC	TATCACAATG	900
	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCAIT	TGAACTCATC	960
	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCCTTAAG	1020
15	TTCAACCTTC	AGGGCAAAACC	TCCGTGCCTC	AGACGTTTAG	CCATAGTCTG	AAATTTCTCT	1080
	CCATAGTTTG	ACTCCCTGTA	ACCCCGGTTT	GTCTCAGCTT	GTTATCCTGT	TTTTTTCTTC	1140
	CCTCCATTCC	CAGGATGAGC	TTGTTGCTTC	TGTCTATGA	GACATTAGAT	TCCTTTTCTT	1200
	TGGTACCCGA	GTAAATCCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGT	TCTTATAGCG	1260
	CTGGATGCG	ACTAGCTGA	GAAGACCAT	ATTCAATTTT	GGAAATCTTT	ATCTCAGATA	1320
20	TTTCTCTTTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTITAG	TCCATCAACG	CCCCATTAGT	1380
	CTATTCCCG	ACTTCAATCA	GGGAACCTAT	ACCTCTTAAA	CTCATTGAGA	GACTCAAAAC	1440
	ATATATATTT	ATACAGGAGA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
	GTGAGAAAT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTTCAG	1560
	CCTATGTGTT	TCTGGCACCT	TGTTGTAGAT	AAATCTCCT	TGACTTTTGT	ATGTGCTGAG	1620
25	AAAACAAACT	CAGGCTCTGT	GTTAAAAAGG	GCCCATGACA	ATACCAAGTG	TTGGGGAGAA	1680
	TGTGGAGAAA	TCGAACTCT	ATTCACGGTC	GGTTGGAATG	CACACTTGTG	CAGATTCTTA	1740
	TGGAGAAGAG	TCTGGCATTT	CCTCAAAATG	TTAACCTTGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCATTCAT	AGGTTTATAC	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACAAACATCAT	TATTCATAAT	AGTAAAAGGA	TGAAAACAAC	ACAAATGTCC	1920
30	ATCAACTTAT	GATTAAGAAA	AATCTGGTCT	ATTCATAGAA	TGGAATATTA	TTCCAGCCACA	1980
	AAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACACTAGA	2040
	TTAAGAAGC	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGG	2100
	ATAGGCAAT	CCATAGAAAC	AGGAGGTAGA	TTCTCTGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
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35	GATGATAGCA	CAACTTTGTG	AATATAATAA	AATCATTGAA	TTGTACAGTT	GAATTTATGG	2280
	TATATAAAT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTCAGGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTTCTTCAG	TTACAGATTA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
40	AAACAGAAAG	ACCATTGAGA	AATGTTGTGA	TCTTGACAGG	TCAAGCAATT	TATTTTTCGG	2520
	CTTCATTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT	2580
	GCTCTTCTCA	GTGTCAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAAATGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGGAGGCT	CAGAATCACA	GTAGGAGGCA	AAAGTTATTC	TTACATGGTG	GCTGCAAGAG	2760
45	AAGATGAGGA	AGAGCAAAA	GAAGAAACCC	CTGATAAAC	CATCGATCT	CCTGAGGCTT	2820
	ATTAACATAT	ATGAGAATAG	CACAAGAAAG	ACCGCCCCCC	ATGATTCAAT	TACCTCTACC	2880
	TGGGTCCCTC	CAATAACATG	TGGAATTTCT	GGTAGATACA	ATTCAGTTTG	AGATTTGGGT	2940
	GGGAACACAG	CCAAACCAT	TCACTCAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
	AACAGAAAC	CATCTGGGAT	GGTTGTAAAG	GGCAGAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAGAGTGA	CATCAGGAG	AAGGCAATAG	AATCCTATTC	TCCATAGTAT	GCTATAAGAT	3120
50	ACTGAAGTAC	ACTTCTTCAC	TATCTCTTTG	GACTTAGAAT	TAGCACTACA	TTCTTGTGTA	3180
	TACAGAAAAA	TTACTAAGGA	AATTCATAGG	ATGACAAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAA	CTTTTGTAGT	CTTTGGTATT	CGAAGTATGC	CTAAAAAGCA	ATGCAAAATC	3300
	CAAGAAAGGA	ATGGTGGGGT	TTTGTGTTGT	TTGTTTGTGT	TTTGTGTTTA	CAGCTGGAGT	3360
	AGAATACAAA	GGGATGGAGT	TGAACAAAAT	GAGAGGAAAT	TGGAATTTCT	AACCTATTCT	3420
55	CATTGGCAAT	AGAAAGGCAC	CTACATGTAT	TTACATGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAAAAGG	AGGTACAATG	GTAGAACTGT	AATCCTGTCC	3540
	TTTGTCTATA	TTTTCATAT	TCATAAAGGT	GAGTGTATGC	CCGCTTGTGA	AATCTGAAGT	3600
	TGAGTAACCT	CAATACTATA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCACC	CTTCATTCCA	CAGACACACA	CAGCCTCTCT	GCCCACTCTC	GCTTCTCTTA	3720
60	GGAAACACAG	TAGAGCTTTC	AAGCCTCTCC	AGCTTAATAA	CATGAAATAT	TTTTGAGAAAT	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGTCTGATT	ATATTTTACT	3840
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	GAGAGTCTTG	AAGGAGATGT	CAGGGAAGCA	TCTTAACAGC	TGGTTGGATG	TGATCCACAG	4020
65	AGGTCTCTCG	TTAGCATTTCA	TTGTAAGGCC	ATCCTAACCTA	GCTCTAGTGT	AAACCAGCAAT	4080
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	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTTC	4260
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70	TGATGCTTTT	CCAGGAGTTT	CAGATCACAT	CGAGTTCAAC	ATGAATTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTATGTTTCG	ATCTGTTCCA	ACAGTTTACA	AAATCAAAAG	AGAAACAACAT	4440
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	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCAG	4560
	TTTTTCTCTG	GTTCCGTGGG	CTAGCAAGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
75	AGCACAGGGG	GCTGTGCAAG	AATCCCATTA	ACTGTGAGAC	CAGTCACTTA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTGTGC	CGGCTTCATG	TCTCTTCCAG	GTTCTTCACT	TTGATCAAGT	4740
	CACAGAGAAC	ACCACAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CACTCTGATT	4800
	CAGCTTTAGA	TCCCTTGAACA	GGTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACCTAAGAA	4860
	AGGCCAGTTT	TAGGAAAAAT	CTTGGACACA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
80	TTCAATGGCA	ATAAATTTTA	TTCTCTATTT	CTGGTTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGTCTGGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTCTTCAC	5040
	AAATGATGAA	TAAAGACAGG	ACACAACTGC	TCCGAGTCCC	AGTGACCTCA	TCCAGAAAAA	5100
	TTAAGGGTAA	GAAAAAATCT	GACTCAATAC	ATGCAAAATC	ATGCAAAATG	TTACAACAGT	5160
	GCCTTGCCCA	TAAAGTTCAT	AATAAATGTT	ATTAAATTTA	TAAAGTAGCT	ATAAATATAC	5220
	TAATCATAA	AATGTGAAAA	TAATTTAATT	TTCAATGAGT	CATTAATGAG	ATTCAGAGGA	5280

	ATAAGCACAA	GTCCAAGTAT	ATTTTGGAAA	ATGATTGCTA	TGGAATATAT	TGGTTTAGAG	5340
	CCTTAATAGT	GCAAAATGCT	TTGCTGGAG	GTAGAAAGTT	CTAGATTAA	ACAGGCTTAG	5400
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5	TGAGCTTTCT	TGTGTTTATC	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAAGTCC	5520
	TTAGCCATGG	ACCTGGCATA	CACCTCTTCT	ACGTGCAGAG	AATGACCATC	ATGAGGAAAG	5580
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	CCTGGCATAA	TCTATTTAAA	ATATCCAACC	TTCAACATAC	TCGTATCCTT	GATGACTGTT	5700
	AGAAAGTAAA	TATGGTCCTT	GCCCATAGG	AGCTGAGAGT	TAACTGGGA	AGCTAAACCT	5760
10	AACCCCTTAA	ACCAACAAGG	AGAAAATCTA	CTGGTAGACA	GCGCTGCATC	TTTAGTTCAG	5820
	AAGAGAAAAG	AATGCAGTAC	GTTAGAGCAA	GAAGAATTTT	CTGGAAGAAG	TCAAATATAA	5880
	GGTGAGTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAG	5940
	GTCTCAATG	AGACTACCA	CAITTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTACATTG	ATACAGCAAT	TGAATGATCT	CCTTTTTTGA	TGTTTGAAGG	TTGATAGGTC	6060
	AGGAAATGTT	CATCACCAGT	TTCAAAAGCT	TCTGACTGAA	TTCAACAAAT	CCACTGATGC	6120
15	ATATGAGTAT	AGATGCGCCA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAAT	TTTTACAGGT	6180
	AAATTTCACT	GGCTTACCCA	CATTTCATTT	GCATCCTGAT	GTCTGTGTCT	CTGAGTGGCC	6240
	AAATGGAAAG	AGCAAGGACA	GATGAGCCTG	GCCGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTTOCA	CAACTCTCCC	CCACTGGAGT	GTCCGAGACC	CCAACGATAC	6360
20	ATCACTGAGG	TGTGGATTTA	GGGATAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAAATAGG	6420
	TGAGTAAGAG	TAATAGTAA	TAAGATACCA	TOGATAAACT	GGCACTGACT	CAGTCACATA	6480
	CGATACATCT	TGGTGGGAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTCTT	GAGAATAGTT	GAGGAAGTAC	CAGGAAATAT	TGAATGCACA	GGATGAAAGA	6600
	CAAAAACAAA	GATCAGAAAC	ATCATGGTTA	AAATTACTGG	AGAGAAGTCT	GAGAAGCAAT	6660
25	GAATCTCCTT	CAGGGAAGCC	TGCTCTGCAG	TTTGCAAAAC	ACAGCCTCTT	CTGCTTCTGC	6720
	CTTTTGGCAA	GATGATATTG	ACCTTCAGTG	ACCTCTTTCT	TGTGCCAGCC	CACATTCCCC	6780
	TTTTGCATTG	CCTCATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGCATCT	6840
	ATTCAGGGTC	TGGATTCAGC	TTACTGTTGT	TACAAATAAG	TAAGTTTGGT	AATATATAGT	6900
	TACATAAATT	ACTCCTAATT	CCTTCTATCT	CTTTCATATC	TCAAAGGAAT	ATTTAGATGC	6960
30	CATCAGAAA	TTTTTACAGA	CCAGTGTGGA	ATCTACTGAT	TTTGCAATG	CTCCAGAAAG	7020
	AAGTCGAAG	AAGATTAACT	CCTGGGTGGA	AAGTCAAAG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTGAGA	AACTATGCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
	GAACAGGTGT	GGGATTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTGTC	CAATGAATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
35	GCCAATTAGA	TGGAAACACA	TCTGGAGAAT	TATTTGCTTA	TGGCCCTGCA	TGACAAATAGC	7320
	TTTGTGGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCCTTT	ACTTTAAATC	7380
	AGACTCAAT	TTTTATGATG	AATATTTAAT	AGAAAACATT	AGAAAGCGTC	TCTCGTCTCC	7440
	TTTACTAATT	GGGAACCAAG	CAGCTCTCTG	GTAATCACC	CTTTTGTCTC	TGAGCTGGAG	7500
	CTGCCTGGAT	CACATCTGTA	GCCAATGTGT	TCTGCAGGGA	TTATCAGAGC	TCTCTTCCCC	7560
40	ATCAGGGGCA	AAGAGCTTGA	CAAGTCTCC	ATCTACAGA	CATCTTCTT	ACCTCCCAAC	7620
	TCTCATTACA	GGCCAAACTT	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCGC	7680
	GAAGTAGTGT	CTGACAGCTC	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
	CTAAAATGCA	ATCAGGGGCT	CCTTCCCTCT	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
45	AAGTAGGAAG	AGGAGGGAGG	GAGAAAGGAA	AGACACATGT	TGGAGAGGTA	GACAAAATCA	7860
	GTTTATCAGT	ATTTCAAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACCTC	7920
	TTCTCTATCA	CAAGAAGTGA	TGTCTCCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	ATCTGGTGAA	CCACTGGTCA	GTGAGTCTAA	CAATTCAAAG	ATCAAAGTCA	8040
	GTGAGTCTCA	AGCAGGGGAT	TGGGTCAATA	ATTAAAGATC	AGTCAAGAAC	ATTTGCAAGG	8100
50	CATCTCCAG	ACAGGCCATT	TGTAGCTTGT	GTAAAAGACT	CTTTTATCTT	TCCCTTGCA	8160
	GAAAAAATTA	AAAACTATT	TCTGATGGG	ACTATTGGCA	ATGATACGAC	ACTGTTCTCT	8220
	GTGAAGGCAA	TCTATTTCAA	AGGGCAGTGG	GAGAATAAAT	TTAAAAGAGA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGGCCAAA	CAAGGTATTG	TCTATATTTT	ATTATATAG	TGTAATATGT	8340
	TAATACATGG	AATGTTAAAC	ATTTCTGATG	GAATGTAAAC	TGATAAGTAA	AAAAATAAAA	8400
55	TTGTTTATGT	CTGTTATTTT	GTTGTTTTAC	TCTTATAACT	TTATTTAGTT	AGGAATACCT	8460
	GAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATTAATAT	TATCTTTTTT	GTCTTGTGTT	TCAGTGTTTA	TTTGTGGGAC	8580
	ACATTGATTT	TAGATTAAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCTT	8640
	TTAATTTTGC	CTTGCTGGAG	GATGTACAGG	CCAAGGTCCT	GGAAATACCA	TACAAAGGCA	8700
60	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATCGA	TGGTCTGCAG	AAGGTAGGAA	8760
	CTTGCACTTA	CAACTCTTCC	TTCTACTGCC	GGACATTTTT	CCAAAGATAC	CAAGTTTAAA	8820
	CAAGGTAAAA	GCTTATGACC	GAGTTGCTCT	AAAAATGATG	AAAATTCTAA	ATGAGGAATG	8880
	ATGACTCACC	TTCATATTAC	AAATATTGGA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
	GTTTGTGTTT	GTTTGTGTTT	TTTTATTATT	ATTATTATAA	TACTTTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGCAGGTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
65	CCATTAACTC	ATCATTTAGC	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCCCCCCC	9120
	CACCCACAAA	CAGTCCCTCAG	AGTGTGATGT	TACCTTCTGT	TGTCCAAGTG	TTCTCATTTG	9180
	TCAATTCCCA	TCTATGATTT	AATTCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
	TTACATGCAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAAATAGGCC	GAGTAGAAAA	GGGAATACAA	9360
70	ATTTAGGAAT	TTAGGGAATT	ACAAITTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GAAAAATATG	ATGAGCCTAT	TAAAAATTGA	CACATGTAGT	AGGCTGTGAG	CACAGAAAT	9480
	AGTGATACAT	ACAGTTCATT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACACATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATAT	9660
75	TTTTACTTAT	TAGAATAATA	ATGTCTATTA	AAGTGAACTT	TCTGTATTTT	ACATTTATTG	9720
	CCAAAATAAC	GAATCTCCAC	ATAGTCAATT	CATTGTTAAG	GTGTATTAGA	GATGACAGAT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTGTT	ATAGCTTGAA	GAGAACTCA	CTGCTGAGAA	9840
	ATTGATGGAA	TGGACAAGTT	TGCAGAATAT	GAGAGAGACA	TGTGTGATTT	TACACTTACC	9900
	TGGGTTCAAA	ATGGAAGAGA	GCTATGACCT	CAAGGACAGC	TTGAGAACCA	TGGGAATGGT	9960
80	GAATATCTCT	TAGGGGAGAT	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GCTCTCAGT	10020
	ATCTAAAGTC	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACGCT	GTAGTAGTAG	TGGAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTTG	10140
	TAATCACCTT	TTCTTATTTT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCATAGA	TGCAATTAGT	CTGTCACTCC	ATTAGAAAA	TGTTCACTTA	10260
	GAGGTGTTCT	GGTAAACTGA	TTGCTGGCAA	CAACAGATTC	TCTTGGCTCA	TATTTCTTTT	10320

5 CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTAA ATGATTAAAA TAGCATGCCT 10380  
 TTCTCTCTTT CTCTTAATAA GCCCAGATAT AAATGTACTT TTCCTTCCAG AAAAATTTCC 10440  
 CTTGAGGAAA AATGTCGAAG ATAAGATGAA TCATTTAATA CCGTGTCTTC TAAATTTGAA 10500  
 ATATATTCTT GTTTCTGACC TGTTTTAAAT GAACCAAAAC AAATCATACT TTCTCTTCAA 10560  
 10 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTTAGGT GATACCTAAA TCCTTCTTAT 10620  
 GTTTCTAAAT TTGTGATTC TATAAACAC ATCATCAATA AAATAATGAC ATAAATCAT 10680  
 TTTTGTCTTA CCTGTTTTCT CTCTGGAAG GGCAAGTGT CAGTTACACA TAGGAAAGAT 10740  
 AATTAGAGA TATATTAATC ATATATAAAG GAAATTAATA AACAGAGTAG TTCATGATGA 10800  
 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACCACA TAGGAACCTC 10860  
 15 CTATTTTATG CTAAGGGAT AAGAACTCA TTACAGGCTT TGATGGTTGT TTGTCAAAGA 10920  
 GGGGCATAAA ATTATCATAT CCACATCTAG AAAATACATC TCTGGCTACG CTGATATCAA 10980  
 TGGATCGGAG GAAAGAACAG TGTGGTTACC ATATATAAAT TAGGAAATCA TTAGAGTATT 11040  
 GGGAGTGGAA ATGGAGAGAA AGAAAGAGCC TGGGGGAATT ATTTAGGAAA TAATAGTTAC 11100  
 AGAAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGGAAGAATA TCTTGTCTCT 11160  
 20 GAGAGAAAAA AAGACTTTGG GTTTAAATTT GTACTTGATG AATTAAGGTA CTTTAAATAT 11220  
 TCAAAATGAT TTGCTGGCA GGCACCTGAA GATATTAGTC TAAATCTCAG AAACAGAATA 11280  
 TGATCTGAAG CTCCTAAATT GTGATATTCA ATATAAATAC TTTAGAGTCA TTGGGATAAA 11340  
 TATGTTAGTT GTAGCTAAAA GCAAAATTA GATACTAGGG AGAAAGGATA AAGTTAGAAG 11400  
 AAAGAGAAAT CTAGAATTGA CCTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460  
 25 CATTTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTACTCC CATAGATTCT 11520  
 TCCC

#### 25 A76 Protein sequence:

25 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor  
 30 Unigene number: Hs.227948  
 Probeset Accession #: AB015089  
 Protein Accession #: BAB21525  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Serine Proteinase Inhibitor domain: 13-390  
 Cellular Localization: secreted

35 1 11 21 31 41 51  
 MNSLSEANTK FMFDLFQQFR KSKENNIFYS PISITSALGM VILGAKDNTA QQISKVLHFD 60  
 QVTENTTEKA ATYHVDRSGN VHQFQKLLT EFNKSTDAYE LKIANKLFGK KTYQFLQBYL 120  
 40 DAIKKFYQTS VESDFANAP EESRKKINSW VESQTNKIK NLFPDGTIGN DTTLVLVNAI 180  
 YPKQWENKF IKENTKREKF WFNKNTYKSV QMRQYNSFN FALLEDVQAK VLEIPYKGGK 240  
 LSMIVLLPNE IDGLQKLEEK LTAELMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300  
 TMGMVNIENG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAV VVELSSPSTN 360  
 EEFCCNHPFL PFIQNKTNIS ILFYGRFSSP

#### 45 A77 DNA SEQUENCE

45 Gene name: hypothetical protein FLJ13459  
 Unigene number: none found  
 Probeset Accession #: XM\_047266  
 50 Nucleic Acid Accession #: XM\_047266  
 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 55 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC 60  
 CACCATGCCA GGCCCTCTTA ACCTCTTCAA GTCTGTTTTC TCATCTGCAG AACAGAGGTA 120  
 ATAAGATCAG TATCTTCTTA ATGGAAGCAC CTGGACTACA TTTTTCAT TCATTGTTAT 180  
 CATAAATGAG GACTAAACCTG TCTCCCGTTG GGAGTTTGA ACCTAGACCT CATGCTTCA 240  
 TGAGTCTATC ACTGCCCCAG GCCAGCTGT GTCCCTACAC CAGCCCCAGC TGACGATCT 300  
 60 TCTTTTCTG CCTGTAGAGA TGGTTACAAT GCCTGGCGTG ATGCATTCTG GCCTTCGCAG 360  
 ATCCTGGCGG GGCTGTGCCA AGCTGTGGC CTCCCTGCC CTGAATACCG AGCGGTGCT 420  
 GTCAAGGTGG GCAGCAAGT CTTCCTGACA CCACCGGAGA CCTGCCCC AGGATCTCT 480  
 TCACATGTGG ATTGACATCT TTCTCAAGA TGTGCTGCT CCACCCCGAG TTGACATCAA 540  
 GCCTGGCAG CCAATCAGCT ATGAGCTCAG AGTTGTCTATC TGGAAACGG AGGATGTGGT 600  
 65 TCTGGATGAC GAGAATCCAC TCACCGGAGA GATGTGAGT GACATCTATG TGAAGAGCTG 660  
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGACGTT CACTTCAACT CCTGACTGG 720  
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT CCGCTTTGAC TACCTGCCA CGGAGCGGGA 780  
 GGTGAGCGTC TGGCGCAGGT CTGGACCCTT TGCCCTGGAG GAGGCGAGT TCGGCGAGCC 840  
 TGCAGTCTG GTCTCTGAGG TCTGGGACTA TGACCGCATC TCTGCCAATG ACTTCCTTGG 900  
 70 ATCCCTGGAG TTGCAGCTAC CAGACATGGT GCGTGGGGCC CGGGGCCCG AGCTCTGCTC 960  
 TGTGCAGCTG GCCCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTGGCT GCGCGCGCCT 1020  
 GAGGGGCTGG CTGACTGTGG AGGAGGCGGA GAAACGGCCA GTGGGAAGG GCGGAGCGCA 1080  
 GGAGGCTCAG GCTGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCAGAGGA 1140  
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCTCT ACGGGCAAGG TGGAGGCAGA 1200  
 75 GTTTGAGCTC CTGACTGTGG AGGAGGCGGA GAAACGGCCA GTGGGAAGG GCGGAGCGCA 1260  
 GGCAGAGCCT CTGGAGAAAC CAGCCGCCCC CAAACTCTCC TTCAACTGGT TTGTGAACCC 1320  
 GCTGAAGAGC TTTGCTTCT TCACTGGCG CCGTACTGG CGCACTCTGG TGCTGCTGCT 1380  
 ACTGGTGTG CTCACCGTCT TCCTCTCTCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG 1440  
 CCAGGTCTATC TTCCGTCCCC TCACAAGTGG ACTCTGGCTG ACCTTGGACA CTCACCCAGG 1500  
 80 GTGCCAACCC TTCAATGCCT GCTCCTGGAA GTCTTTCTTA CCATGTGAG CTACCCCGAGA 1560  
 GTCTAGTGCT TCCTCTGAAT AAACCTATCA CAGCCACTG

#### A78 Protein sequence:

Gene name: hypothetical protein FLJ13459

Unigene number: none found  
 Probeset Accession #: XM\_047266  
 Protein Accession #: XP\_047266  
 Signal sequence: none found  
 Transmembrane domains: 291-313  
 C2 domain: 27-86  
 Cellular Localization: plasma membrane / ER

1 11 21 31 41 51  
 MWIDIFPQDV PAPPVDIKP RQPISEYELRV VIWNTEDVVL DDENPLTGEM SSDIYVKSXWV 60  
 KGLEHDKQET DVHFNLSLTGE GNFNWRFPVFR FDYLPITEREV SVWRRSGPPA LEEAEFRQPA 120  
 VLVLVQVWDYD RISANDFLGS LEIQLPDMVR GARGPELCSV QLARNAGAPR CNLPRCRRLR 180  
 GWNFPVKLKE AEDVEREAQE AQAGKKKRKQ RRRKGRPEDL EFTDMGNNVY ILTGKVEAEF 240  
 ELLTVBEAEK RPYGKGRKQP EPLEKPSRPK TSPNWFVNPL KTFVFFIWR RYRVLVLLLL 300  
 VLLTVFLLLV FYTIPGQISQ VIFRPLHK

20 A79 DNA SEQUENCE  
 Gene name: Homo sapiens mRNA; cDNA DKFPz434K0322 (from clone DKFPz434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Nucleic Acid Accession #: AL137708  
 25 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 30 GGCAITGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60  
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120  
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180  
 ATGGCCTGGG CTGGGCCCCC GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240  
 CTCTGTGGG CAAAGCAGGG GAGGCGCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300  
 35 CTGCTCTCTG GAGCGGGTGG AGTCAGGAA GAGCTAGCT GGGAGTCAC CCTGGGCTGT 360  
 GGGTCACGCT AGGCCCATG TAGCACCTGT GTTCCCTGTC CTGTAGGTGA CAGGAGCCAG 420  
 CCCAGCCAGG TGTGCTCCCT CCCAGGCCCT TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480  
 CGCCGCCCCC ACCTTCTCTT CCACCCACAT GCGGAAGGGT GGCCAGGCAG GCAGGTGGAC 540  
 GAGTCCAGGC AGCGCTGAG TCAGTGTGTG TGAATGTTC TGGCCGCTCC CAGCTGCACC 600  
 40 CTGCCCTCTG CTGCCACCAC CTCACCTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCTGTC 660  
 CAGGAATGCA CCTTTAGCCC AGGCTGTCTC AGTGAGCTCC GCGCAGAGCC AGCCCTGTCT 720  
 CTCCGCCCAT GACCTGTGAG ACCCTCTGCG GCTTCCAGT TCCTGGGGGC TGCAGTGAAC 780  
 ATGCTCCACC TGATGCGCTG GCAAAACATG GTGGGCCCCA GCTGTGTGTC GTGCTGGGGT 840  
 45 AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGATGAGA TGGGACCCCC 900  
 AGGCAGGGCC CAGGGTCCAG GGGCCAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCCTGG 960  
 TGGAGGACGC ATCTACAGT GGGGCAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020  
 AGGCTGCCCA GGCCTGCTCT GCTTGGCTGG GGTGGGGGTC TGCTGGGAGG TGGCTGGGAG 1080  
 GCTGGGCTCT GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCCTTCAG 1140  
 50 CTCTCTGCTG CACGAAACCC TCGCCCTGCG CCACCCCGTG CTGCCTCTTT GCGCTGGCAG 1200  
 ACCCAGCACT GGTGTGCTGT AGTCAGATGG GGTAGCGGGC AGGGGCGGGA GGGGCCACCC 1260  
 TCCCACTGTA CCGAGCTCTT TGGGCCGCTT CTTCCAAACC AGCAGGGTAG AAAGATGGGG 1320  
 CACCCACAGG TCTCTCCAGC TGCCCGCGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380  
 ATTCCAGACC TTGTGCGCGG GACCCCTGTG GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440  
 55 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCTCTACC 1500  
 CCAGGGCCCC GCTGGGCTCT CATTTGCCGC GCGCTTGGCG CGGGGCTGCT CCTGTCTTCC 1560  
 TGCTCTCTCT GTGCTGCTGT CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGAGCAAG 1620  
 GAGTCCGTGG GTCTGGGCGG TGCCCGCGGC ACCACCAACA CCACCTGGT GAGGAGCGGC 1680  
 60 TCCTTGTCTC CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740  
 GGCAGATTCA GCCCCAGGGA TGGTTAACC CCCACAGAGG CAGGGCGTTG AGGACCTTCC 1800  
 TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCAT 1860  
 GGGCCCGAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920  
 TTTGGGTGGG TTTGGCGCGT CTCACAGAGC GAAGCCGACG ATTTGTGCTT GTTGGGTGGC 1980  
 CTGGCTTGA GCGCGGGGGT CTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCAGGG 2040  
 65 CTCTGATGAG GCATGATGTC AGCAACACCT GCCCTTGTTC CCAACTCACT CCAGGTGCAA 2100  
 CCTGATGTGG ATGGCTTGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCTGTCAG 2160  
 CTCTCCCTGG AGTTGACCTT TGGAAAGCAG GAGGTGAAGG GCGCCGCTGC GCAGGACCA 2220  
 CGGTTCTGCG AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCTGGGGTGG 2280  
 TGGGGAGCTG ACAGGGCAGG GGCCTTGGC TGAGCCCAAC CGCTGGCTC CCAGATCAGG 2340  
 70 GTGGGCTGTA GGCAGGAGC CGAAGTGAAG CCTGGGGGCA CGGTGACCC CTATGCCCGG 2400  
 GTCAGCGTCT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGACCGG AGGCAOGCTC 2460  
 TGCCCGCTGT TTGACGAGAC CTGCTGCTTC CAGTGAGTTC AGGATGGTTC GGTGGGTGG 2520  
 GCCTGGACCG CTGATAGGCG CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580  
 GCTGGGTGGG CCTGAGCTAG GGCAGCAGGG CCTGGCTCAC GCGCTGCGCT CAGATCCGCG 2640  
 75 AGGCGGAGCT CTGTGCTGCC ACCCTGCAAG TGCACTTTT CAACTTCAAG GCCTTCTCGG 2700  
 GGCATGAGCC CCGGGGTGAG CTCCGTCTGC CACTGGGCAC CGTGGATCTG CAGCATGTTT 2760  
 TGGAGCACTG GTACCTGCTG GGCCTGCGCG CTGCCACTCA GGTGAGGTGC TGGTCAACAG 2820  
 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CTTGCCCTAT GGGCATCGG AAAGACAGGC 2880  
 CTGATGGGCA GCATTTTCGG GGTCTGAGC CCAACTCGG CCAGATTCAC CCTCCCGGGC 2940  
 80 TGAAGCCCTT CTGTGCTGCC ACAGCCCGAG CAGGTGGGGG AGCTGTGCTT CTCTCTCGG 3000  
 TACGTGCCCA GCTCAGGCCG GCTGACCGTG GTGGTGTCTG AGGCTGAGG CCTGGTCCA 3060  
 GGACTTGCAG AGCCCTAAGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG 3120  
 AGAAGAGAGC CACCAAAAAA GGGCAAGGCG GCGCCCTACT TCAATGAGGC CTTCACTTTC 3180  
 CTGGTGCCTT TCAGCCAGGT CCAGAAATGTG GACCTGGTGC TGGCTGTCTG GGAOCGAGC 3240  
 CTGCGCTCC GAACTAGGCC GTAGGCAAG GTGCACCTGG GTGCCCGGCG CTGGGGCAG 3300

CCOCTGCAGC ACTGGGCAGA CATGCTGGCC CAGCCCCGC GGCCCATTCG CCAGCGGCAC 3360  
 CCOCTGCGGC CAGCCAGGGA GGTGGACGCG ATGCTGGCCC TGCAGCCCCG CCTTCGCGTG 3420  
 CGCCTGCOCCT TGCCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCGG CTGAGCCACG 3480  
 GCATTGCCCC AGGCGCGCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

**A80 Protein sequence:**

Gene name: Homo sapiens mRNA; cDNA DKFp434K0322 (from clone DKFp434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Protein Accession #: CAB70885  
 Signal sequence: none found  
 Transmembrane domains: 69-85  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGHPVPSPSA PAFAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA 60  
 STPGPRWALI AGALAAGVLL VSCLLCAACC CRRHRKKPR DKESVGLGSA RGTITTHLVR 120  
 SGLLTQSRRE GLKSLRLQSPG QRGEFSPRDG LTPTEAGR

**A81 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51  
 GCGGAACACC GGCCCCCGCT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60  
 TCCTCTGTGG ACCTCTCGCG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGCAGCG 120  
 CCTCCGAGCC GTCCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGAGG GCGGAGGCGG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCGCT GGGCAAGAGC 240  
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360  
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAGGGGTC 420  
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGCCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540  
 AGACAGGCTG GTTGTGTGTT AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600  
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GAGACCCATG AACATCTCCA 660  
 TCATCGTGAC CGACAGAAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720  
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCG ACAGATGAGG 780  
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840  
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900  
 CCAGTGGCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020  
 ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080  
 GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGACACG CCCCACCTCA CCAGGCTGGC 1140  
 GTGCCACCTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200  
 CTGAGAGCAA CCAGGGGATC CTGACAACCA GGAAGGGTTT GGATTTTGGG GCCAAAAACC 1260  
 AGCACACCCCT GTACGTTGAA GTGACCAACG AGGCCCCCTT TGTGCTGAAG CTCCCAACCT 1320  
 CCACAGCCAC CATAGTGGTC CAGGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380  
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCTACTG GGAGCCTGTG TGTGTCTACA 1440  
 CTGCGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CGCATCCTG AGAGACCCAG 1500  
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCA AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCACTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAGAC CCTGTGCGCC 1740  
 ACGTGTGAA CATCAOAGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCCAGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTGAAAC CTGCGCTGGA CCGTGGAAAG GAGGTTTCAT CCTCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGCTAA CACAGACCCC ACAGCCCGCG CTAAGACAC CCTCTTGGTG TTGACATATG 2400  
 AGGCGACGGG TCCGAGCGCC GGTCCCTGA GTCCTCTCAC CTCCTCCGCC TCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACGTGGCGG GAGGAGCAGC TAGCGGCGCT GCCTGCAGGG CTGGGGACCA AAGTTCAGGC 2580  
 CACAGAGCAT TCCAGAGGCG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640  
 GGAAGTGGCC GTTCAACACT GCGGAGGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCTTACGCTC TTACAGATGG AGGAATGTGG CAGATTGAC TTCAGCACTG AAAACCTCTC 2760  
 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820  
 TGCTCAACCC TGTGTCCTGG GCCTGGGCGT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA AGCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940  
 TCAAAAGGTT AGAGAAAGTT CTTCAAAGT GCAGCCAGA GCTGCTGGGC CCACTGGCGG 3000  
 TCTGTCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GATGATGATCT CTGCTTTTTT 3060  
 ATACTAGTGT TGCCTAGGTT GCCCTTATT TTTTATTTC CCGTGTGGGT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAAGTTTTT TATTAAAGAA A

**A82 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)

Cellular localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MGLPRGPLAS LLLQVQCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGPPFPQRLNQ LKSNKDRDRTK IPYSITGPGA DSPPEGVPAV EKETGWLLLN KPLDREBIAK 180
YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GUVAYSIHSQ EPKDPEDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAEVPEP AVGHEVQRLT VTOLDAPNSP 360
AWRATYLMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAEVVF VPFSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
DPAGMLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
VNDHGPFPEP RQITICNQSP VREVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL 660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVYF YBEGGGGEDD QDYDITQLHR 720
GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIIE NLKAAANTDPT APPYDTLLVF 780
DYESGSDAA SSSSLTSAS DQDQDYDYLN BWGSRFKILA DMYGGEDED

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**A83 DNA SEQUENCE**

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Probeset Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
AGCACTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCAGCGTGG CTGTGGCCTC 60
GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTITGGA TTTGGTGGC TTTTCTTCAT 180
GCGCCAATTG TTAAAGACTC ATGAGATAAG TCAATATGTT GTACAGGTGA TCTTCTCCGT 240
GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
GAATAGCAGC TCCCGTTATT TTTCACTGAA AATGAACCTG TGCCTAATTC TGCTGATCCT 360
GGTTTTCATG GTGCCTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
TAAACAACGA CTGCTTTTTC CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
ACTAGGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
CATCAGCCGG GTTGGGTGTA TTGGAGTGAC TCTCATGGCT CTTCTTTCTG GATTGTGTGC 600
TGTCACATGC CCATACACTT ACATGTCTTA CTTCTCAGG AATGTGACTG ACACAGATAT 660
TCTAGCCCTG GAACGGCGAG TGCTGCAAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720
GATGGCAATG GCACGGAGAA CAATGTTCCT GAAGGGGGAA GTGCATAACA AACCATCAGG 780
TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT 840
TATTCAACAG GAAGTGGATG CTTTGGGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
TGATCTATAT GCTACCAAGG AGAGAAATAGA ATACTCCAAA ACCTTCAAGG GGAATATATT 960
TAATTTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
TGTGAATTAT CTGGGAATCC AATTGTATGT GAAATTTTGG TCCCAACACA TTCTCTTCAT 1140
TCTTGTGGA ATAATCATCG TCACATCCAT CAGAGGATTG CTGATCACTC TTACCAAGTT 1200
CTTTATGCC ATCTTAGCA GTAAGTCTC CAATGTCAAT GTCTGTCTAT TAGCAGAT 1260
AATGGGCAAG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTGAATA 1320
COGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTGTGTT 1380
TGATGTGATC TTCTGGTCA GCGCTCTCTC TAGCATACTC TTCTCTATT TGGCTCACA 1440
ACAGGCCACA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500
CAGTGTGTTT AAAATTAGTA TATAAGAGGG GGGAAAAATG GAACCAAGGC CTGACATTTT 1560
ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACTTCA TAGCATACTC CTTCCCCCTC 1620
AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTCAG 1680
ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
CAAAGAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGTTAGC 1800
TGAGCCAAAC ACGTAGGATT TCCGTTTAA GTTTCATCAT GAAAAGGTTA TAGCTTTGCC 1860
TTGAGATTGA CTCATTAATA TCAGAGACTG T

```

**A84 Protein sequence**

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Protein Accession #: NP\_057418.1  
 Signal sequence: none found  
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402,  
 424-446  
 Cellular localization: plasma membrane

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1      11      21      31      41      51

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	MSFLIDSSIM	ITSQILFFPG	GWLFFMRQLF	KDYBIRQYV	QVIPSVTFAF	SCTMFELIIF	60
	EILGLVNSSS	RYFHWKQNL	VILLILVFMV	PFIYGYFIVS	NIRLLHKRQL	LFSCLLWLT	120
5	MYFFKLGDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYFLRN	180
	VTDTDLAL	RELLQTMDMI	ISKKKRMAMA	RRTMFPQKEV	HNKPSGFWGM	IKSVTTSASG	240
	SENLTLIQBE	VDALIELSRQ	LPLETADLYA	TKERIEYSKT	FKGKYFNFILG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKTDVPT	RGIEITVNYL	GIQFDVKFWS	QHISFILVGI	IIVTSIRGLL	360
10	ITLTKFFVAI	SSSKSSNVIV	LLLAQIMGY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYHRWFDVIF	LVSALSSILF	LYLAHQAPE	KQMAP			
	<u>A85 DNA SEQUENCE:</u>						
	Gene name: TTK protein kinase						
	Unigene number: Hs.169840						
	Probeset Accession #: M86699						
15	Nucleic Acid Accession #: NM_003318						
	Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)						
20	1	11	21	31	41	51	
	GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGGCAC	ATCTCAGCTT	ACTGCAACCT	CCGCTCCCG	GGTCAAGCG	ATTCTCCTGC	120
	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACATAATT	180
	CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
25	ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAAGTGCTA	GGATTACAGC	CGTGAAACTG	300
	TGCTGGCTG	ATTCTTTTTT	TGTTGTGGA	TTTTTGAAC	AGGGTCTCCC	TTGGTCGCC	360
	AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATAAACC	TCCACCTCCT	GGTTTCAAGT	420
	GATCTCCCA	CTTTAGCTTC	CTGAGTAGCT	GTGATTACAG	GGGTGCACCA	CCACACCCGG	480
	CTAATTTTTG	TATTTTTTAT	AGAGACAGGG	TTTCAACATG	TTGGCCAGGC	TGTTCTCAAA	540
30	CTCCTGGACT	CAAGTAGTCC	GCCTGGCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACCATG	CCTGACCTTA	TAATCTTAA	GTCATTTTTT	CTGTCCATT	TCTTCCTTAG	660
	GGTCTCTACA	ACAAATCTGC	ATTAGGCGGT	ACAATAATCC	TTAACTTCAT	GATTCACAAA	720
	AGGAAGATGA	AGTGATTTCAT	GATTTAGAAA	GGGGAAGTAG	TAAAGCCCAT	GCACACTCCT	780
35	GGATGATGAT	CCTAAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
	TTTGGTTTAA	ATTAATTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
	ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCCCAG	960
	TGCAGTTTTT	TGTAGAAAAT	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
	CCATAATGAA	CAAGTGAGAG	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
40	AACTAAGCTT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAAGT	GTTAACCAAA	1140
	TTATGATGAT	GGCAACAAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
	ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATGTAT	TGGTCGTAC	AGTCAAGCAA	1260
	TTGAAGGCT	TCCCCAGAT	AAATATGGCC	AAATAGAGAG	TTTTGCTAGA	ATTCAAGTGA	1320
	GATTTGCTGA	ATTAAAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAATGG	1380
45	CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTTATATATC	TTTTCACAA	TTTGAAGTGT	1440
	CACAAGTAA	TGTCAAAAAC	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGAGCAG	1500
	TACCACTAGA	AATGCTGGAA	ATTGCCCTGC	GGAATTTAAA	CCTCCAAAAA	AAGCAGCTGC	1560
	TTTCAGAGGA	GGAAAGAAG	AATTTATCAG	CATCTACGGT	ATTAAGTCCC	CAAGAAATCAT	1620
	TTTCGGTTC	ACTTGGGCTT	TTACAGAATA	GGAACAACAG	TTGTGATTCC	AGAGGACAGA	1680
	CTACTAAAGC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
50	ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAACACAGT	ATGCCCATTT	GGAAGAGTCC	1800
	CAGTTAACT	TCTAAATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACTCT	1860
	GTTTTATGAA	AAGACAACCC	TCTAGATCAG	AATGCOGAGA	TTTGGTTGTG	CCTGGATCTA	1920
	AAACCAAGTG	AAATGATTCC	TGTGAATTAA	GAAATTTAAA	GTTCTGTTCA	AATAGTCATT	1980
55	TCAAGGAACC	TCTGGTGTCA	GATGAAAAGA	GTTCTGAAGT	TATTATTACT	GATTCAATAA	2040
	CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
	AAGAAACAGA	GGTTCCAGAG	AGTAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
	GTATTAAACA	GAATCCTGCT	GCACTTCTAA	ATCACTGGCA	GATTCGGGAG	TTAGCCCGAA	2220
	AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGAGCAACC	TGCTTTTCA	GTTTCAAAAC	2280
60	AGTCACCACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
	GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTTAGAAC	TCCAGTTGTA	AAGAATGACT	2400
	TTCCACCTGC	TGTTCAGTTG	TCAACACCTT	ATGGCCAAAC	TGCTGTTTTC	CAGCAGCAAC	2460
	AGCATCAAT	ACTTGCCACT	CCACTTCAAA	ATTACAGGTT	TTTAGCATCT	TCTTCAGCAA	2520
	ATGAATGCAT	TTGGTTTAAA	GGAAGAATTT	ATTCCATATT	AAAGCAGATA	GGAAGTGGAG	2580
65	GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAATATG	2640
	TGAATTAAGT	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
	TGAATAAACT	ACAACAACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCAAGG	2760
	ACCAATACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
	AGAAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCAG	2880
70	TTCAACAAT	CCATCAACAT	GGCATGTGTC	ACAGTGATCT	TAAACCAAGT	AACCTTTCTGA	2940
	TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATGTC	AAACCAAAATG	CAACCAAGATA	3000
	CAACAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAAAGCAA	3060
	TCAAGATAT	GTCCTCCTCC	AGAGAGATG	GGAATCTTAA	GTCAAAGATA	AGCCCAAAAA	3120
	GTGATGTTG	GTCCTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCATTTT	3180
75	AGCAGATAAT	TAAATCAGAT	TCTAAATTAC	ATGCCATAAT	TGATCCTAAT	CATGAAATTG	3240
	AATTTCCCGA	TATTCAGAG	AAAGATCTTC	AAGATGTGTT	AAAGTGTGTT	TAAAAAAGGG	3300
	ACCCAACACA	GAGGATATCC	ATTCTGAGC	TCCTGGCTCA	TCCATATGTT	CAAAATCAAA	3360
	CTCATCCAGT	TAAACCAATG	GCCAAGGGAA	CCACTGAAGA	AATGAATAT	GTTCTGGGCC	3420
	AACCTGTTGG	TCTGAATTTCT	CCTAACTCCA	TTTTGAAAGC	TGCTAAAACT	TTATATGAAC	3480
80	ACTATAGTGG	TGGTGAAAGT	CATAATTCTT	CATCCTCCAA	GACTTTTGAA	AAAAAAGGG	3540
	GAAAAAATG	ATTGCAAGTT	ATTGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGAGT	3600
	GTTATACTCT	TGAATCCCTG	TGGAAATCTA	CATTGAAGA	CAACATCAT	CTGAAGTGT	3660
	ATCAGCAAAA	AAAATTCAGT	GAGATTATCT	TTAAAAAGAA	ACTGTAAAAA	TAGCAACCCAC	3720
	TTATGGCACT	GTATATATTG	TAGACTTGTT	TTCTCTGTTT	TATGCTCTTG	TGTAATCTAC	3780
	TTGACATCAT	TTTACTCTTG	GAATAGTGGG	TGGATAGCAA	GTATATTCTA	AAAAACTTTG	3840



TAAATAAAGT TTTGTGGCTA AAATGA

**A86 Protein sequence:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51  
 15 MNKVRDIKVK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLKLEKNS 60  
 VPLSDALLNK LIGRYSQAIE ALPPDKYQGN ESFARIQVRF AELKAIQEPD DARDYFQMAR 120  
 ANCKKFAFVH ISFAQPELSQ GNVKKSQQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180  
 EEEKKLSAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARPLYGENM PPQDAEIGYR 240  
 20 NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGSKP 300  
 SGNDSCELRN LKSVQNSHPK EPLVSEKSS ELIITDSITL KNTKESSLLA KLEETKEYQE 360  
 PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTPE QPVFVSRSQS 420  
 PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTFVVKNDFF PACQLSTPYG QPACFQQQOH 480  
 25 QILATPLQNL QVLASSANE CISVKGRIYS ILKQIGSGGS SKVPQVLNEK KQIYAIKYN 540  
 LERADNQTLN SYRNEIAYLN KIQHSDKII RLYDYEITDQ YIYMVMECGN IDLSNWLKKK 600  
 KSIDPWERKS YWKMLEAVH TIHQHGIHVS DLKPANPLIV DGMKLKIDFG IANQMOPDTT 660  
 SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYY MTYGTPTFPQ 720  
 IINQISKLHA IIDPNHIEF PDIEKDLQD VLKCKLRDP KQRISPELL AHPYVQIQTH 780  
 PVNQMAKGT EEMKYVLGQL VGLNSPNSIL KAAKTYEHY SGGESHNSSS SKTFEKKRGK 840  
 K

**A87 DNA SEQUENCE**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719  
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 GGGGCGCAGG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CTGCCCCCT 60  
 CTGCCACCTG GGGCGGTGGG GGCOCGAGC CGGAGCGCGG GGTAGCGCGT AGAGCCGGCG 120  
 CGATGCACTG GCGCTCACTG CGAGCTGCGG CGCGGCACAG CTTCGTGGCG CTCTGGGCAC 180  
 45 CCCTGTCTCT GCTGCGCTCC GCCCTGGCGG ACTTCAGCCT GGACAAAGAG GTGCACTCGA 240  
 GCTTCATCCA CGCGCGCTCC GCAGCCAGG AGCGCGGGGA GATGCAGCGC GAGATCCTCT 300  
 CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360  
 CCATGTTTAT GCTGAGACTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGGG 420  
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 50 GCCTGCAAGA TAGCCATTTT CTCACCGACG CGGACATGGT CATGAGCTTC GTCAACCTCG 540  
 TGGAAACATGA CAAGGAATTC TTCCACCCAC GCTACCAACA TGAGAGTTTC CGGTTTGATC 600  
 TTTCCAGAT CCAGAAAGGG GAAGCTGTCA CGGCGAGCGA ATTCGGGATC TACAAGGACT 660  
 ACATCGCGGA ACCTCTCGAC AATGAGAGCT TCGGATCAG CGTTTATCAG GTGCTCCAGG 720  
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGTACCCCTC TGGGCTCGG 780  
 55 AGGAGGGCTG GCTGTGTGTT GACATCAGC CCACAGCAA CCACTGGGTG GTCAATCCGC 840  
 GGCACAACT GGGCCTGCGG CTCTCGGTGG AGAOGCTGGA TGGGACAGC ATCAACCCCA 900  
 AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960  
 TCTTCAGGC CAGGAGGTC CACTTCGCGA GCATCGGTC CAGGGGAGC AAACAGCGCA 1020  
 60 GCCAGAACCG CTCCAAGAG CCCAAGAAC AGGAAGCCCT GGGATGGCC AACGTGGCAG 1080  
 AGAACAGCAG CAGCGACGAG AGGCAGGCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140  
 GAGACCTGGG CTGCGAGGAC TGGATCATCG CGCTGAAGG CTACGCGGCC TACTACTGTG 1200  
 AGGGGGAGTG TGCTTCCCT CTGAACCTCT ACATGAAAGC CACCAACCCG GCCATCGTGC 1260  
 AGACGCTGCT CCACTTCATC AACCCGGAAG CGGTGCCAA GCCCTGTGTG GCGCCACGCG 1320  
 65 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAAOGTCATC CTGAAGAAAT 1380  
 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GGCACAGCT OCTCGAGAA TTCAGACCTC 1440  
 TTGGGGCCAA GTTTTCTCG ATCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500  
 CTGCTTTTGG TGAGACCTTC CCTCCCTAT CCCCACCTT AAAGGTGTGA GAGTATTAGG 1560  
 AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620  
 70 TCTTCAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAAA ACAACGCATA AAGAAAAATG 1680  
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 TTATGAGGCG CTACAGGCA GGCCACCCAG CGTGGGAGG AAGGGGGCGT GGCAGGGGGT 1800  
 GGGCATTG GTGTCTGTGC GAAAGGAAAA TTGACCGGA AGTTCTGTGA ATAAATGTCA 1860  
 CAATAAAGC AATGAATG

**A88 Protein sequence:**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Protein Accession #: NP\_001710.1  
 Signal sequence: 1-30  
 Pfam domains: TGF $\beta$  propeptide [37-281]  
 Transmembrane domains: none found  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
5  MHVRSRLRAA PHSFVALWAP LPLLRSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60
   ILGLPHRPRP HLQGHNSAP MFMLDLNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
   LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRYKYDY 180
   IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVEFDITA TSNHVVVNPR 240
   HNLGLQLSVE TLDGQSINPK LAGLGRHGP QNKQPFMVAF FKATEVHPRS IRSTGSKQRS 300
10  QNRSKTPKNQ BALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWDWIIA PEGYAAYYCE 360
   GECAFFLNSY MNATNHAIVQ TLVHPINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
   RNMVVRACGC H

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A89 DNA SEQUENCE:

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15  Gene name:      Homo sapiens mRNA; cDNA DKFp56401763 (from clone DKFp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Nucleic Acid Accession #: AC012478
   Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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20  1      11      21      31      41      51
   |      |      |      |      |      |
25  ATGCGGCGCG TGCCTGCTGC CGCCCCGCTC CTGCGCTGCG TGCTGCTGCG GCTCCTGGCC 60
   GCTCCGCGCG CCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
   CGCGAGTCGC GGCACCGCC CGGCCCGGGG CCGGGGAACA CCACCGGTT TGGGTCTGGG 180
   GCGGCGGGCG GCAGCGGCG CTCCAGCTCC AACAGCAGTG GCGACGCTT GTGACCCGCG 240
   ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCAG CCGTGATCGT GCGTTCGCGC 300
   TTACACCCCT TCCTCATCGC CTGCGCTGCT CTGCGGTCTC TCAGGTGCGG AAAGAGGTTA 360
   AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGA AATGGGCCCA 420
   CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
   TCCTTGCGCG CTGCACTGAG ACGTCAGCTG CCAGGCTGCC AGACGCTACT GACAGTTCCT 540
   GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCAGCAA GATGCAGTGG AAGGCCGTGAT 600
   GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCTGCTG GGCATCTCTG GGAAAGTTGG 660
   TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAAG CCTCTGCGT CGGAGGTGTT 720
35  GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC 780
   TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCAAA TGGAGTTGCT TCTGCCACCC 840
   TTGGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGTTTTTGG ACAACTGCAG 900
   TCGAATCTCA TGGAAAAGCT GGATTCTCTC GCCTTAAGCA GAAACACCCG GGCTCCATCT 960
   GCCAGTGCT TGGCACTGGT CCGGCGAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
40  CCTTGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAACCATG 1080
   AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCGGCGCAGC GGGGCACCTT TTGTGAAGAC 1140
   AGAGCAGTGA CTAAGGTTCT CCAGGCTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
   GCCCTAGAGA TCGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
   ACCCATCTCG TCAGGTTGCG TCGTTAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
45  AGGGTGTTC GCGCTCGCG CAGTCTCTG CATGGCGAG GGTGAGCGG TACCGCAACT 1380
   TGCCCTTTGG TTTTGAAGAT TCTGTTGAGG GCGCATCCTC ACCTTGACCT CTTCTACAAA 1440
   ATCTGTCTCC CCGTCTGTGC CGTGAACAC CTAAGGGAAG CCAAGAGAAG CTCAGTGACT 1500
   GTCTTGTGCT CATTTGAGCA GAGCCCAACA AAGGCAGCTG CTGCCCAAGG GAGCCTGTCT 1560
   AAACGAGGGC CAGTGGGCA ATTGAACAGA CACATGACC CTGGCTGGGG GATCACACAT 1620
50  GCGAACCTCG AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCAAGTGA GGATGTCACT 1680
   CACCCTGGAG GAGACTTGGA TGGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
   GATGGCAGAT GCCAAGAT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
   TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCTCT 1860
   TCCCCCGGAC AGCCCTGTG TCTGTCCAGG CCTTGA

```

A90 Protein sequence:

```

60  Gene name:      Homo sapiens mRNA; cDNA DKFp56401763 (from clone DKFp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Protein Accession #: FGENESH predicted
   Signal sequence: 1-27
   Transmembrane domains: 94-115, 448-469
   Cellular Localization: not determined

```

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65  1      11      21      31      41      51
   |      |      |      |      |      |
70  MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTRPGSG 60
   AAGSGSSSSS NSSGDALVTR ISILLRLDPT LKAAVIVAF FTLIIACLL LRVFRSGKRL 120
   KKTRKYDIIT TPAERVMAP LNEEDEDED STVPDIKRV SLPAALRQL PGQTLTLP 180
   VPPFFILDID LPARCSGRPD GGIRPGKTCF PAWHPVESW SAATNGVKDW TWKPSCVGGV 240
   ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHPPKVPEPT STPHGFRQLQ 300
   LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAESDLFN PWWHFSATGS PIKTLTYQTM 360
   STLGLDVFCG AGQRTFCED RAVTKVLQGS SPSKQLRWKP ALESQFPFHL RLLRECPPLS 420
75  THPVRLARSD ARGQASLTGR RVFRFRQSL HGGSGSATAT CLLVLKILLR RHPHLDLPYK 480
   ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHGEPV KRQPSQGLTR HTCPGWGITH 540
   ANLQTIPTDQ GQSGPREVDV HPGGDLGVA NFYLESEGFQ DGRQKQWVLM SEDGPPSLTG 600
   CERLTGSHHF SSHSKSWFL SPRQPLFLSR P

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EWINGA91 DNA SEQUENCE

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Gene name:      G protein-coupled receptor 64
Unigene number: Hs.184942

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Probeset Accession #: AA435577  
 Nucleic Acid Accession #: NM\_005756  
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

1      11      21      31      41      51
|      |      |      |      |      |
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTCTGAA 60
CTCGCGGTCA GGAATGTTTT CTCTGTGAGG CAGTGTGGCC ATGTGGGCAG AACTGAAGAA 120
GTTTCTAGCA CGTTCAAGAT ATTCTTGTTC ATCATTTGTC TTCATGTCGT TCTGGTAACA 180
TCCTCGGAAG AAGATACTGA TAAATCCAGT TTGTCAACAC CACCTGCTAA ATTATCTGTT 240
GTCAGTTTTG CCCCTCTCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAAACA CTATAGTAAA AACCTTCAAT 360
GCCTCAGGCG TCAGAACCCA GAGAAATATC TGCAATTGTT CATCTATTGT CAATGACTCA 420
GCATTTTCTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT 480
CAACATATAA CGAATGGCAC CTAACTGGGA GTCTGTCTCT TAAGTGAATT AAAACGCTCA 540
GAGCTCAACA AAACCCCTGA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCCAAA GCACATTAAT TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660
TTGTCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTGAGC CAATGGAACA CTGCTGCTGT 720
TCTGTGAGTA TACCTGCCCC TTCTCTCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA 840
TCCATCCCAG TGGTGCCTCG GGCCACTGTG CTTTCCAGG TCCCAAAAGC TACCTCTTTT 900
GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
CAACCCCTTT CACCCAGGCC TTCAGCTCCC ATAGCTTCCA GGCCTGCCAT TGACATGCCC 1020
CCACAGTCTG AAGCATCTCT TCCCTATG TGCCCAACCC ATGTCTCCGG CACCCAGACT 1080
CCTGTGAAGC CCTCATTTTC CTCTCCACCC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC 1200
CAAGTGTGTC AGATGGAGAA GGCTCTGTTC TTGGGCAGCC TGGAGCCTAA CCTCGCAGGA 1260
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCGCCGC CTGACATGCT GGGCCCTCTG 1320
GCTCAAAGAT TGCTGAAGT AGTGGATGAC ATTGGCCTAC AGCTGAACCT TTCAAACAGC 1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAATC TTCAGTTTC TCTGGAACCC 1500
CAAGCTCTG AGAACAGTAT TGGCACAATT ACTCTTCTTT CATCGCTGAT GAATAATTTA 1560
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAAGTTA ATTTTTTTGA AACACCTGCT 1620
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680
GTTGCACAA TCACCGTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
AACCCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800
GGCAGGAGG CAGTGTGAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAACCC 1860
ATCTGTACCT GTAGCCATCT AACAGCTTC GCGTCTGTC TGGACCTATC TAGGACATCT 1920
GTGCTGCTG CTCAATGAT GGCTCTGAGC TTCATTACAT ATATTGGTTG TGGGCTTTCA 1980
TCAATTTTTC TGTCACTGAC TCTGTAAACC TACATAGCTT TTGAAAAGAT CCGGAGGGAT 2040
TACCTCTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TCTCTGTGAA CCTGGTCTTC 2100
CTCCTGAGTG CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA 2160
TTTCTTCATT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCTAGAAAGC ATTCCATATG 2220
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTGTC 2280
ATTGTGCTGT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCTGACTAT ATCCCGAGT 2340
AACTATGGGC TTGGATCCCTA TGGGAAATTC CCCAATGGTT CACCGGATGA CTTCTGCTGG 2400
ATCAACAACA GCTGATATCT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTGT 2460
CTGAACGTCA GCATGTTTCA TGTGCTCTCT GTTCAGCTCT GTCGAATTAA AAAGAAGAAG 2520
CAACTGGGAG CCCAGCGAAA AACCAATATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580
TTTTACTGTT GAATAACTTG GGGCTTTGCC TTCTTTGCTT GGGGACCACT TAACGTGACC 2640
TTCAATGATC TGTGTTGCCAT CTTTAATACC TTACAAGGAT TTTTCTATAT CATCTTTTAC 2700
TGTGTGGCCA AAGAAATGTT CAGGAAGCAA TGGAGGCGGT ATCTTTGTTG TGGAAAGTTA 2760
CGGCTGGCTG AAAATCTGTA CTGGAGTAAA ACTGCTACTA ATGTTTAAA GAAGCAGACT 2820
GTAACCAAGG GAGTGTCCAG CTCTTCAAA TCCCTACAGT CAAGCAGTAA CTCCACTAAC 2880
TCCACACAC TGCTAGTGAA TAATGATTGC TCAGTACAGC CAAGCGGAAA TGGAAATGCT 2940
TCTACAGAGA GGAATGGGTT CTCTTTTATG GTTCAGAAAT GAGATGTGTG CCTTCAAGAT 3000
TTCACTGAGT AACAGCACAT GTTTAAGCAG AAGGAAGATT CCTGCAATGG GAAAGGCGGT 3060
ATGGCTCTCA GAAGGACTTC AAAGCGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
CTTTCTCTTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAAAT TTACTCTTTA 3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAAGCAT 3240
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
TTTAGACATT TCTGATTGTT TTTCTTATCT TTCATTTTAT AAGAAGGTTG GTTTTAAACA 3360
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
TTTTAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTTGA CTTGAGCCTG 3480
TTGGTGAGTT TAGTTGTGCA TGCCCTTTGT GTATATAAGC TAAATCTAG TGACCCATGT 3540
GTCAAAATC TTAATCTTAC ATTTTCTTGT ATTTATTTTC TACTGTGTAA ATGTATCTCT 3600
TTGTAGAATC ATGTTGTTT TGTCTCACGT GATAATTCAG AAAATCCTTG CTCGTTCCGC 3660
AAATCTTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
TCAAGAAATA ATGATCCAG CCAGACTGAG AAAATGTAAG CAGACAGTGC CACAGTATGC 3780
TCATACAGTG CCTTTAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
TGGGTGATGG TTTGACAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
GTGCAGGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCATCCC CTGACCGCAT 3960
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
AGAGGGATGA ACTGCTATCC AGACCATGTG TCAGGAAAT TGTGAACGTA GATGAGGTAC 4080
ATACACTGCC GCTTCTCAAA TCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140
CTTCTCTTAA AAAGGTACAT ATATATGGA AAAAATCATA TTGCCGTTCT TTAAGAGCA 4200
ACTGCTATGT ACATTGTTGA TTGTTATGAC TGGTACACTC TGGCCAGGCC AGAGCTATAA 4260
TTGTTTCTTA AATGTGCTTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
GGGAACCTGC CTACACTGCT ATTGTTGCTA CATGTATOGA GCCTTGATTG CTCCTAGTTA 4380
TATACAGGGT CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCTCT AAGTACATCC 4440
TTATTAGGAA CATTTCAAAC CCTTTTGTAG TAAGTCTTTC ACTAAGGTTT TCTTGATAT 4500
ATTTCAAGTG AATGTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
CTGACTGTGC TTTGCAATAT TTCTTTCTG ATTTATTATA TTTTCTTGTA TTTATATGTT 4620

```

AAAATCAAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

# A92 Protein sequence

Gene name: G protein-coupled receptor 64  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
15 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPF PAKLSVVSPA 60
PSSNEVETTS LNDVTLSELLP SNETERTKIT IVKTFNASGV KPQRNICLS SICNDSAPFR 120
GEIMFQYDKE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAS 180
TLNCTFTIKL NNTMNAACAI AALERVKIRP MEHCCSVRI PCPSSPEELG KLQCDLQDPI 240
VCLADHPRGP PFSSSQSIFV VPRATVLSQV PKATSPAEPP DYSPVTHNVP SPIGEIQFLS 300
PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTPPPVKA SFSSPTVSAP ANVNTTSAPP 360
VQTDIVNTSS ISDLNQLVQ MEKALSLGSL EPNLAGEMIN QVSRLLHSPF DMLAPLAQRL 420
LKVVDDIGLQ LNFSTNTISL TSPSLALAVI RVNASSFNTT TFVAQDPANL QVSLETQAPE 480
NSIGTITLPS SLMNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVISSSVANL 540
TVRNLTRNVT VTLKHINPSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600
SHLTSPFVLL DLSRTSVLPA QMMALTFTY IGCGLSSIFL SVTLVTYIAF EKIRRDYPSK 660
25 ILIQLCAALL LNLVFLDLS WIALYKMQGL CISVAVFLHY FLVSPFMWG LEAFHMYLAL 720
VKVFNTYIRK YILKFCIVGW GVPVAVVTII LTISPNDYGL GSYGKFPNGS PDDFCWINNN 780
AVFEYITVGY FCVIFLLNVS MFIVVLVQLC RIKKKQLGA QRKTSIQDLR SIAGLTFLLG 840
ITWGFAPFAN GPNVNTFMYL FAIFNTLQGF FIFIPYCVAK ENVRKQWRY LCCGKLRLAE 900
30 NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDSCVHA SGNGNASTER 960
NGVSFSVQNG DVCLHDFGK QHMFNEKEDS CNGKGRMALR RTSKRGSLHF IEQM

```

## Fibrosis

### A93 DNA SEQUENCE

Gene name: BGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

```

40 1      11      21      31      41      51
|      |      |      |      |      |
CGCGAGAGGA GCCTCGGCCA GGCTAGCCAG GCGGCCCCCA GCCCTCCCC AGGCGCGGAG 60
CGCCCCCTGCC GCGGTGCGCT GCCTCCCCTC CCAGACTGCA GGGACAGCAC CCGTAACGTG 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGGCC GCGGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGGGAGA 240
ATGCTCTTGC CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
GGGAACCGGG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCAOGTCA GCGTGGGTC 360
TGCTACTATG GAACATAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGAAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGGC CAGTCCCAAC CAGATGTGTG AATACACAAG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAAGTCTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
TCAGGACTCC GCTTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
AAATGTCACA TTGTTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGGTCCCTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTCTTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACTG GTAACATCAA AGACAGAATC 1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAAG CAAAAATTAA AAATGTTACC 1140
CCGAACCCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGOGA 1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGATT 1380
CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAAA TATCTCGGTT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAACTCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA 1560
GGTCAACAAG AAGACATTGG CCGATTGAAA CTCTCCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCGGAGACAA AAGTGGGAA ACTTGGAGTG 1680
TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCAAGAGTGA GGATGAAAAG 1740
TGAAGACAG GGAATAATCA GTTGATATCA GGAAGTATG CTACCAAAAG CATCATTTTT 1800
GAAGCAGAAC GTGCAAGGGC CAAACCGGC GAAATGCGAG TGGATGGGOT CTGCTTGT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTTGT ATGTGAGTGT CCGTGGTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCTT 2040
TCTTGATATA GATATGCCAA TATTGCTTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAATG GTCAGTTTAT CTCCCCTCT 2160
CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TCTTAGAAAA 2220
TAGAAAAAAA AGCACAAGAA AATGTTTAACT TGTTTGACTC TTATGATACT TTTGGGAAAC 2280
TATGACATCA AAGATAGACT TTTGCTTAAG TGGCTTAGCT GGTCTTTTCA TAGCCAAACT 2340
TGTATATTTA AATCTTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

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A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

1 11 21 31 41 51  
 15 MPLPWSLALP LLLSWVAGGF GNAASARHFG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60  
 CEATCEPGCK FGECVGFNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRVC NTHGSYKCF 120  
 LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEPQCLCPSS SGLRLAPNGR DCLDIDECAS 180  
 GKVICPYNRR CVNTFGSYIC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240  
 20 GSPKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KGLLAHNSNM KKKAKIKNVT 300  
 PEPTRTPTEK VNLQPFNYEE IVSRGNSHSG GKKGNEBKMK EGLEDEKREE KALKNDIEER 360  
 SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHIGCD WRQDREDDFD 420  
 WNPADRDNAI GFYMAVPAFA GHKKDIGRLK LLLPDLQPS NFCLLFYRL AGDKVGKLRV 480  
 FVKNNSNALA WEKTTSEDEK WTKGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV 540  
 25 SGLCPDSLLS VDD

GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51  
 35 AGCAACGACG CGGGGCAGCG GGAGCGCGCG CGCGCCCATG TGGCTGCTGG GCGCGCTGTG 60  
 CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGAACAACT TCAACCAATGA 120  
 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180  
 40 GTGTGACGGG CTGCGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 GTGAAATGTG GGCCTCAACT TCTTCCCTCG TGCCAGCGGC ATCCATTGCA TCATTGGTGG 300  
 CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCCCTCT CTTTGTCTCA CGCCCGGCTA CCACTGCAAG AACGCCCTCT GTATTGACAA 420  
 GAGCTTCATC TGGGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 45 AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540  
 TTACCCGACG ATCACTTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 CCTGCTGGCA CTGGTCTTGC ACCACCAAGG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660  
 GCACCGGCTG CAGCACCTGT TGCTGCTGTC CGGCTGGTGG GTCCCTGGACC ACCCCACCCA 720  
 CTGCAACGTC AACTACACCG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 50 GAATGCGTGG GAAGTAGGCT CCCCACCTCT CTACTCCGAG GCCTTGCTGG ACCAGAGGCC 840  
 TGCGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
 CGACCTGCCC CCCTACCGCT CCGGTCGCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960  
 CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGCA 1020  
 GGGCAGCTGT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 55 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTGG 1140  
 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 AACTATCTCT GCATTCCTCT CCTCCCCAG ACTTCAGAGA TGTTTTCTTG GCGTCTCAGT 1260  
 TGACATGATC TGTGTGCGGT CTTTCTGCTC AGGTCACTCT TCCTTGGGA CCGAGATCA 1320  
 CACCCCTCAT TTTCACATTA TTCTGTTTCT GTTGAGAGAG CAGCATATAA AACAGTATTG 1380  
 60 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATCTCTCTG GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500  
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATT CCATTTGAGC 1560  
 ATCAAAACCT GCTTTGCACA ATCTATTGTT ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620  
 AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTGGC AACGTTATTT TGGTTTGTG 1680  
 65 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTGG CCCAAGAATG 1740  
 CTCAATCTGA GAGCTTTCTC CAGCAGCATA TATCATCAGC CTCATCCTAA AATAGGCAGG 1800  
 GAGCCCTCTC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860  
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCACGCTG 1920  
 ACCTGCCCCG AGCCAGGAAA TGAGGAOCTA ACTTGAGTTG GCCCAAGGCT TGAACCTGGT 1980  
 70 GTATGTCCCT GTGGCCACCA CCCAGCCTGT CTTGCTCAIT CATGCAGCTC CAACACTGGC 2040  
 CTCCAAAGTT CCCTTAACAC TTGCAAGTCT CTTTCTACCT GTGCATTGAG ACTTGAGGAC 2100  
 ACTGGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTGAGGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
 75 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAATGCATT 2340  
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 AGCTGTCTCT TTTTGTGTTT TTCTTTTAA AGGTGCCAAA GAAGAGTGCA AAAGGAGATC 2460  
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 ACATTGTGTC ATTGTGTCAC TTTGAGGTTA TTATTTATCA AGTCTCTGAA GGAAGCAGAA 2580  
 80 AGAGGACTCT CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640  
 TTCTCTGTGT CCACTGACCC ACAGGGCCCC CTTCCCTGCA GGAAATAGGG GTAAAAAGTT 2700  
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5 TGATCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTCAGAA 2940  
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 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATGT 3300  
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 10 TGATTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGGTTT 3420  
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 TTATACTTTC TAATAAAATT GCAGTTTCAT TCTTCTGTGT TGTGCAAAAG GWMCTAMARM 3840  
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTAAACA CCACCTCGGG 3900  
 TGGGCCGGCG GGGCCACGCT AGGTACGGCG ACCACGGCGG CCCAAACGGG ACCCCAGAAG 3960  
 20 GAAACCCCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACCCGCCGGG 4020  
 GGAAACCGCA GAGTGTTCGC TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

25 A96 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AN043782  
 Protein Accession #: none found  
 30 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51  
 MWLLGLPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60  
 EKECEPKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCPDG SDEENTANP LLCSTARYHC 120  
 40 KNGLCIDKSP ICDQNNQD NSDEBCESS QEPGSGQVFP TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLRHQKRR NNLMTLPVHR LQHPVLLSRL VLDHFHHCN VTYNVINGIQ 240  
 YVASQABQNA SEVSGPPSYS EALLDQRPFW YDLPPFPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTEEV

#### 45 LUNG

50 A97 DNA SEQUENCE  
 Gene name: putative GPCR, Weakly similar to dJ365012.1  
 Unigene number: Hs.256897  
 Probeset Accession #: BE001836  
 Nucleic Acid Accession #: BE001836  
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 ATGGCCGTCA AATCTTTTC CTTCACACT GGAATGATG GGCTAGACCC AGACCCAATC 60  
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 GGTTAGGCC CACATAGCAC TAAAGTCTT CAACATGCAA TTAGAAGCTC AAATGTTGAC 180  
 60 GGGAATATTG TCACTCTAA AAAAGATGTT TCTATTAGAA TTTACTACT CTTTCATGAA 240  
 AACATAGATG CTCTCTCTTT CTGATTAGT GATGGCCATC AGTTAACCCA AGTGCACTCA 300  
 GAGAAGTCAA ATTCTGACAC AATCCAGCAA GTAACTATAA AAACGTATGG CCCAGTCGAA 360  
 GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAAA AGATTGAGA 420  
 AATTTTCTGA AGCTCTTGAA GCCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480  
 65 AGAGCAAAAG CTACCACAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA 540  
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 GCTGGAGCAC TCCCAAGCTG TGAATGTCAT CTCAACAACC TCAGCCAGAG TGTCAATTTC 660  
 TGTGAGAGAA CAAGATTGTT GGGCATTTC AAAATTAATG AAAGGTTTAC AAATGACCTT 720  
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 70 AAAGCATATG AAAGAATTCA AGGTTTGTAG TCGGTTCAAG TCACCCAATT TCGAAATGGA 840  
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 75 TGTGAGTCTT CTGGGTGGCA GGTCACTAGG GAGACTTGTG TGCTCTCTCT GCTTGAAGAA 1140  
 CTGAACRAGA ATTTCAATGAT GATTGTAGGC AATGCCACTG AGGCAGCTGT GTCATCCTTC 1200  
 GTGCAAAATC TTCTGTCTAT CATTGGGCAA AACCCATCAA CCACAGTGGG GAATCTGCTG 1260  
 TCGGTGTGTG CGATTCTGAG CAATATTCCA TCTCTGTGTC TGGCCAGCCA TTTCAAGGTG 1320  
 TCCAATTCAA CAATGGAGGA TGTCTACAGT ATAGCTGACA ATATCTCTAA TTCAGCTTCA 1380  
 80 GTAACCAACT GGACAGTCTT ACTGCGGGAA GAAAAGTATG CCAGCTCAAG GTTACTAGAG 1440  
 ACATTAGAAA ACATCAGCAC TCTGGTGCTT CCGACAGCTC TTCTCTGAA TTTTCTCGG 1500  
 AAATTCTATT ACTGGAAGG GATTCCAGTG AACAAAAGCC AACTCAAAAG GGGTTACAGC 1560  
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 GGTTCAGAGC AATTCAGAG ATCCCTTCCA GAAACTATTA TCAGATGCGC CTGCTTGACT 1680  
 CTGGGGAACA TTCTACCCGT TTCCAAAAAT GGAAATGCTC AGGTCAATGG ACCTGTGATA 1740

5 TCCACGGTTA TTCAAACTA TTCCATAAAT GAAGTTTTC TATTTTTC CAAGATAGAG 1800  
 TCAAACTGA GCCAGCTCA TTGTGTGTT TGGGATTCA GTCAATTGCA GTGGAACGAT 1860  
 GCAGGCTGCC ACCTAGTGAA TGAAACTCAA GACATCGTGA CGTGCCAAATG TACTCACTTG 1920  
 10 ACCTCTCTCT CCATATTGAT GTCACTTTT GTCCCTCTA CAATCTTCCC CGTTGTAAAA 1980  
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 15 TTCTACCTCT CTTTGTCTT CTGGATGCTC ATGCTTGGCA TCCTGCTGGC TTACCGGATC 2280  
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 TATGGGTGCC CTCTCATTAT ATCTGTGCTT ACCATTGCTG TCACGCAACC TAGCAATACC 2400  
 TACAAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAACC ACTCTGGCT 2460  
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 20 ACAAAGCTCT GGAGGCCGAC TGTGGGGAA AGACTGAGTC GGGATGACAA GGCCACCATC 2580  
 ATCCGCGTGG GGAAGAGCCT CCTCATCTG ACCCTCTGC TAGGGCTCAC CTGGGCTTT 2640  
 GGAATAGGAA CAATAGTGGA CAGCCAGAT CTGGCTTGGC ATGTTATTTT TGCTTTACTC 2700  
 AATGCACTCC AGGGATTTTT TATCTTATGC TTTGGAATAC TCTTGGACAG TAAGCTGCGA 2760  
 CAATCTTGT TCAACAAGTT GTCTGCTTA AGTTCTTGA AGCAAAACAGA AAAGCAAAAC 2820  
 TCATCAGATT TATCTGCCAA ACCCAAATTC TCAAGCCTT TCAACCCACT GCAAAACAAA 2880  
 25 GGCCATTATG CATTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940  
 GTCTCAATG AATAA

#### A98 PROTEIN SEQUENCE

25 Gene name: putative GPCR, Weakly similar to dJ365012.1  
 Unigene number: Hs.256897  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Pfam domain: 7tm\_2 [561-820]  
 30 Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789  
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51  
 | | | | |  
 MHALLLCFSV LINGASGLSL QSPVEEYQLL LQVYRDSKE KRDLRNFLKL LKPPILLWSHG 60  
 LIRIIRAKAT TDCNSLNGVL QCTCEDSYTM FPPSCLDPNQ CYLHTAGALP SCECHLNLS 120  
 QSVNFCERTK IWGTFKINER PTNDLLNSSS AIYSKYANGI EIQLKKAYER IQGFESVQVT 180  
 QFRNGSIVAG YEVVGSSSAS ELLSAIEHVA EKAKTALHKL PFLDGSFRV PGKAQCNDIV 240  
 40 PFGSKDDEV TLPCSSGYRG NITAKCESSG WQVIRETCVL SLLEBLNKNF SMIVGNATEA 300  
 AVSSFVQMLS VIIRQNPSTT VGNLASVVS LSNISLSLSA SHFRVSNSTM EDVISIADNI 360  
 LNSASVTNWT VLLREEKYAS SRLLETLENI STLVPPTALP LNFSRKFIDW KGIPVNSQL 420  
 KRGSYQIKM CPQNTSIPIR GRVLIGSDQF QRSLEPETIIS MASLTILGNL PVSXNGNAQV 480  
 NGPVLSTVIQ NYSINEVFLF FSKIESNLQ PHCVFWDPSH LQWNDAGCHL VNETQDIVTC 540  
 45 QCTHLTSFSI LMSFPVPSTI FVVKWITYV GLGISIGSLI LCLIEALFW KQIKKQSTSH 600  
 TRRIOMVNIA LSLLIADVNF IVGATVDTV NPSGVCTAAV PFTHFFYLSL FFWHLMLGIL 660  
 LAYRIILVPH HNAQHLMAV GPCLGYGCP L IISVITIAVT QPSNTYKRD VCLWNWSNGS 720  
 KPLLAFFVPA LAIVAVNFV VLLVLTKLWR PTVGERLSRD DKATIIRVGK SLLILTPLL 780  
 LTWGFIGITI VDSQNLAMHV IFALLNAFQV RTVTITYCIV K

#### A99 DNA SEQUENCE

55 Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Probeset Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51  
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 AGCACCTGGG AAAAGGCAGA CGTGTGAGG GGGCTGTGG CCCAGCGTG CTGTGGCCTC 60  
 GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120  
 CTCCAGCATC ATGATTACCT CCCAATACT ATTTTGTGGA TTTGGGTGGC TTTCTTCAT 180  
 65 GCGCCAATTG TTTAAAGACT ATGAGATAGC TCAGTATGTT GTACAGGTGA TCTTCTCCGT 240  
 GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300  
 GAATAGCAGC TCCGTTATT TTCACTGGAA AATGAACCTG TGCCTAATTC TGCTGATCCT 360  
 GGTTTTCATG GTGCCCTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420  
 TAAACAACGA CTGCTTTTTT CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480  
 70 ACTAGGAGAT CCTTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540  
 CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTCTTTCTG GAITTGGTGC 600  
 TGTCAACTGC CCATACACTT ACATGTCTTA CTTCCTCAGG AATGTGACTG ACACAGATAT 660  
 TGTAGCCCTG GAACGGCGAC TGCTGCAAA CAGGATATG ATCATAAGCA AAAAGAAAAG 720  
 GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780  
 75 TTTCTGGGGA ATGATAAAAA GTGTACCAC TTCAAGCATCA GGAAGTGAAG ATCTTACTCT 840  
 TATTCAACAG GAAGTGGATG CTTTGGGAAGA ATTAAGCAGG CAGCTTTTTT TGGAAACAGC 900  
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 TAAITTTCTT GGTACTTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020  
 CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080  
 80 TGTGAATTAT CTGGGAATCC AATTGTAGT GAAGTTTGG TOCCAACACA TTTCTTCTAT 1140  
 TCTTGTGGA ATAAATCATG TCACATCCAT CAGAGGATG CTGATCACTC TTACCAAGTT 1200  
 CTTTATATGC ATCTCTAGCA GTAAGTCTCT CAATGTCAAT GTCTGCTAT TAGCAGAGAT 1260  
 AATGGGCATG TACTTTGTCT CCTCTGTCT GCTGATCCGA ATGAGTATGC CTTTGAATA 1320  
 CGCACCATTA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACGTTGGTT 1380  
 TGATGTGATC TTCTGTGTC GGGCTCTCTC TAGCATACTC TTCTCTATT TGGCTCACAA 1440

	ACAGGCACCA	GAGAAGCAA	TGGCACCTTG	AACCTAAGCC	TACTACAGAC	TGTTAGAGGC	1500
	CAGTGGTTTC	AAAAATTTAGA	TATAAGAGGG	GGGAAAAATG	GAACCAGGGC	CTGACATTTT	1560
	ATAAACAAAC	AAAATGCTAT	GGTAGCATTT	TTCACTCTCA	TAGCATACTC	CTTCCCCCTC	1620
5	AGGTGATACT	ATGACCATGA	GTAGCATCAG	CCAGAACATG	AGAGGGAGAA	CTAACTCAAG	1680
	ACAATACTCA	GCAGAGAGCA	TCCCGTGTGG	ATATGAGGCT	GGTGTAGAGG	CGGAGAGGAG	1740
	CCAAGAACT	AAAGGTGAAA	AATACACTGG	AACCTCTGGG	CAAGACATGT	CTATGGTAGC	1800
	TGAGCCAAAC	ACGTAGGATT	TCCGTTTAA	GGTTCACATG	GAAAAGGTTA	TAGCTTTGCC	1860
	TTGAGATTGA	CTCATTAAAA	TCAGAGACTG	T			
10	<u>A100 Protein sequence</u>						
	Gene name:		putative G-protein coupled receptor				
	Unigene number:		Hs.16085				
	Protein Accession #:		NP_057418.1				
	Signal sequence:		none found				
15	Transmembrane domains:		5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446				
	Cellular Localization:		plasma membrane				
20	1	11	21	31	41	51	
	MSFLIDSSIM	ITSQILFFGF	GWLFFMRQLP	KDYEIRQYVV	QVIFSVTFAP	SCTMPELIIP	60
	EILGVLNSSL	RYFHWKMLNC	VILLILVFMV	PPYIGYFIVS	NIRLLHKQRL	LFSCLLWLTP	120
	MYFFWLKGGP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYPLRN	180
	VTDTDLALE	RRLQLTMDMI	ISKKKRMAMA	RRTMPQKGEV	HNKPSGFWGM	IKSVTTSASG	240
25	SENLTLLIQE	VDALIEELSRQ	LPLETADLYA	TKERIEYSKT	FKGKYFNFLG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKTDPTV	RGIEITVNYL	GIQFDVKFWS	QHISFILVGI	IIVTSIRGLL	360
	ITLTKFFYAI	SSSKSSNVIV	LLLAQIMGY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYHRWFDVIF	LVSALSSILF	LYLAHKQAPE	KQMAP			
30	<u>A101 DNA SEQUENCE</u>						
	Gene name:		ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]				
	Unigene number:		Hs.19322				
	Probeset Accession #:		AA088458				
	Nucleic Acid Accession #:		AA088458				
35	Coding sequence:		862-1995 (underlined sequences correspond to start and stop codons)				
40	1	11	21	31	41	51	
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	CTGAAGAAA	AGGAGCTGGA	GCAGGAGAAG	GAGGTGCTGC	TGCAGGTTT	GGAGATGATG	120
	GCGCGGGCC	GCGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCGCG	180
	CTGGGCGAGA	GCAGAGCCAG	CGCCGACTTT	GGGCTGCAG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTGC	CCAAGGTACA	AGAGGTGGCC	CGTGCCTGG	GGGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GGGCGCTGCC	CCCGTCTCC	TCCGGGCCCC	CCTGCCCTGC	CCTGACGTCC	360
45	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGACTC	420
	CTCACCCGAG	AGGTGACCGA	GAAGAGTGAG	GCATCAACG	AGCTGGAGCA	GGAGAACTCG	480
	GCGCTCATT	AGCAGCTGTT	TGAGGCCCGC	GCCCTGAGCC	AGCAGGACGG	GGGACCTCTG	540
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50	GCCGAGGAC	AGTCCCGGAG	TGGGCGCCTT	CCTGCGCGCC	TTGCCAGATG	GGCTCCCGAG	720
	GCTTGCCTCC	GGCTGTGCC	CGCACCGAGC	GCTTGAATCC	GTTTGGGCTC	CTGGTTGYTG	780
	ACATGGGCTG	GGGCTCTCTT	TGAGTCCGCA	TAGTCCGCG	CTACTACTGG	CCGCTGTCAG	840
	TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	OGTCCCCCGG	TTTCCAGCGG	TGCGCGCTCG	900
	GGTCCCATCT	TCAGGAAAG	GCACTGCCCC	CGCCAGGCTG	CACTTCCAAC	AACGGGCGAG	960
55	AGAGGGGCG	GGGCGGCTCC	GACGCGGGTC	CAAGGGCAGC	TTCCCGCTCA	ACCAGGGCAC	1020
	CAGGAGGAGG	TGGCTGTAGC	TGGGACGAGC	GGAAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAGCGGGG	GGTGCCTGCC	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTGCG	ACTTCAGGTT	1140
	CTGGCCAGG	CTGAGGAGCC	CTGGCTGCAG	CGGATCGGCA	OGCGGGGTGG	GCGAGAGCTT	1200
	GGCTGTGATG	TGCCCTCCAC	AGACCCTGGG	GTGATGGCCT	TCCCCCTCTT	GGCGGGGAGC	1260
60	TTGCCCCAGC	TTGAGTCCCA	CACAACATCC	TGTGAGCCTG	GCTCCCCAGG	AGGGCCCCCA	1320
	GACAGCTCCC	AGGCACTGCA	TAGGCAAAAG	CTGTTTCCCC	CGACTCAGGA	TTTCCAGGCG	1380
	CTGGGGTCC	GCTCACCCCC	CTTTGCTCTC	ACGCCCCAGC	TGTCCCCAGG	TTTCACTGGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAAC	GAGAACCCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCTGCCCCA	GGCCCACTCC	CGCTGGTGCT	1560
65	GGAGTAGCA	CTGTGGGGGG	GGCCCTGCTC	AGCCCACTCT	GGAGGGTCCC	AGTGTACCA	1620
	GAACCAAGGG	CAACGCAACA	GCATCGATGG	GTCTCTGAGC	CCAGGGCCCC	CGATGCGGGG	1680
	TCAGTGTGTG	TGGGGCGCAG	GGCCTCCGAT	GCGGGGTGAG	TGCGTGGGGG	GCGCAGGGCC	1740
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70	CCTTCGGGAG	CCCACTCCCA	TGCTAACCTG	CCCAAGCAAA	CCCCACAGAG	CCACATTCCC	1920
	TGCTGCACCT	GGTCTGCAGG	GGTGTCCCAG	GACAGGCCCA	AGTCAGGCCA	GCATGCGAGT	1980
	GCCCTCTTAC	CTGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCTGGG	2040
	ACCTCTCTGG	CAGGAAAGGG	TGCAGGTCTT	GAGGGCCTGT	GCCCCACAGC	CCCAAGCAACC	2100
	AGGTGAGCTG	CAGCGCAGTG	GGTGGGCCAG	TGGCAGCCAG	GGAGAAGCCC	CCCGTCAGCA	2160
75	GGCTGGGGTC	TGCCCCACAG	GGCCTCCCCA	CGTCTGCCCT	TGAGGGGTGCC	TGCCATGCCC	2220
	TGGGGGATCC	TGGCATCTTT	ACTGGAGTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTAGCTTCA	TGAGGAGACC	GCCCCATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACTCCCG	GAAAACTGCG	CTTTCAAGCT	TGGTGTTCGG	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAAGTG	CCCTGGAGAC	2460
80	CACGAGGGGA	GAATTTAAAG	GCCCCGGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCCCT	CCTGGAGCCT	GCCTTAGGAC	GCTGGGGGGG	TGAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CTGGGCTCTT	ATCCGGGAGG	TGCCAGTAGC	GTGTGAGGAT	ACATACAGTG	2640
	GCGTGACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
	CAGAAAGTGT	CCCAAGTTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTGTGTGTT	ATCAAGTTCC	AAGGAAAAGG	ACATCTCAG	CCGGGGGTGG	TGGTTCACGC	2820



5 CTGGAATCCC AGCACTTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACAAAAAAAG AAAAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

**A102 DNA SEQUENCE**

10 Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

15  
 1 11 21 31 41 51  
 | | | | | |  
 ACCGGGCACC GGAAGGCTCG GGTACTTTGG TTCTTAATTA GGTTCATGCCC GTGTGAGCCA 60  
 20 GGAAGGGCTG GTGTTTATGG GAAGCCAGTA ACACATGTGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180  
 AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAAATA GTCCCTGTTC ACCAGATGCA 300  
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCAATGA AGTTTTTTCC AATCATCGTC 360  
 25 ATTGGGATCA TTGCATGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTGG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACSCAAATGT TGCCTGTGCC CAACGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAAECTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720  
 30 CACCTCTGAC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCCCTCG GCCACGTGGT TACCTTGAGG TGACAGCCT GTGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCGTGTGGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 35 CTAGTTTCCC TGTGTGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAT 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTTGCCCA ACTCTGAAGA GAACTTCCCC 1200  
 GATGGAAGAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTGCC TGAACCAAGC GGCCTGCTCC TTGATTTCCA ACAAGATCTG CAACCAAGG 1320  
 40 GAGTGTAGC GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
 GTGCACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACCGC CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCGGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 45 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCG AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCGGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAAACCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800  
 50 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCGCTCCGCT CCCTGGTTCA AGCGATTCTC 1860  
 TTGCTTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CACACCAACC CAACTAATTT 1920  
 TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAATGA TGTGCTGCTC TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040  
 ACGCTAGGCC TCAGCTCCTT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGG AAAATTCCTG 2160  
 55 ACGAGTAAAG CAGTTATGTG ACCTCAGGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCTCTCTA GGGACAGAA 2280  
 CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCCTAT TTTATGATT TCTTTGATG ATTGGTGCT TGACGTATTA 2400  
 60 TTGTCCCTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAA

**A103 Protein sequence:**

65 Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 70 Tryp\_Spc domain: 216-444  
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51  
 | | | | | |  
 MGENDPPAVE APFSPFRSLFG LDDLKISFVA PDADAVAAQI LSLLPLKFPF IIVIGIIALI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLPVF 120  
 TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDX 180  
 VTALHHSVYV REGCASGEHV TLQCTACGHR RGYSSRIVGG NMSLLSQNFW QASIQFQGYH 240  
 80 LCGGSVITPL WIIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QVCLFNSEE NFFDGRKVCWT SGWGATEDGA GDASPVLNHA 360  
 AVPLISNKKI NHRDVYGGII SPSMLCAGYL TGGVDSQCGD SGGFLVQGER RLMLVVGATS 420  
 PGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM\_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51  
 | | | | |  
 ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCGGC CAAGCGCTCC 60  
 GGCTGCCCGG GCTGTGGGCG CAACGCCTCG GACGGCCAG TCCTTCGCC GGGGGCCGTG 120  
 GACGCCTGGC TCGTGCCGCT CTCTTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC 180  
 TCGCTGGTCA TCTACGTCAT CTGCCGCCAC AAGCGGATGC GGACCGTGAC CAACTTCTAC 240  
 ATGCCAACCC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300  
 CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT GGTCAACTAC 360  
 ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCCG 420  
 TGGTACGTGA CCGGTGTTCC GTTGCGCGCC CTGCAACGCC GCACGCCCCG CTTGGCGCTG 480  
 GCTGTACAGC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCGGT GCTCGCCCTG 540  
 CACCGCCTGT CACCGGGGCC GCGGCGCTAC TGCACTGAGG CCTTCCCGAG CCGCGCCCTG 600  
 GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCGCT GCTCGCCACC 660  
 TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGGGG TCGCGGTGCG CCGCGCGCCC 720  
 GCGATACGCG CCTGTCAGGG GCAGGTGCTG GCAGAGCGGG CAGGCGCGGT GCGGGCCAAAG 780  
 GTCTCGCGGC TGGTGGCGGC CGTGTCTCTG CTCTTCGCGG CTGCTGGGG CCGCATCCAG 840  
 CTGTTCTCTG TGGTCAAGCG GCTGGGCGCC GCGGGCTCCT GGCAACCAAG CAGTACGCC 900  
 25 GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCGC GCTGAACCCG 960  
 CTGCTCTACG CTTCTCTGGG CTCGCACTTC CGACAGGCTT TCCGCGCGGT GTGCCCTTGC 1020  
 GCGCGCGGCC GCGCGCGCGG CCGGAGCCCT CCGGAGCCGC AGCCCCACAC 1080  
 GCGGAGCTGC ACCGCTGGG GTCCCAACCG GCGCGCGCA GGGCGCAGAA GCCAGGGAGC 1140  
 AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

A105 Protein sequence

Gene name:

Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number:

Hs.208229

Protein Accession #:

AI819198

Signal sequence:

none found

Pfam domains:

7tm\_1 [59-323]

Transmembrane domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization:

plasma membrane

40

1 11 21 31 41 51  
 | | | | |  
 MHTVATSGPN ASWGAPANAS GCPGCGANAS DGFVPSRAV DAWLVPLFFA AIMLLGLVGN 60  
 SLVIYVIRH KPMRTVTNFI IANLAATDVT FLCCVPFTA LLYPLGWL GDFMCKPVNY 120  
 IQQVSVQATC ATLTAHSVDR WYVTVFPLRA LHRTTFLAL AVSLSIWVGS AAVSAPVLAL 180  
 HRLSPGPRAY CSEAFPRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240  
 ADSALQGVVL AERAGAVRAK VSRLVAHVVL LPAACWPIQ LFLVLQALGP AGSWHPRSYA 300  
 50 AYALKTNHAC MSYSNSALNP LLYAFLGSHF RQAFRRVPCP APRRRPRRR PGPSDPAAPH 360  
 AELHRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

A106 DNA SEQUENCE

Gene name:

integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM\_002214

Coding sequence:

680-2990 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51  
 | | | | |  
 CCCAGAGCCG CCTCCCGCTG TTGCTGGCAT CCGAGCTTC CTCCTTGCC AGCCAGGACG 60  
 CTGCCGACTT GTCTTTGCCG GCTGCTCGCG AGACGGGCT GCAAAGCTGC AACTAATGGT 120  
 GTTGGCCTCC CTGCCCACTT GTGAAGCAA CTGCGCTGAT TGATCGGCCA CAGACTTTTT 180  
 TCCCTCGAC CTGCGCGCGG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTATAC 240  
 TAGGGTGGTT TCCCCCCCAG CTGCGGCTT TGTTTGGGTT TGATTGTGT TGGCTCTTCG 300  
 CTAAGCTGAT TTATGCAGCA GAAGCCCGAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT 360  
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTGGCC GCGGGGCCCT 420  
 TGGCCGTGCA AGGAGGTGCT TCTGCGGAG ACCCGGGGAC CCGCGGTGCC GAGCCGGGAG 480  
 GCGCGTAGGG GCGCTGAGAT GCGAGCGGT GCGCGGGGCC GCTTACCTGC ACCGCTTGCT 540  
 CCGAGCGCGG GGGTCCGCTT GCTAGGCTTG CGGAAAAGT OCTAGCGACA CTCGCCCGCG 600  
 GGGCGGGAGT TCGCCCGGGA GCGCGAGCCC GGTTCGGGAA GGCAGCCAGG CCGCGGGGCG 660  
 GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CCGCCCTGGC TTTTATACC GCTGCATTGG 720  
 TCTGCTGCA AAGGACCGG CGAGGTCCCG CCTGTTCTT CTGGGCGAGC TGGGTGTTTT 780  
 CACTTGTCTT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCACTTCA AATGCAGCAT 840  
 CCGTGTCCAG GTGCTTGGG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTC 900  
 TTTCAAGTGG ATCAAGAGT GAACGTTGTG ATATTGTTTC CAATTAAATA AGCAAAGGCT 960  
 GCTCAGTTGA TTCAATAGAA TACCATCTG TGCACTTAT AATACCCACT GAAATAGAAA 1020  
 TTAATACCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCGGAAGCTA 1080  
 ATTTTATGCT GAAAGTTTCT CCTCTGAAGA AATATCCTGT GGATCTTAT TATCTGTGTT 1140  
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAAATAAA TTCCGTTGGA AACGATTTAT 1200  
 CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTGCTCTTGG ATTGGCTCA TACGTTGATA 1260  
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCACTGACT 1320  
 ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGCTTTG ACAGAGAACA 1380  
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440

5	AAGGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCTCATCTC	GCTCTTGATA	1560
	GCAAAATTGGC	AGGCATAGTG	GTGCCCAATG	ACGGAAACTG	TCATCTGAAA	AACAACGTCT	1620
	ACGTCAAATC	GACAACCATG	GAACAOCCTT	CCTAGGCCA	ACTTTCAGAG	AAATTAATAG	1680
	ACAACAACAT	TAATGTCTATC	TTTGCACTTC	AAGGAAAACA	ATTTTCATGG	TATAAGGATC	1740
	TTCTACCCCT	CTTGCCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAAGGCT	GCAAACCTCA	1800
	ATAATTGTGT	AGTGGAGGCC	TATCAGAAAGC	TCATTTCAGA	AGTGAAAGTT	CAGGTGGAAA	1860
	ACCAGGTACA	AGGCATCTAT	TTTAACATTA	CCGCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
10	TTACAATGAA	AAAATGTGAT	GTACACAGGAG	GAAAAAATA	TGCAATAATC	AAACCTATTG	2040
	GTTTTAATGA	AACCGCTAAA	ATTCTATATC	ACAGAAACTG	CAGCTGTCTG	TGTGAGGACA	2100
	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AAACTTTTCT	AGATTCCAAG	TGTTTCCAGT	2160
	GTGATGAGAA	TAAATGTCTAT	TTTGATGAAG	ATCAGTTTTC	TTCTGAGAGT	TGCAAGTCAC	2220
	ACAAGGATCA	GCTTGTTTGC	AGTGGTCTGAG	GAGTTTGTGT	TTGTGGGAAA	TGTTTCATGTC	2280
15	ACAAATTTAA	GCTTGGAAAA	GTGTATGGAA	AATACTGTGA	AAAGGATGAC	TTTTCTTGTC	2340
	CATATCACC	TGGAAATCTG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
	TCAATTCAAA	GGGCCAAGTG	TGCAGTGGAA	GAGGCACTGT	TGTGTGTGGA	AGGTGTGAGT	2520
	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
20	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTCACTCTCA	CAATTGTGCT	CAGGCTATAC	2640
	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	GACCAAACTT	2700
	CAGAATGTTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTT	CATCATTTTC	ATAGTTACAT	2760
	TCTTGATTGG	GTTCCTTAAA	GTCCCTGATCA	TTAGACAGGT	GATACTACAA	TGGAATAGTA	2820
	ATAAAATTAA	GTCTCTCATCA	GATTACAGAG	TGTCAAGCTC	AAAAAAGGAT	AAGTTGATTC	2880
25	TGCAAAAGTGT	TGTCACAAGA	GCAGTCACCT	ACCGACGTGA	GAAGCCTGAA	GAATAAAAAA	2940
	TGGATATCAG	CAATTTAAAT	GCTCATGAAA	CTTTCAGGTG	CAACTTCTAA	AAAAAGATTT	3000
	TTAAACACTT	AATGGGAAAC	TGGAATTGTT	AATAATTGCT	CCTAAAGATT	ATAATTTTAA	3060
	AAGTCACAGG	AGGAGACAAA	TGCTCAAGG	TCATGCCAGT	TGCTGGTTGT	ACACTCGAAC	3120
	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTCAGAGA	3180
30	AAAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTGTTGTA	GCACITTTACT	GTAATATATA	3240
	ACTTATTTAG	ATCAGCATAG	AATGTAGATC	CTCTGAAGAG	CACGTATTAC	ACTTTACAGG	3300
	TACCTGTTAT	CCCTACGCTT	CCCAGAGAGA	ACAAATGCTGT	GAGAGAGTTT	AGCATTGTGT	3360
	CACCTACAAGG	GTACAGTAAAT	CCCTGCACCTG	GACATGTGAG	GAATAAATA	ATCTGGCAAG	3420
35	TATATTCTAA	GGTGTCCAAA	CACCTCAACA	GTGTGTTGTT	GAATAGACAA	GAACAGCTAG	3480
	ATGAATAAAT	GATTGTGTTT	TCACTCTTTC	AAGAGGTGAA	CAGATACAA	CTTAATCTTA	3540
	AAAGATTATT	GCTTTTAA	GTGTGTAGTT	TTATGCATGT	GTGTTTATGG	TTTGCTTATT	3600
	TTTGCAAGAT	GGATACTAAT	TCCAGCATTC	TCTCTCTTTC	GCCTTTATGT	TTTGTTTTCT	3660
	TTTTTACAGG	ATAAGTTTAT	GTATGTACAA	GATGACTGGA	TTAATTAAGT	GCTAAGTTAC	3720
40	TACTGCCATA	AAAAACTAAT	AATACAATGT	CACCTTTATCA	GAATACTAGT	TTTAAAGCT	3780
	GAATGTTAA						

A107 Protein sequence:

45	Gene name:	Integrin, beta 8
	Unigene number:	Hs.52620
	Probeset Accession #:	AA479726
	Protein Accession #:	NP_002205.1
	Signal sequence:	1-39
50	Transmembrane domains:	682-704
	EGF domain:	552-584
	INB domain:	54-469
	Cellular Localization:	plasma membrane

55	1	11	21	31	41	51	
	MCQSALAFFT	AAFVCLQNDR	RGPASFLWAA	WVPSLVGLG	QGEDNRCASS	NAASCARCLA	60
60	LGPEOGWCVQ	EDFISGSSRS	ERCDIVSNLI	SKGCSVDSIE	YPSVHVIIPT	ENEINTQVTP	120
	GEVSIQLRPG	AEANFMLKVR	PLKYPVDLY	YLVDVSASM	NNIEKLNSVG	NDLSRKMAFP	180
	SRDFRLGFGS	YVDKTVSPYI	SIHPERIHNQ	CSDYNLDCMP	PHGYIHVLSL	TENITEFEKA	240
	VHRQKISGNI	DTPEGGFDM	LQAACVESH	GWRKEARRLL	LVMTDQTSHL	ALDSKLAGIV	300
	VPNDGNCHLK	NNVYVKSTTM	EHPSLQQLSE	KLIDNNINVI	FAVQKQFHW	YKDLLPLLP	360
65	TIAGEIESKA	ANLNNLVVEA	YQKLISEVKV	QVENQVQGIY	FNITAICPDG	SRKPGMEGCR	420
	NVTSDNDEVLF	NVTVTMKKCD	VTGGKNYAI	KPIGFNETAK	IIHNRNCSQ	CEDNRGPKGK	480
	CVDETFLDSK	CFQCDENKCH	FDQDQSSSES	CKSHKQPV	SGRGVCVCGK	CSCHKIKLGK	540
	VYGYKCEKDD	FSCPYHHGNL	CAGHGECEAG	RQCFPSGNEG	DRQCPSAAA	QHCVNSKQV	600
	CSGRGTCVCG	RCECTDPRSI	GRFCEHCPTC	YTACKENWNC	MQCLHFNLS	QAILDQCKTS	660
70	CALMEQQHYV	DQTSECFSSP	SYLRIFPIIF	IVTFLIGLLK	VLIRQVILQ	WNSNKKSSS	720
	DYRVASASKD	KLILQSVCTR	AVTYRREKPE	EIKMDISKLN	AHETFRCNF		

A108 DNA sequence

75	Gene name:	ESTs
	Unigene number:	Hs.128899
	Probeset Accession #:	AA983251
	Nucleic Acid Accession #:	AA983251
	Coding sequence:	1-1749 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	ATGCTGTCTG	GCTTCTTGAT	GAGTCCCACT	ACCCAGCACA	GAGCACAGTA	CACTCCCGGA	60
	GGAAAGAAAC	TTCCGTGGGA	GGCTTCCATC	GGTGCGCACA	CCTCCGAGG	GCGAGGCAGC	120
	GACCGGAGGA	GGGAGAGCCG	GCGGAGGCT	GCGGGCTCC	TGTGGGACCG	CGCTGCAGCC	180
	GGGGAGGCGG	AGAAGGGGAA	CCGGGGCGAG	CCGCCCGCCT	GGATCCGCGC	CCAGCAGCAG	240

5	CGCGGGCCGC	CGCCAGCTGG	GCAGGCTCCC	GGGACTGCGG	CTGGGGGCGC	GCAGGACCCCT	300
	CGCCTGCGTC	CTGGAGCTTC	CGGGGGGAGG	GTCCGGTTGC	CAGTGAAACC	TCCAGAGGCT	360
	TCCGAGCGAC	AGCCCCGGGG	GCCTTCTGAC	TGCATCCOGA	GATTTCCATC	AGCGAGTGCA	420
	ACTCATAAAG	CAGTCCCTAA	GGGACCCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCCTGGAC	CTAGGGCCCG	CGGTGGTGGC	CTCCTGGGCG	TGCGGCGAGA	GGGGAGTGGC	540
	CGCGCGGAA	AGCGCOCGCG	GACAGTCAGT	GACGAGGCCG	GGGGGTGCGC	GGGGCCACGA	600
	CTTCTCGGAG	ACCGTCTCTG	GCTCTCTGGA	GACGCGCTGT	CGCGGCCAG	GGTGGTGCCA	660
	TGTGGGGCGC	TGCGCGCTCG	TCCGTCTCTC	CATCCTGGAA	CGCGGCTTCG	CTCCTGCAGC	720
10	TGCTGCTGGC	TGCGCTGCTG	GCGCGGGGGG	CGAGGGGCCA	GCGGCGAGTA	CTGCCACGGC	780
	TGGCTGGACG	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCGAGCG	CTTCGACGGC	840
	GGGAGCGCCA	CCATCTGCTG	CGGCAGCTGC	GCCTTGGCGT	ACTGCTGCTC	CAGCGCCGAG	900
	GCGCGCCTGG	ACCAGGGCGG	CTGCGACAAT	GACGCGCAGC	AGGCGCGTGG	CGAGCCTGGC	960
	CGGGCGGACA	AAGACGGGCC	CGGACGGCTC	GGCAGGGCTT	CATGCTTAG	GGGTACCCAA	1020
15	GGAGACGGCG	AGGGTGCGCC	CCCACCCGTG	AGGGCCTGGC	AGCGGTGCTC	CCCTGAAGGC	1080
	TCCCGAAGAG	GAAGGCAGCT	CCTCAGGGCT	TTCCCGGGGC	TGCTGCCCGG	TGCCAGACGC	1140
	CGCGGATTCC	CATCTTCTCC	ACGCGGCGGC	CCCTCTCCCG	TGCAGCGGCC	CGCCTTGCCC	1200
	ATCTACGTGC	CGTTCTCTAT	TGTTGGCTCC	GTGTTTGTGG	CCTTATCAT	CTTGGGGTCC	1260
	CTGTGGGCG	CTGTGTGCTG	CAGATGTCTC	CGGCTAAGC	AGGATCCCCA	GCAGAGCCGA	1320
20	GCCCCAGGGG	GTAACCGCTT	GATGGAGACC	ATCCCATGTA	TCCCCAGTGC	CAGCACTCTC	1380
	CGGGGCTGCT	CCTCAGGCCA	GTCCAGCACA	GCTGCCAGTT	CCAGCTCCAG	CGCCAACTCC	1440
	GGGGCGCGGG	CGCCCCCAAC	AAGGTACAG	ACCAACTGTT	GCTTGCCGGA	AGGGACCATG	1500
	AACAACGTGT	ATGTCAACAT	GCACAGCAAT	TTCTCTGTGC	TGAACGTGCA	GCAGGCCAAC	1560
	CAGATTGTGC	CACATCAAGG	GCAGTATCTG	CATCCCCCAT	ACGTGGGGTA	CACGGTGCAG	1620
25	CACGACTCTG	TGCCCCATGAC	AGCTGTGCCA	CCCTTTCATG	ACGGCTGCA	GCCTGGCTAC	1680
	AGGACAGATC	AGTCCCCCTT	CCCTCACACC	AACAGTGAAC	AGAAGATGTA	CCGAGCGGTG	1740
	ACTGTATTAAC	CGAGAGTCAAC	TGGTGGGTTT	CTTTACTGAA	GGGAGACGAA	GGCAGGGGTG	1800
	GATTCTCGAG	GTGGAAGTCC	GCACATGTGC	GTGTAATTGA	TGGCAGGATT	CCTTTGGATG	1860
	GCTTCATTTC	CCCCCAGACT	GTATGAAAAC	ATCTCCGAAT	TAGCATTTCT	GGATATGTTT	1920
30	CATCCAGGGT	ATCATTTGAT	TATGATGGAA	AACCGGCTCT	AGCTGGAGAT	GACTGTGATG	1980
	TGCTGATGG	GTGTATAACA	AATGCTTGAG	TCCGAAGTGC	CCTTGAGATA	TGGTTGACGA	2040
	AGAAATTTTA	TAAACTGATA	AATTAAGGAT	TTTTATTATG	TGTTATTAT	TATTTCTTTT	2100
	TGTTGTTTGA	CTGCACAGGA	TCAAAATGCC	TGTTATCTCC	CTTTACTGCG	GACTTTTTTT	2160
	TTTTTTTTTT	TTTTTTTTAA	TCAGACAGGG	TCTTGCTCTG	TGCCCCAGGC	TGGAGTGCAG	2220
35	TGTTGGGATC	TGCGGCTCACT	GCAACTTCAG	CCTCCTGGAT	TCAGGCAACA	CTCCTGCTCT	2280
	AGCCTCCAC	GTGGCTGGGA	TTACAGGTGC	CTGCCCCCAT	GGCTAATTTT	TGTTATTTTT	2340
	TGTAGAGATG	GGGTTTCACC	ATGTTGGCTG	GGCTGGTCTC	ACTCTCCTGA	CCTCAAGCAA	2400
	CTGSCCTGTC	TCAGCCTCCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	GCCCCAGGCC	2460
	TGAGCCTTTT	TTTTTTTCTA	ATGCATCCAA	GGTTAAGGGG	AAGACGCAAA	TAACAGGACT	2520
40	ATTTCAAAAG	GAACCTGTTT	TGAACTCTGT	GAGATCAGTC	ATCAGTCTCA	GTATTCCACA	2580
	GGCACACCTT	AATTTTCATTG	TAAAAAGATA	TATATATTTT	GTCTATTTTT	GTGCTTTTGG	2640
	GGGCTATTTT	TGTCCTTTTT	TACCTTATGT	AGAGATCTTA	TTACAAAGTG	ATTTTCTACA	2700
	TTAAAAAGAG	ACTGAATAAA	ATTGTATAGT	TACTTAACCTA	ATGAAGACAT	TTCAAGACTC	2760
	TGGGATGATT	TTAATCTTGA	AGTAGTAGGT	GGTATAGTCA	TAAACCAATT	CATCCCCCTC	2820
45	TTGATTGTAT	CTTAATTTTC	TGGCTTTAAG	GTGACATCTG	AGAGGTAATG	CATCTTTTTT	2880
	TATATTGAAA	TCATAAACTA	TCACCCGCTG	CTTCTCTGAG	TTACTTTTAA	TTTTGCCTTG	2940
	TGGTTATGGT	TTGGCGTTTC	CTTCTGTTTG	GTTTTCAGAG	CCCCATGTCT	ATATAGTCTC	3000
	GAGTGCAAGT	AATTACTATA	CTGTAAATG	AAGATCAGTA	TTTCTGCTTA	GATCTGATAA	3060
	AAAAATTTAT	TTGCTTTAGT	TATAAAAAAT	CAAAAGAAATG	TGTTACAAAG	ATACTTAGTA	3120
50	TAGCTCCTCA	GCCATTAACCT	GAGACTTGGG	ATGAAATTTA	AACCAGATAC	GATTACTTTT	3180
	GCAGATCATA	AGGCTTTTTA	TACTCTTGTT	ATCAAAATGG	CTTATTTTTC	AGGCACTAAG	3240
	GATTGTTAAG	AGAAAAGCTT	TTCAACGAAG	GATTGCCTTT	CTTCTCCAC	ACTGTTCTTG	3300
	ATTTCTCTCT	TCPTTCAGGC	CTCAACAGGC	ACTGTATTTA	TTGCCAATGT	TCCAAATAT	3360
	CAAAATCARR	RGPSGECYCH	WLDAGQVWRI	GFQCFERFDG	GDATICGSG	ALRYCCSSAE	3420
55	ATGTGCAAGT	ACATTTCCAA	CTGCTAGCAC	AACCAATATT	TTGTAATTA	ACAAATCGCT	3480
	GTATGATATG	GTCTTCTACA	CATTTATGTC	TATAGATATC	TATGATCAT	CTTTCTATTC	3540
	TGTTTCATGA	CTGAATAAAT	TAAACCAAGT	GTTGGCAATT	GATATCATCA	ATGATACTCA	3600
	TTTTTTAATA	ACCAAGGCA	GGGAAAAATC	ATTTTACTTA	TTAATAAATA	TTTTATGATG	3660
60	TGAAAAAAA	AAAAAAA	AAAAAAA				

**A109 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

70	1	11	21	31	41	51	
	MLSGFLMSPS	TOHRAQYTPG	GKKLPWEASI	GAHTRSRGRS	DREERSRPEA	AGLLWDRAAA	60
	GEAEKGNRGE	PPAWIRAQQQ	FRPPFPAGQAP	GTAAGGAQDP	RLRPGRSRGR	VRFPVKPPEA	120
75	SGRQPRGSPD	CIPRFPASASA	THKAVPKGTG	PPAEDGDGLG	APGPRARRRR	LLGVAAEGSG	180
	PRGRRGTVS	DEARGSPGPR	LLGDRPALSG	DALSAPRVVP	CGALAAARPS	HPGTPLRSCS	240
	CCWLRCWRRG	RGPSGEYCHG	WLDAGQVWRI	GFQCFERFDG	GDATICGSG	ALRYCCSSAE	300
	ARLDQGGCND	DRQQGAGEPG	RADKDGPRRL	GRASCLRGTO	GDGEGAPPVF	RAWQRCSPDG	360
	SPKGRQLLRA	PPGLLPARRR	RGFPSSPRGG	PSPLQRPALP	IYVPLIVGS	VFVAFIILGS	420
	LVAACCCRL	RPKQDPQQR	APGGNRLMET	IPMIPSASTS	RGSSSRQSST	AASSSSSANS	480
80	GARAPPTRSQ	TNCCLPBGTH	BNVYVNMPTN	FSVLNCCQAT	QIVPHQGGYL	HPFYVGYTVQ	540
	HDSVPMTAVP	PFMDGLQPGY	RQIQSPFPHT	NSEQNMYPV	TV		

**A110 DNA SEQUENCE:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCAGCTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCACAG TTTCTTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAAGAG GCCTCTCAG AACTCTCAA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCCTGA GATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300
   CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
   GAAACCACTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
   GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTACCC CCTATTGATA GAAAAACATG AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTAT 600
   GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
20 TTACTATTTA GTTTTITTTAA TGTTTGTGCA ATAGTCTTAT TAAAAATAAT GTTTTITTTAA 720
   TCTGAAAAAA AAAAAAAA AAAAAAAA

```

### 25 A111 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

30

```

35 1      11      21      31      41      51
   |      |      |      |      |      |
   MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEB GLFYAQKSKK 60
   PLMVIHHLSD CQYSQALKKV PAQNBEIQEM AQNKFIIMNL MHETTDKNLS PDGQYVPRIM 120
   FVDPSSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

### 40 A112 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

```

1      11      21      31      41      51
|      |      |      |      |      |
50 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TGGATGTCAA ACCCTGCGC 60
   AAAACCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
   CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCTCATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCTT GGGGCGAGCC TCTCCACTTC ATCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGCGCT 300
   GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGGGCCACA 360
   GGGAACTGGT TCTCTGCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
   GGGCCCTGTC TCTCAGGCTC CTGGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
   AAGACCCCCC GTGTGTTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
   AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGAGCC CCACTGGGTC 720
   CTCACGGCAG CCACTGCTT CAGGAAACAT ACOGATGTGT TCAACTGGAA GGTGCGGGCA 780
   GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCAATTGAA 840
   TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCGCCCTA TGAAGCTGCA GTTCCCACTC 900
   ACTTCTCTAG GCACAGTCAG GOCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
   GGTACCAGG GGGAAAGTCA CAGAAAGATG ATGTGTGAGC GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCGCA GCACCCGAGG AGTATACACC 1260
   AAGGTCTCAG CTAATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

```

### 75 A113 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

80

	1	11	21	31	41	51	
5	MLQDPDSQDP	INSLDVKPLR	KPRIPMETFR	KVGIPILIAL	LSLASIIIVV	VLIKVILDKY	60
	YFLCGQPLHF	IPRKQLCDGE	LDCPLGEDEE	HCVKSPFEGP	AVAVRLSKDR	STLQVLDSAT	120
	GNWFSACFDN	FTEALAEATC	RQMGYSKPT	FRAVEIGPDQ	DLDVVEITEN	SQELMRNNS	180
	GPCLSGSLVS	LHCLACGKSL	KTPRVVGEE	ASVDSWPNQV	SIQYDKQHVC	GGSIIDPHWV	240
	LTAACHCFRKH	TDVFNWVKRA	GSDKLGSPFS	LAVAKIIIE	FNFMYPKDND	IALMKLQFPL	300
10	TFSGTVRPIC	LPFFDEELTP	ATPLWIIIGW	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
	AYQGEVTEIM	MCAGIEGGV	DTCQDSDGGP	LMYQSDQHWV	VGIVSWGYGC	GGPSTPGVYT	420
	KVSAYLNIWY	NVWKAEI					

A114 DNA SEQUENCE:

Gene name:	TTK protein kinase
Unigene number:	Hs.169840
Probeset Accession #:	M86699
Nucleic Acid Accession #:	NM_003318
Coding sequence:	1026-3551 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
20	GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACCT	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CCGCCTCCCG	GGTTCAGGCG	ATTCTCCTGC	120
25	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACTAATTT	180
	CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
	ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAGTGCTA	GGATTACAGC	CGTGAACCTG	300
	TGCTCGGCTG	ATTCCTTTTT	TGTTGTTGGA	TTTTTGAAC	AGGCTCTCCC	TTGGTCCGCC	360
	AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATAAACC	TCCACCTCCT	GGTTTCAAGT	420
30	GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	CGGTGCACCA	CCACACCCGG	480
	CTAATTTTTG	TATTTTTTAT	AGAGACAGGG	TTTCAACATG	TTGGCCAGGC	TGTTCTCAAA	540
	CTCCTGGACT	CAAGGGATCC	GCCTGCCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACCATG	CCTGACCTTA	TAATTCCTAA	GTCAATTTTT	CTGGTCCATT	TCTTCTTAG	660
	GGTCTCTACA	ACAAATCTGC	ATTAGGGGGT	ACAATAATCC	TTAATCTCAT	GATTCACAAA	720
35	AGGAAGATGA	AGTGATTTCAT	GATTTAGAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
	GGATGATGAT	CCTAATATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
	TTTGGTTTAA	ATTAATATATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
	ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCCCAG	960
	TGCAGTTTTT	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGTAT	1020
40	CCATAATGAA	CAAAGTGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
	AACTAAGCTT	GAATAAAAT	TCTGCTGATA	CTACAGATAA	CTCGGGAAC	GTTAAACCAA	1140
	TTATGATGAT	GGCAAAACAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
	ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTGGTTAC	AGTCAAGCAA	1260
	TTGAAGCGCT	TCCCCAGAT	AAATATGGCC	AAAATGAGAG	TTTGTCTAGA	ATTCAAGTGA	1320
45	GATTTGCTGA	ATTTAAGCTT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAATGG	1380
	CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTCTATATATC	TTTTGCACAA	TTTGAAGTGT	1440
	CACAAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGAGCAG	1500
	TACCACATGA	AATGCTGGAA	ATTGCCCTGC	GGAATTTAAA	CCTCCAAAAA	AAGCAGCTGC	1560
	TTTCAGAGGA	GGAAAGAAAG	AATTTATCAG	CATCTACGGT	ATTAATGCC	CAAGAAATCAT	1620
50	TTTCCGGTTC	ACTTGGGCAT	TTACAGAATA	GGAAACAACAG	TGTGTATTCC	AGAGGACAGA	1680
	CTACTAAAGC	CAGGTTTTTA	TATGAGAGAG	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
	ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAACAGATC	ATGCCCATTT	GGAAAGATCC	1800
	CAGTTAACTT	TCTAAATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
	GTTTTATGAA	AAGACAAACC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
55	AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAAATTTAAA	GTCTGTTCAA	AATAGTCAAT	1980
	TCAAGGAACC	TCTGGTGTCA	GATGAAAAGA	GTTCTGAACT	TATTATTACT	GATTCAATAA	2040
	CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
	AAGAACCAGA	GGTTCCAGAG	AGTAAACAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
	GTATTAACCA	GAATCCTGCT	GCACTTCTCA	ATCACTGGCA	GATTCGGGAG	TTAGCCCGAA	2220
60	AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGACCAACC	TGCTTTTTC	GTTTCAAAAC	2280
	AGTCACCACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
	GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTTAGAAC	TCCAGTTGTA	AAGAATGACT	2400
	TTCCAACCTG	TGTTCAAGTG	TCAACACCTT	ATGGCCAACC	TGCCTGTTTC	CAGCAGCAAC	2460
	AGCATCAAT	ACTTGCCACT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
65	ATGAATGCAT	TTCGGTTAAA	GGAAGAAATTT	ATTCATATT	AAAGCAGATA	GGAAAGTGGAG	2580
	GTTCAAGCAA	GGTATTTTCA	GTGTTAATATG	AAAAGAAACA	GATATATGCT	ATAAAATATG	2640
	TGAATTAAGA	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	COGGAACGAA	ATAGCTTATT	2700
	TGAATAAACT	ACAACAACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCAAGG	2760
70	ACCAATACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
	AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCGAG	2880
	TTCAACAAT	CCATCAACAT	GGCATTTGTC	ACAGTGATCT	TAAACCAAGT	AACTTTCTGA	2940
	TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATGTC	AAACCAATG	CAACCAAGTA	3000
	CAACAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACGTTAA	TTATATGCCA	CCAGAAGCAA	3060
	TCAAAGATAT	GTCCTTCTCC	AGAGAGAAATG	GGAATCTTAA	GTCAAAGATA	AGCCCCAAAA	3120
75	GTGATGTTTG	GTCCTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCAATTTC	3180
	AGCAGATAAT	TCTAAATTAC	ATGCCATAAT	TGATCCTAAT	CATGAAATTG		3240
	AAITTCOCGA	TATTCAGAG	AAAGATCTTC	AAAGTGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
	ACCCAACAAC	GAGGATATCC	ATTCCTGAGC	TCTCGCTCA	TCCATATGTT	CAAAATCAAA	3360
80	CTCATCCAGT	TAACCAAAATG	GCCAGGGGAA	CCACTGAAGA	AATGAAATAT	GTTCTGGGCC	3420
	AACTTGTGTT	TCTGAATTTCT	CCTAACTCCA	TTTTGAAAGC	TGCTAAAAC	TTATATGAAC	3480
	ACTATAGTGG	TGGTGAAGAT	CATAATTCTT	CATCCTCCAA	GACTTTTGAA	AAAAAAAGGG	3540
	GAAAAAAATG	ATTTGCAAGT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
	GTTATCTCT	TGAATCCCTG	TGGAATCTA	CATTGAAGA	CAACATCACT	CTGAAGTGT	3660
	ATCAGCAAAA	AAAATTCAGT	GAGATTATCT	TTAAAGAGAA	ACTGTAAAAA	TAGCAACAC	3720

TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780  
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTGG 3840  
 TAAATAAAGT TTTGTGGCTA AATGA

5

**A115 Protein sequence:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

10

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1	11	21	31	41	51	
MNKVRDIKKN	FKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	LLLLKLEKNS	60
VPLSDALLNK	LIGRYSQAIE	ALPPDKYQON	ESFARIQVRF	AELKAIQEPD	DARDYFQMAR	120
ANCKKFAFVH	ISPAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLEIALRN	LNLQKKQLLS	180
EECKKRLSAS	TVLTAQESFS	GSLGHLQNRN	NSCDSRGQTT	KARPLYGENM	PPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDDSVVPCF	MKRQTSRSEC	RDLVVPFSKP	300
SGNDSCELRN	LKSVQNSHPK	EPLVSEKSS	ELIITDSITL	KNKTESSLLA	KLEETKGYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	NTEQKHITFE	QPVFVSQKS	420
PPISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTFVVKNDFP	PACQLSTPYG	QPACFQQQOH	480
QILATPLQNL	QVLASSANE	CISVKGRIS	ILKQIGSGGS	SKVFQVLNEK	KQIYAIKYN	540
LEEADNQTLT	SYRNEIAYLN	KLQQHSKII	RLYDYEITDQ	YIYMVMCEGN	IDLNSWLKKK	600
KSIDPWERKS	YWKMLAEVH	TIHQHGIVHS	DLKPANFLIV	DGMLKLIDFG	IANQMPPDTT	660
SVVKDSQVGT	VNYMPPEAIK	DMSSSRENGK	SKSKISPKSD	VWSLGCILYY	MTYGRTPFPQ	720
IINQISKLHA	IIDFNHEIEF	PDIPEKDLQD	VLKCCLEKRP	KQRISIPELL	AHPYVQIQTH	780
PVNMAGKGT	EEMKYVLGQL	VGLNSPNSIL	KAATLYEHY	SGGESHNSSS	SKTPEKGRCK	840
K						

**OVARIAN**

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**A116 DNA SEQUENCE**

Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Nucleic Acid Accession #: NM\_001508  
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51	
<u>ATGGCTTCAC</u>	CCAGCCTCCC	GGGCAGTGAC	TGCTCCCAAA	TCATTGATCA	CAGTCATGTC	60
CCGAGTTTGG	AGGTGGCCAC	CTGGATCAAA	ATCACCCCTTA	TTCTGGTGTA	CCTGATCATC	120
TTGGTGTATGG	GCCTTCTGGG	GAACAGCGCC	ACCATTCGGG	TCACCCAGGT	GCTGCAGAAG	180
AAAGGATACT	TGCAGAAGGA	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
TTGGTGTTC	TCATCGGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCTTGACC	300
ACGTCCAGCT	ACACCTGTCT	CTGCAAGCTG	CACACTTTCC	TCTTCGAGGC	CTGCAGCTAC	360
GCTACGCTGC	TGCACGTGCT	GACACTCAGC	TTTGAGCGCT	ACATCGCCAT	CTGTCACCCC	420
TTCAGGTACA	AGGCTGTGTC	GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTCGTCTGG	480
GTCACCTCOG	CCCTGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCTTG	540
GTGAAGCTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCGG	CCACCACGAG	600
CAGCCCGAGA	CCTCCAAATAT	GTCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660
CAGTCCAGCA	TCCTCGGCGC	CTTCGTGGTC	TACCTGTGGG	TCCTGCTCTC	CGTAGCCTTC	720
ATGTGCTGGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GGCCGGGGGC	780
ACGCGGCTTC	CGCAGCTGAG	GAAAGTCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840
ACCATCATCT	TCCTGAGGCT	GATTGTGTGT	ACATTTGGCG	TATGCTGGAT	GCCCAACGAG	900
ATTGCGAGGA	TCATGGCTGC	GGCCAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCGGG	960
GCGTACATGA	TCCTCTCTCC	CTTCGCGGAG	ACGTTTTTCT	ACCTCAGCTC	GGTCATCAAC	1020
CGCTCCTGT	ACACGGTGTC	CTCGCAGCAG	TTTCGGCGGG	TGTTGCTGCA	GGTCTGTGTC	1080
TGCGCGCTGT	CGCTGCAGCA	CGCCAAACCA	GAGAAGCGCC	TGCGGTGACA	TGCGCACTCC	1140
ACCACGACGA	GCGCCGCTCT	TGTGCAGCGC	CGTTGTCTCT	TGCGTCCCG	GCGCCAGTCC	1200
TCTGCAAGGA	GAACGAGAAA	GATTTTCTTA	AGCACTTTTC	AGAGCGAGGC	CGAGCCCGAG	1260
TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	AGTCAGGCGC	GAAACGAGCC	1320
AATTCTGCTG	CAGAGAATGG	TTTTCAGGAG	CATGAAGTTT	<u>GA</u>		

**A117 Protein sequence:**

Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Protein Accession #: NM\_001508, NP\_001409  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [72-172, 224-344]  
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MASPSLPGSD	CSQIIDHSV	PEFEVATWIK	ITLILVYLII	FVMGLLGNSA	TIRVTQVLQK	60

- 5 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTPLFEACSY 120  
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LPAMGTEYPL 180  
 MCVNPSIRGLT CNRSSTRHHE QPETSNNISIC TNLSSRWTVF QSSIFGAPVV YLVVLLSVAF 240  
 MCNMMQVIM KSKQKSLAGG TRPPQLRKSE SEESTARRQ TIIPLRLIVV TLAVCNMNPQ 300  
 IRRIMAAKP KHDWTRSYFR AYMILLPFSE TPFYLLSSVIN PLLYTVSSQQ FRRVFVQVLC 360  
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPO 420  
 SKSQSLSLES LEPNSGAKPA NSAAENGFOE HEV
- 10 A118 DNA sequence  
 Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.87223  
 Probeset Accession #: AA250737  
 Nucleic Acid Accession #: NM\_001203  
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

15  
 1 11 21 31 41 51  
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 CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTCGGGAGA CCGCGGCGCT 60  
 GAGGACGCGG GAGCOGGGAG CGCAGCGCGG GGGTGGAGTT CAGCCTACTC TTCTCTAGAT 120  
 GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180  
 CATAACCAAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
 TGCCATAAGT GAGAAGCAAA CTTCTTGAT AACATGCTTT TGCGAAGTGC AGGAAATTA 300  
 AATGTGGGCA CCAAGAAAGA GGATGCTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC 360  
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGACGACA 420  
 GACGATATTT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTGCGCTGT GGTCACTTCT 480  
 GGTGCGCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACACCTCCAT TCCTCATCAA 540  
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCCTACA 600  
 CTGCTCTCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCTTTACTT 660  
 ATATCTGTGA CTGTCTGTAG TTGCTCTTGT GTCCTTATCA TATTATTTTG TTACTTCCGG 720  
 TATAAAGAC AAGAAACACG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780  
 ATTCTCTCTG GAGAAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAAGTGA 840  
 TCAGGCTCTC CTCTGCTGGT CCAGAGGACT ATAGCTAAGC AGATTCAGAT GGTGAAACAG 900  
 ATTGAAAAAG GTGCTATGAG GGAAGTTTGG ATGGGAAAGT GCGTGGGCGA AAAGGTAGCT 960  
 GTGAAAGTGT TCCTTACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020  
 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080  
 GGGTCTTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140  
 TATCTGAAT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTC 1200  
 AGTGGCTTAT GTCATTTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260  
 CATCGAGATG TGAAAGATGA AAACATTTCT GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320  
 GACCTGGGCC TGGCTGTATA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
 ACTCGAGTTG GCACCAAAACG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440  
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500  
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 CTAGTCCCA GAGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620  
 CGCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAA GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740  
 ACACCTGCCA AAATGTGAGA GTCCACGAGC ATTAACACTCT GATAGGAGAG GAAAAGTAAG 1800  
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860  
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCTGCTTCC CAGTGGGTT CAGACCTCAC 1920  
 CTTTCAAGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCOGTG 1980  
 TCTGTTTGTG GCGCGAGAAA COGTGGGTA ACTTGTTCAT GATATGATGC AT

- 40  
 45  
 50
- 55 A119 Protein sequence  
 Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

65  
 1 11 21 31 41 51  
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 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCFE DSVNNICSTD GYCFTMIEED 60  
 DSGLFVVTSQ CLGLEGSDPQ CRDTPIPHQR RSIEOCTERN ECNKDLHPTL PPLKNRDFVD 120  
 GPIHRRALLI SVTVCSLLLV LIILPCYPRY KRQETRPYRS IGLEQDETYI PPGESLRDLI 180  
 EQSQSSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFPTEBAS 240  
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHEIF STQKPAIAH RDLKSNILV KKNGTCCIAH LGLAVKPISD 360  
 TNEVDIPNT RVGTRKYMPP EVLDESINRN HPQSYIMADM YSPGLILWEV ARRCVSGGIV 420  
 EBYQLPYHDL VPSDPSYEDM REIVCIKCLR PSFPNRWSSD ECLRQMKRLM TECWAHPAS 480  
 RLTLARVKKT LAKMSQSQDI KL

- 75  
 80 A120 DNA SEQUENCE  
 Gene name: LIV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Probeset Accession #: U41060  
 Nucleic Acid Accession #: NM\_012319.2  
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51



5  
 10  
 15  
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CTCGTGCGCA | ATTCGGCAGC | AGACCGCGTG | TTCGCGCGCT | GTAGAGATTT | CTCGAAGACA 60  
 CCACTGGGCC | CGTGTGGAAC | CAAACCTGCG | CGCGTGGCCG | GGCGGTGGGA | CAACGAGGCC 120  
 GCGGAGACGA | AGGCGCAATG | GCGAGGAAAT | TATCTGTAAT | CTTGATCCTG | ACCTTTGCCC 180  
 TCTCTGTAC | AATGCCCTTT | CATGAACATA | AAGCAGCTGC | TTTCCCCAG | ACCACTGAGA 240  
 AAATTAGTCC | GAATGGGGAA | TCTGGCATTG | ATGTTGACTT | GGCAATTTCC | ACACGGCAAT 300  
 ATCATCTACA | ACAGCTTTTC | TACCGCTATG | GAGAAAATAA | TTCTTTGTCA | GTTGAAGGGT 360  
 TCAGAAAATT | ACTTCAAAAT | ATAGGCATAG | ATAAGATTAA | AAGAATCCAT | ATACACCATG 420  
 ACCACGACCA | TCACTCAGAC | CACGAGCATC | ACTCAGACCA | TGAGCGTCAC | TCAGACCATG 480  
 AGCATCACTC | AGACCAAGAG | CATCACTCTG | ACCATGATCA | TCACCTCTAC | CATAATCATG 540  
 CTGCTTCTGG | TAAAAATAAG | CGAAAAGCTC | TTTGCCAGA | CCATGACTCA | GATAGTTTCA 600  
 GTAAAGATCC | TAGAAACAGC | CAGGGGAAAG | GAGCTCACCG | ACCAGAACAT | GCCAGTGGTA 660  
 GAAGGAATGT | CAAGGACAGT | GTTAGTGCTA | GTGAAGTGAC | CTCAACTGTG | TACAAACATG 720  
 TCTCTGAAGG | AACTCACTTT | CTAGAGACAA | TAGAGACTCC | AAGACCTGGA | AAATCTTTCC 780  
 CCAAAGATGT | AAGCAGCTCC | ACTCCACCCA | GTGTCAATC | AAAGAGCCGG | GTGAGCCGGC 840  
 TGGCTGGTAG | GAAACAAAT | GAATCTGTGA | GTGAGCCCGG | AAAAGGCTTT | ATGTATTCCA 900  
 GAAACACAAA | TGAATTCCT | CAGGAGTGTT | TCAATGCATC | AAAGCTACTG | ACATCTCATG 960  
 GCATGGGCAT | CAGGTTCCG | CTGAATGCAA | CAGAGTTCAA | CTATCTCTGT | CCAGCCATCA 1020  
 TCAACCAAT | TGATGCTAGA | TCTTGTCTGA | TTCAATCAAG | TGAAAAGAAC | GCTGAATCC 1080  
 CTCCAAGAGC | CTATTCATTA | CAAATAGCCT | GGGTTGGTGG | TTTTATAGCC | ATTTCCATCA 1140  
 TCAGTTTCTT | GTCTCTGCTG | GGGGTTATCT | TAGTGCTCTT | CATGAATCCG | GTGTTTTTCA 1200  
 AATTTCTCTT | GAGTTTCTTT | GTGGCAGTGG | CGGTTGGGAC | TTTGAGTGGT | GATGCTTTTT 1260  
 TACACCTTCT | TCACATTTCT | CATGCAAGTC | ACCACCATAG | TCATAGCCAT | GAAGAACCCAG 1320  
 CAATGGAAT | GAAAGAGGA | CCACTTTTCA | GTCACTGTGC | TTCTCAAAAC | ATAGAAGAAA 1380  
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 AGAAGAAACC | TGAATATGAT | GATGATGTGG | AGATTAAGAA | GCAGTTGTCC | AAGTATGAAT 1560  
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 GGTGCAAGAA | TAAATGCCAT | TCACATTTCC | ACGATACACT | CGGCCAGTCA | GACGATCTCA 1800  
 TTCACCAACA | TCATGACTAC | CATCATATTC | TCCATCATCA | CCACCAACAA | AACCAACATC 1860  
 CTCACAGTCA | CAGCCAGCGC | TACTCTCGGG | AGGAGCTGAA | AGATGCGCGG | GTGCCACTT 1920  
 TGGCTGGAT | GGTGATAATG | GGTGATGGCC | TGCACAATTT | CAGCGATGGC | CTAGCAATTTG 1980  
 GTGCTGCTTT | TACTGAAGGC | TTATCAAGTG | GTTTAAGTAC | TTCTGTTGCT | GTGTTCTGTC 2040  
 ATGAGTTGCC | TCATGAATTA | GGTGACTTTG | CTGTTCTACT | AAAGGCTGGC | ATGACCGTTA 2100  
 AGCAGGCTGT | CCTTTATAAT | GCAITGTCTG | CCATGCTGGC | GTATCTTGGA | ATGGCAACAG 2160  
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 GTTTTGAAT | TATGTTACTT | ATTTCCATAT | TTGAACATAA | AATGTTGTTT | CGTATAAAT 2400  
 TCTAGTTAAG | GTTTAAATGC | TAGAGTAGCT | TAAAAGTTG | TCATAGTTTC | AGTAGGTCTAT 2460  
 AGGGAGATGA | GTTGTATGTC | TGTACTATGC | AGCGTTTAA | GTTAGTGGGT | TTTGTGATT 2520  
 TTGTATGAA | TATTGCTGTC | TGTACAAAG | TCAGTTAAAG | GTACGTTTAA | ATATTTAAGT 2580  
 TATTCTATCT | TGGAGATAAA | ATCTGTATGT | GCAATTCACC | GGTATTACCA | GTTTATTATG 2640  
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 TTTTCAAGAA | CTAACACAGT | TATTCCTATA | CTGGATTTTA | GGTCCTGAA | GAAGTCTGG 2760  
 TGTTTAGGAA | TAAAGATGTG | CATGAAGCCT | AAAATACCAA | GAAAGCTTAT | ACTGAATTTA 2820  
 AGCAAGAGAA | TAAAGGAGAA | AAGAGAAGAA | TCTGAGAATT | GGGGAGGCAT | AGATTCTTAT 2880  
 AAAAATCACA | AAATTTGTTG | TAAATTAGAG | GGGAGAAATT | TAGAATTAA | TATAAAAGG 2940  
 CAGAAATTAG | AGAGTAGTAA | TTCAATTAAC | AATTTTGTCA | AGATTATTTT | CGTAAAAAC 3000  
 GTAGTAGACA | CTCTCATATA | CTAATTAGTG | TACATTTAAC | TTTGTATAAT | ACAGAAATCT 3060  
 AAATATATT | AATGAATTTA | AGCAATATAC | ACTTGACCAA | GAAATGGGAA | TTTCAAAATG 3120  
 TCTGTCGGG | TATATACCA | GATGAGTACA | GTGAGTAGTT | TATGATACAC | CAGACTGGGT 3180  
 TATTGCCAAG | TTATATATCA | CCAAAAGCTG | TATGACTGGA | TGTCTGAGTT | ACCTGGTTTA 3240  
 CAAATATTAC | AGAGTAGTAA | AACTTTGATA | TATATGAGGA | TATTAAACTT | ACATAAGTA 3300  
 TCATTGTATT | CGATTCAAG | AGTACTTTGA | TATCTCTCAG | TGCTTCAGTG | CTATCATTGT 3360  
 GAGCAATTGT | CTTTATATAC | GGTACTGTAG | CCATACTAGG | CCTGTCTGTG | GCATTCTCTA 3420  
 GATGTTTCTT | TTTTACAAA | TAAATTCCTT | ATATCAGCTT | G

## A121 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Protein Accession #: NP\_036451  
 Signal sequence: 1-21  
 Pfam domain: Zip[591-743]  
 Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745  
 Cellular Localization: plasma membrane

70  
 75  
 80

1 11 21 31 41 51  
 MARKLSVILI | LTFALSVTNP | LHELKAAAPP | QTTEKISPNW | ESGINVDLAI | STRQYHLQQL 60  
 FYRYGENNSL | SVEGPKLLQ | NIGIDKIKRI | HIHHDHDSHS | DHEHSDHER | HSDHEHSDH 120  
 EHSDHDSHS | HNHAAASGN | KRALCPDHD | SDSSGKDPN | SQGGAHRPE | HASGRNRVKD 180  
 SVSASEVTST | VYNTVSEGT | FLETITPRP | GKLPKDVSS | STPPSVTSKS | RVSRLAGRKT 240  
 NESVSEPRRG | PMSYRNTNEN | PQECFNASKL | LSHGMGIQV | PLNATEPNYL | CPAIINQIDA 300  
 RSLCLHTSEK | KAIIPPKTYS | LQIAWVGFI | AISIISPLSL | LGVILVPLMN | RVFPKPLLSF 360  
 LVALAVGTL | GDALFLHLLP | SHASHHSHS | HEPPAMENKR | GLFSLHLSQ | NIEESAYFDS 420  
 TWKGLTALGG | LYPMFLVEHV | LTLIKQPKDK | KKKNQKKPEN | DDDVEIKQL | SKYESQLSTN 480  
 EERKVDITDRT | EGYLRADSQ | PSFEDSQQA | VLEEEVMIA | HAHPEVYNE | YVPRGCKNKC 540  
 HSHFHTDQ | SDDLHSHH | YHILHSHH | QNHHPHSHS | RYSREELKDA | GVATLAWMVI 600  
 MGDGLNPFSD | GLAIGAAFT | GLSSGLSTSV | AVFCHLPHE | LGDFAVLLKA | GMTVKQAVLY 660  
 NALSAMLAYL | GMATGFIGH | YAENVSMWIF | ALTAGLFMYV | ALVDMVPEML | HNDASDRGCS 720

RWGYFFLQNA GMLLFGIML LISIFERKIV FRINF

5 A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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CGGCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCTCCTCC AGGCCGCGAG 60
CGCCCCCTGCC GGGTGCCTTG GCCTCCCTC CCAGACTGCA GGGACAGCAC CCGTAACTG 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGGCC GGCCTCCCTC CGAGGGG3GC TCAGGAGGAG GAAAGGAGAC CCGTCCGAGA 240
ATGCTCTGCG CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
GGGAACGCGG CCAATGCAAG GCATCAAGGG TTGTTAGCAT CGGCAOGTCA GCCTGGGGTC 360
TGTCATATG GAACTAAACT GGCTGCTGCG TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGAAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACAGG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGCCG ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAATGTC AGTACAGCTG TGAAGACACA GAAGAAGGCG CACAGTGCCT GTGTCCATCC 720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
AAATGTGACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATAGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGGTCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCTC AGAGCACCTG GTACCATCAA AGACAGATC 1080
AGAAGTGTGC TTGCTCACA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC 1140
CCAGAACCCA CAGGACTCC TACCCCTAAG GTGAACTGCG AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
GAGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT 1380
CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAAT TATCTGGT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAACTCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCG GGCCTTGGCA 1560
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AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCGGAGAGCA AAGTCGGGAA ACTTCGAGTG 1680
TTTGTAAGAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
TGAAGACAG GGAATATCA GTTGTATCAA GGAAGTATG CTACCAAAG CATCATTTT 1800
GAAGCAGAAG GTGGCAAGGG CAAAACGGC GAAATCGCAG TGGATGGCGT CTGCTTGTT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTTGT ATGTCAATTG CTTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCCT 2040
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TTTCTGAATC TTTCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCTCTCT 2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACACACT TTCTAGAAAA 2220
TAGAAAAAAA AGCACAGAGA AATGTTTAA TGTTTGACTC TTATGATAC TCTTGAAAC 2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTCA TAGCCAAACT 2340
TGTATATTTA AATTCCTTGT AATAATAATA TCCAAATCAT CAAAAAATA AAAAAAAA

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55 A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

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MPLPWSLALP LLLSVVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRSKGV 60
CEATCEPGCK FGECVGFNKC RCFPGVTGKT CSQDVNECGM KRPQCHRCV NTHGSYKFC 120
LSGHMLMADA TCVNSRTCAM INQYSCEDT EGGPQLCPSP SGLRLAPNGR DCLDIDECAS 180
GKVICPYNRR CVNTPGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSETC SHHANCFTNQ 240
GSPKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLIAHNSM KKKAKIKNVT 300
PEPTTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEKMK EGLEDEKRE KALKNDIEER 360
SLRGDVPPPK VNEAGFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD 420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLPQPS NFCLLPDYRL AGDKVKGKLRV 480
FVKNSNNALA WKTTTSEDEK WTKGIQLYQ GTDATESIIF EAERGKKTG EIAVDGVLLV 540
SGLCPDLSLS VDD

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80 A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGGCT AGAGCCGGCG 120
CGATGCACTG GCGCTCACTG CGAGCTGCGG CGCCGACAG CTTCGTGGCG CTCTGGGCAC 180
CCCTGTTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
10 GCTTCATCCA CGGGCGCTCC CGCAGCCAGG AGCGGGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTGCGCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCA CTGGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
GCCAGGGCTT CTCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACCGAGC CCGACATGGT CATGAGCTTC GTCAACCTCG 540
15 TGGAAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAAGG GAAGCTGTCA CGGCAGCGCA ATTCCGGATC TACAAGGACT 660
ACATCCGGCA ACGCTTCGAC AATGAGAAGT TCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTTCGG 780
AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACAGCAA CCCTGGGTG GTCAATCCGC 840
GGCAACACTT GGGCTGCGAG CTCTCGGTGG AGACGCTGGA TGGGAGAGC ATCAACCCCA 900
AGTTGGCGGG CTGATTGGG CGGCACGGGC CCCAAGCAA GCAGCCCTTC ATGTTGGCTT 960
20 TCTTCAAGGC CACGAGGTC CACTTCCGCA GCATCCGTC CACGGGAGC AAACAGCGCA 1020
GCCAGAACCG CTCCAAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
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30 TTGGGGCCAA GTTTTCTGAG ATCCTCCATT GCTCGCTTGG GCCAGGAACC AGCAGACCAA 1500
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35 TTATAGCGC CTACCAAGCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
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40 **Al25 Protein sequence:**  
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Protein Accession #: NP\_001710.1  
 45 Signal sequence: 1-30  
 Pfam domains: TGF $\beta$  propeptide [37-281]  
 Transmembrane domains: none found  
 Cellular Localization: secreted

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50 1      11      21      31      41      51
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MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE RREMOREILS 60
ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
15 LQDSHPLTDA DMVMSFVNLV EHDKEFPFPR YHREPRFDL SKIPEGEAVT AAEFRIYKDY 180
IRERFDNETP RISVYVLQLE HLGRESDLFL LDSRTLWASE EGMLVFDITA TSNHNVNPR 240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWDWIIA PBGYAAYTCE 360
60 GECAPPLNSY MNATNHAIVQ TLVHPINPET VPKPCAPFTQ LNAISVLVFD DSSNVILKKY 420
RNMVVRACGC H

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65 **Al26 DNA SEQUENCE**  
 Gene name: integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Nucleic Acid Accession #: NM\_002214  
 Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

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75 TAGGGTGGTT TCCGCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
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TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCCGC GCGGGCCCT 420
TGGCCGTGCA AGGAGGTGCT TCTCGCGGAG ACCCGGGGAC CCGCGTGCC GAGCCGGGAG 480
GGCCGTAGGG GCCCTGAGAT GCGAGAGGGT GCGCGGGCCC GCTTACCTGC ACCGCTTGCT 540
80 CCGAGCGCGG GGGTCCGCTT GCTAGGCGCT CGGAAAAAGT CTAAGCGACA CTGCCCCGCG 600
GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGCGC 660
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TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTCTC CTGGGAGACC TGGGTGTTTT 780

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5 CACTGTGTTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840  
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 TTTCAGGTGG ATCAAGAAGT GAACGTGTGT ATATTGTTTC CAATTTAATA AGCAAAAGGCT 960  
 10 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA 1020  
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCGGAAGCTA 1080  
 ATTTATGCT GAAAGTTTAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140  
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55 **A127 Protein sequence:**  
 Gene name: Integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 60 Signal sequence: 1-39  
 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 INB domain: 54-469  
 Cellular Localization: plasma membrane  
 65

1 11 21 31 41 51  
 70 MCGSALAFPT AAFVCLQND RGPASPLNAA WVPSLVGLG QGEDNRCASS NAASCARCLA 60  
 LGPECGWCVC EDFISGGRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENHINTQVTP 120  
 GEVSIQLRPG ABANFMLKVH PLKKYFVDLY YLVDVSASMH NNIEKINSVG NDLSRIMAF 180  
 SRDFRLGFGS YVDKTVSPYI SIHPERIHNO CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240  
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 75 VPNDGNCHLK NNIVYKSTTM EHPSLGQLSE KLIDNNINVI FAVQGRQFHW YKDLLPLLP 360  
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 CVDETFLDLQ CFQCDENKCH FDEQPFSES CKSHKDQPV C SGRGVCVCGK CSCHKIKL 540  
 VYGYCEKDD FSCPYHGNL CAGHGECEAG RCQCFSGWEG DRQCPSAAA QHCNVSKGV 600  
 80 CSGRGTCVCG RCBCDTPRSI GRPCEHCPTC YTACKENWNC MQCLHFNLS QAILDQCKTS 660  
 CALMEQQHYV DQTSCEFSPP SYLRIFPIIF IVTFLIGLLK VLIIRQVILQ WNSNKIKSSS 720  
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**A128 DNA SEQUENCE**  
 Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942  
 Probeset Accession #: AA435577  
 Nucleic Acid Accession #: NM\_005756  
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

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5 A129 Protein sequence  
 Gene name: G protein-coupled receptor 64  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 10 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

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 30 AVFYITVVG FCVIPLNVS MFIIVLVQLC RIKKKQLGA QRKTSIQDLR SIAGLTFLLG 840  
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 NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SONGMASTER 960  
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35 A130 DNA SEQUENCE  
 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Probeset Accession #: AA460530  
 40 Nucleic Acid Accession #: NM\_003667  
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

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 70 ACCCATGTC ATTTTCCACT TTGCCATCCC TAATAAGCT GGACCTATCG TCCAACTCC 1500  
 TGTGCTCTTT TCTTATAACT GGGTTACATG GTTTAACTCA CTTAAATTA ACAGGAATC 1560  
 ATGCTTACA GAGCTTGATA TCATCTGAAA ACTTTCCAGA ACTCAAGGTT ATAGAAATGC 1620  
 CTTATGCTTA CCACTGCTGT GCATTGGAG TGTGTGAGAA TGCTATAAG ATTTCTAATC 1680  
 AATGGAATAA AGGTGACAAC AGCAGTATGG ACGACCTTCA TAAGAAAGAT GCTGGAATGT 1740  
 TTAGGCTCA AGATGAACGT GACCTTGAAG ATTTCTGCT TGACTTTGAG GAAGACCTGA 1800  
 75 AAGCCCTTCA TTCAGTCAG TGTTCACCTT CCCCAGGCC CTTCAAACC TGTGAACACC 1860  
 TGCTTGATGG CTGCTGATC AGAATTGGAG TGTGGACCAT AGCAGTTCTG GCACCTACTT 1920  
 GTAACTCTT GGTGACTTCA ACAGTTTTC GATCCCTCT GTACATTTC CCAATTAAC 1980  
 TGTAAATTGG GGTCAATGCA GCAGTGAACA TGCTCAAGGG AGTCTCCAGT GCCGTGCTGG 2040  
 CTGCTGTGGA TGCTTCACT TTTGGCAGCT TTGCACGACA TGGTGCCTGG TGGGAGATG 2100  
 80 GGGTGTGTTG CCATGTCATT GGTTTTGTG CCAATTTTGC TTCAGATCA TCTGTTTCC 2160  
 TGCTTACTCT GGCAGCCTG GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTTGAAA 2220  
 CGAAAGCTCC ATTTTCTAGC CTGAAAGTAA TCAATTTGCT CTGTGCCCTG CTGGCCTTGA 2280  
 CCATGGCCGC AGTTCCCTG CTGGGTGCA GCAAGTATGG CGCTCCCTCT CTCTGCTGTC 2340  
 CTTTGCTTTT TGGGGAGGCC AGCACCATGG GCTACATGGT CGCTCTCATC TTGCTCAATT 2400  
 CCTTTGCTT CCTCATGATG ACCATTGCC ACACCAAGCT CTAATGCAAT TTGGACAAGG 2460

5 GAGAACTGGA GAATATTGG GACTGCTCTA TGGTAAAACA CATTGCCCTG TTGCTCTTCA 2520  
 CCAACTGCAT CCTAAACTGC CCTGTGGCTT TCTTGTCTCT CTCCTCTTTA ATAAACCTTA 2580  
 CATTATATCAG TCCTGAAGTA ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTCTCTGCAT 2640  
 GTCTCAATCC CCTTCTCTAC ATCTTGTTC AATCTCACT TAAGGAGGAT CTGGTGAGCC 2700  
 TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAACT 2760  
 CTGATGATGT CGAAAACAG TCCTGTGACT CAACTCAAGC CTTGGTAACC TTTACCAGCT 2820  
 CCAGCATCAC TTATGACCTG CCTCCAGTT CCGTGCCATC ACCAGCTTAT CCAGTGACTG 2880  
 AGAGCTGCCA TCTTCTCTCT GTGGCATTGT TCCCATGTCT CTAATTAATA TGTGAAGGAA 2940  
 AATGTTTCA AAGGTTGAGA ACCTGAAAT GTGAGATTGA GTATATCAGA CGAGTAATTA 3000  
 10 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

**A131 Protein sequence**

15 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 20 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 | | | | | |  
 MDTSLRGVLL SLFVLQLLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLVFTSY LDLSMNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLV 120  
 LQNNQLRHVP TEALQNLRLS QSLRLDANH SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLALQA MTALANKIHH IPDYAFGNLS SLVVLHLANN RIHSLGKKCF DGLHSLRTLD 240  
 LNNYNNLDEFP TAIRTLNLK ELGFHNNIR SIPEKAFVGN PSLITIHFPD NPIQFVGRSA 300  
 30 FQHLPELRTL TIAGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360  
 YNNLEDLPSF SVQCLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI ALIHPNAPST 420  
 LPSLKLKDL SMLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFFELKV IEMPYAYQCC 480  
 AFGVCENAYK ISNQWNKGDN SSMDDLHKKD AGMFAQDER DLEDPLDPE EDLKALHSVQ 540  
 CSPSPGPKFP CEHLLDGWL I RIGVWTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA 600  
 35 AVNMLTGVS AVLAGVDAFT FGSPARHGAW WENGVGCHVI GFLSIFASES SVFLLTLAAL 660  
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLFPFGE 720  
 STMGYMVALI LLNSLCFLAM TIATYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC 780  
 PVAFLSPSSL INLTPISEPV IKFILLVVVP LPACLNPLLY ILFNPHPKED LVSLRKQTYV 840  
 40 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVFPSPAY PVTESCHLSS 900  
 VAFVPC

**A132 DNA SEQUENCE**

45 Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Probeset Accession #: U25128  
 Nucleic Acid Accession #: NM\_005048  
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 | | | | | |  
 GGCCGGTGGC CGGGGCCCGA CCACCCAGC TGGCGTGTGT TACTGGCCAC AAGTTTGCTC 60  
 TGGGCGAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120  
 TCTTCTCTACA GCGGTTCCGG GCATGGCCGG GCTGGGGGGG TCGCTCCAGC TCTGGGGTTG 180  
 55 GCTAATGCTC GGCAGCTGCC TCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATAC 240  
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300  
 AGCTCAACTC CAGAGGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTG 360  
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGC CCTCTTATA TTTATGACTT 420  
 CAACCATAAA GGAATTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480  
 60 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCCT CGCTTCTGCG AGCCAGATAT 540  
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600  
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT GGTACTTCA GAGGATGCA 660  
 TTGCACTAGG AACTATATCC ACATGCACCT ATTGTGTCT TTTATGCTGA GAGCTACAAG 720  
 CATCTTTGTC AAGACACAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780  
 65 AATAATGCAG GATGACCCAC AAAATCCAT TGAGGCACT TCTGTGGACA AATCACAATA 840  
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900  
 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCCGACAC 960  
 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTCAGC 1020  
 70 ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGGAGGTGTC TGGGAACCTA GTGCTGGAGA 1080  
 CATCAAGTGG ATTTATCAAG CACGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140  
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200  
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATGACACTG GTCTCGTCTC TAGTCTTTGG 1260  
 AGTGCAATAC ATCGTGTTCG TATGCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320  
 75 CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGCT TTTCTTGTGT CTATCATCTA 1380  
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAG AGTGTGAGTC GGTGGAATCT 1440  
 CTCGGTGGAG GTTAAAGGGA CACGCCATG TGGCAGCGCG AGATGGGGCT CAGTGCTCAC 1500  
 CACCGTGAAG CACAGCACA GCAGCCATG ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560  
 TATCTCTGGC AAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCATTATTACC 1620  
 80 TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCTGCCA CACTCTTTCC ACGAGGAGAC 1680  
 CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740  
 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800  
 CATTGTGGC TGACTTTTCT GGGCTGGTCC AATGGCTGTT GTGTGAGAG GGCTTGGCTG 1860  
 ATACTCTCAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920  
 TTTTAGGCTC CATGAATTGG CTCTGTAA TACTAACGAC ATGAAATATC AAGTGTCAAT 1980

5 GGAGTAGITT ATTACCTTCT ATTGGCATCA AGTTTTCTCT TAAATTAATG TATGGTATTT 2040  
 GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100  
 GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160  
 ATTTTCCITT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220  
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280  
 GATCTAAGAA CAAGTACTTG CTGAAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340  
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAG AATATTTTAC 2400  
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGSTCT TCATCTTTTC 2460  
 10 TTCTTTGTAA ACCATGTCAT GTGAAAGAT TTTCTCAGTT AGTGAGCTTG TGTCTGCAA 2520  
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG 2580  
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640  
 T

# 15 A133 PROTEIN SEQUENCE

Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Protein Accession #: NP\_005039.1  
 Signal sequence: 1-25  
 Pfam domain: 7tm\_2 [141-420]  
 20 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419  
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 | | | | |  
 MAGLGASLHV WGLMLGSLC LARAQLDSGD TITIEEQIVL VLKAKVQCEL NITAOQEAGE 60  
 GNCFFEMDGL ICFPRGTGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120  
 NYSDCLRPLQ FDISIGKEF PERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180  
 30 MHLFVSFMLR ATSIPIKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240  
 VMFIYFLATN YYNIIIVGLY LENLIFVAFP SDTKYLWGPFI LIGWGPFAAF VAAMAVARAT 300  
 LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360  
 LAKSTLIVLV VFGVHYIVFV CLPHSPTGLG WEIRMHCELF FNSPQGFVFS IICYCNGREV 420  
 QAÉVKKQWSR WNLSDVWKRT PPGSRRCGS VLTTVTHTST SQSQVAASR MVLISGKAAK 480  
 IASRQPDSHI TLPGVVWSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RFMESNPDTB 540  
 35 GCQGETEDVL

# 40 A134 DNA sequence

Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251.  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 | | | | |  
 ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCAGAGTA CACTCCCGGA 60  
 GGAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGGGCACA CCTCCGAGG GCGAGGCAGC 120  
 GACCGGAGGA GCGAGAGCCG GCGGAGGCTC GCGGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240  
 50 CCGCGGCGCG GCGCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTC 300  
 CGCCTGCGTC CTGACGCTTC CCGGGGGAGG GTCCGGTTGC CAGTGAACCC TCCAGAGGCT 360  
 TCCGAGCAGC AGCCCGCGGG GCCTTCTGAC TGATCCCGGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAGCG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTCCTGGAC CTAGGGCCCG GCGTCGTGCG CTCTGGGCGC TCGCGGCAGA GGGGAGTGGC 540  
 55 CCGCGCGGAA AGCGCCGCGG GACAGTCACT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600  
 CTTCTGGGAG ACCGTCTCTG GCTCTCTGGA GAOGCGCTGT CCGCGCCAG GGTGGTGCCA 660  
 TGTGGGGCGC TCGCGGCTCG TCCGTCTCCT CATCTCTGAA CGCGGCTTCG CTCCTGCAGC 720  
 TGTCTGTGCG TCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780  
 TGGCTGGAGC GCGAGGGGCT CTGGGCGATC GGCTTCCAGT GTCCCGAGCG CTTGACCGGC 840  
 60 GGCAGCGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900  
 GCGGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGGCTGG CGAGCTGGC 960  
 CGGGCGGACA AAGACGGGCC CCGACGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGCGG AGGGTGGGCC CCCACCGGTG AGGGCTGGC AGCGGTGCTC CCTGAAGGC 1080  
 TCCCGAAGAG GAAGGCAGCT CCTCAGGGCT TTCCGGGGGC TGCTGCCCGC TGCCAGAGCG 1140  
 65 CGCGGATTCC CATCTTCTCC AGCGGGCGGC CCTCTCCGCC TGCGGGGCC CGCCTTGCCC 1200  
 ATCTAGCTGC GTTCTCTCAT TGTGGCTTCC GTGTTGTGG CCTTTATCAT CTGGGGTCC 1260  
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 GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCATGA TCCCGAGTGC CAGCACTTCC 1380  
 70 CGGGGGTGGT CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG GCGCAACTCC 1440  
 GGGGCGCGGG GCGCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGAACATG 1500  
 AACAACTGTG ATGTCAACAT GCCCAAGAA TTTCTGTGTC TGAAGTGTCA GCAGGCCACC 1560  
 CAGATTGTGC CACATCAAGG CAGATATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG 1620  
 CACGACTCTG TGCCTATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCTA CCTGSGCTAC 1680  
 AGGCAGATTG AGTCCCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
 75 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTGAGG GTGGAACTCC GCACATGTGG GTGGTATTTA TGGCAAGATT CTTTGGATG 1860  
 GCTTCATTGG CCCCAGACT GTATGAAAC ATCTCCGAAT TAGCAATTCT GGATATGTTT 1920  
 ACTCCAGGGT ATCATTTGATT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 TTTGCTGATG GTGTATAACA AATGCTTGAG TCGAAGTGC CTTGAGATA TGGTTGACGA 2040  
 80 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTCTTTT 2100  
 TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTGCC CTTTACTGAG GACTTTTTT 2160  
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTGTCTCTG TTGCCAGGC TGGAGTGCAG 2220  
 TGCTGGAGT TCGGCTCACT GCAACTTCAG CTTCTGTGAT TCAGGCAACA CTCCTGCCCT 2280  
 AGCTCTCCAC TTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGATTTTT 2340



5 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA OCTCAAGCAA 2400  
 TCTGCTGTCT TCAGCTCTCC AAAGTGTCTG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460  
 TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAA TAACAGGACT 2520  
 ATTCTAAAG GAAACCTGTT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580  
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 10 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880  
 TATATTGAAA TCATAAATA TCACCCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940  
 TGGTTATGTT TTGGCGTTTC CTCTGTTTGT GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000  
 GAGTGCAAGT AATTACTATA CTGTGAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060  
 AAAAAATTTT TTGCTTAGT TATAAAATT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCTCTA GCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTTACTTT 3180  
 15 GCAGATCATA AGGCTTTTAA TACTCTTGT ATCAAAATGG CTTATTTTTC AGGCCTAAG 3240  
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTCTCCACAC ACTGTTCTTG 3300  
 ATTTCTCTCT TCTTTAGAG CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360  
 CAAATCAAG TGAATTATTT TGTGTGTTCT TTAATTATAT AAAAAAGAT AACTTTAAGG 3420  
 20 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480  
 GTATGTTATG GTCTTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTTCTATT 3540  
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTGA 3600  
 TTTTAAATA ACCAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660  
 TGAATAAAAA AAAAAAATA AAAAAAATA

25 **Al35 Protein sequence**  
 Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 30 Transmembrane domains: 402-424  
 Cellular Localization: not determined

35 1 11 21 31 41 51  
 | | | | |  
 MLSGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEAEKGNRSG PPWIRAQQQ PRPPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPEA 120  
 SGRQPRGSPD CTPRPPSASA THKAVFKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180  
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVV C3ALAARPSF HPGTPLRSCS 240  
 40 CCNLRCHRRG RGPSPGYCHG WLDQAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300  
 ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTO GDGEGAPPV RANQRCSPFG 360  
 SPKGRQLLRA FPGLLPRARR RGPSPSPRGG PSPLQRPALP IYVFFLIVGS VFVAFIILGS 420  
 LVAACCCRCL RPKQDPQOSR APGNRLMET IPMIPASAST RGSSSRQSST AASSSSSANS 480  
 45 GARAPPTRSQ TNCCLPBGTM NNYYVNMPTN FSVLNCQQAT QIVPHQGGYL HPPYVGYTVQ 540  
 RDSVPMATAV PFMGLQPGY RQIQSPFPHT NSEQKMYPAV TV

**Al36 DNA SEQUENCE**  
 Gene name: selectin E (endothelial adhesion molecule 1)  
 50 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 | | | | |  
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGG 60  
 GCGTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120  
 CAGCAAAAGT ACACACACCT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180  
 60 TCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240  
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGTCCAGGT 300  
 GAACCCAACT ATAGGCAAAA AGATGAGGAC TGCCTGGAGA TCTACATCAA GAGAGAAAAA 360  
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420  
 GCTGCCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 65 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAACGTG 540  
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 AGCTACAATT TTCTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 ACCATGCACT GTATGCTCTC TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720  
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GSGTTTGTGG AATGTTTCCA AAACCTTGGA 780  
 70 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840  
 GCGCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 GCTGTGACAT GACGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960  
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 TTGACGGGAC CAGCCAGGT TGAATGCACC ACTCAAGGCC AGTGGACACA GCAATCCCA 1080  
 75 GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140  
 CTTCCTAGTG CTCTCTGGAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200  
 GGTTTTGTGT TGAAGGGCTC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260  
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320  
 GTGAGGTGTG CTATTCCCC TATTGGAGAA TTCACCTACA AGTGTCTTGT TGCCTTCAGC 1380  
 80 TGTGAGGAGG GATTGGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440  
 TGGACAGAA AGGTTCTCTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCGGGA 1500  
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCTGTG 1560  
 CCTGAAGGAT GAGCGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620  
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680  
 CTTTGTGCTG CTCTGACTCT CACTCTGACA TTAGCACCAT TTCTCTCTG GCTTGGGAAA 1740

TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800  
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

5

**A137 Protein sequence:**

Gene name: Selectin B (endothelial adhesion molecule 1)  
Unigene number: Hs.89546  
Probeset Accession #: M24736  
Protein Accession #: NP\_000441  
Signal sequence: 1-22  
Transmembrane domains: 555-573  
C-lectin domain: 23-139  
Cellular Localization: plasma membrane

10

15

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1      11      21      31      41      51
|      |      |      |      |      |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRVTHLVAI QNKEEIEYLN 60
SILSYSPSY YWIGIRKVMNV WVMVGTQKPL TEEAKNWAPG EPNRQKDED CVEIYIKREK 120
DVGWMDNERC SKKQLALCYT AACINTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
ECDAVINPAN GFVECFQNPQ SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPQVETCT TQGWTTQIIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420
EKPTCEAVRC DAVHQPPKGL VRCASPIGE FTKSSCAFS CEEGFELYGS TQLECTSQGQ 480
WTEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTINGSA ARTCGATGHW 540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRL CLRKAKKFVP ASSCQSLESD 600
GSYQKPSYIL

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30

**A138 DNA SEQUENCE:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
Nucleic Acid Accession #: AA487468  
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

35

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1      11      21      31      41      51
|      |      |      |      |      |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTGGGTCTT CTGCTCTCTA CTGCTCACAG TTTCTTCCAA CCTTGCCATT 120
GCAATAAATA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACCCTGA GGAATTGTCA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAAITTT ATCACCTGAT GGGCAATATG TGCTAGAAAT CATGTTTGTA 420
GACCTCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTATCC CCTATTGATA GAAAAACATG AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTAT 600
GAGAGAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

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55

**A139 Protein sequence:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
Protein Accession #: none found  
Signal sequence: 1-23  
Transmembrane domains: none found  
Cellular Localization: secreted

60

65

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1      11      21      31      41      51
|      |      |      |      |      |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQSKSK 60
PLMVIHLED CQYQALKKV FAQNEBIQEM AQNKFIIMNL MHETTDKNLS PDGQYVPRIM 120
FVDPSTLTRA DIAGRYNRL YTYEPRDLPL LIENMKKALR LIQSEL

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70

**A140 DNA SEQUENCE**

Gene name: TMPSR3a  
Unigene number: Hs.298241  
Probeset Accession #: AI538613  
Nucleic Acid Accession #: AB038157  
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

75

80

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1      11      21      31      41      51
|      |      |      |      |      |
ACOGGGCACC GGACGGCTCG GGTACTTTCC TTCTTAATTA GGTCAATGCC GTGTGAGCCA 60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACCTGTGG CTACTATCTC TTCCGTGGTG 120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGATGTC 180
AGAGGTCTCT AAATAGTCAC CATGGGGGAA AATGATCCCG CTGCTGTGTA AGCCCCCTTC 240

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TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAATATA GTCTGTGTC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTGG CTCACTCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CCGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCGGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT AGCAAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAAGTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCAGTGGT TACCTTGCAG TGCACAGCCT GTGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900  
 CTTGAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCCTC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAT CTCCCCAAGT CATGGACCCT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGAACA TCCAGCCCA TCCCACTGG TGGAGAAGAT TGTCTACCA 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCOCGGCCA 1140  
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACTTCCCC 1200  
 GATGGAAAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCCTGTCC TGAACCAAGC GCGCGTCCCT TTGATTTCGA ACAAGATCTG CAACCAAGC 1320  
 GACGTGTACG GTGGCATCAT CTCCCCTCC ATGCTCTGCG CGGGCTACTG GACGGGTGGC 1380  
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACCA CTTTGGCATC GGCTCGCGAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCCGTC TCACTCTCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCCGGACAC AGTAGCAGGC CCGAAAGAGG CACCCCTTCA TCTGATTCCA GCACAACCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 TTGCTCTAGC TTCCCACTG GCTGGGACCA CAGGTGCGCG CCACCACACC CAACTAATT 1920  
 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAAATG TGTGCTGTCT TCAGCCTCCC ACAGTGTGCG GATTACAGGC ATGGGCCACC 2040  
 AGCGCTAGCC TCACGCTCTT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGG AAAATTCCTG 2160  
 ACGAGATAAG CAGTTATGTG ACCTCAGCTG CAAAGCCACC AACAGCCCTC CAGAAAAGAC 2220  
 GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCATCTCTA GGGACCAGAA 2280  
 CCAAAACCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCTAT TTTCTGATG TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400  
 TTGCTCTTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAA AAAAAA 2460  
 AAAAAA

**A141 Protein sequence:**

Gene name: TMRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_Spc domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MGENDPPAVE APPSFRSLFG LDDLKISPIVA PDADAVAQI LSLPLKFPF IIVIGIILI 60  
 LALAIGLGIH FDCSGKYRRC SSPKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120  
 TAASWMTMCS DDMKRGHYANV ACAQLGFPSY VSDNLRVSS LEGQFREFFV SIDHLLPDDK 180  
 VTALHSHSVV REGCASGHVV TLQCTACQHR RGYSSRIVGG NMSLLSQHPW QASLQFQGVH 240  
 LOGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGKVCWT SGWGATEDGA GDASPVNLHA 360  
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQGDG SGGPLVCQER RLWKLVGATS 420  
 FGIGCAEVNK PGVITRVTSP LDWIEBQMER DLKT

**A142 DNA SEQUENCE**

Gene name: BSTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CCAACACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60  
 CTGAGATCCT TGCAGTACTG ACATCTCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120  
 CGGCTGCTCC TATTGCTGAG CTGCTGGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180  
 AGACCCAGCT GTGCTCCTGG ATGGTTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240  
 AAGCTGAGGA ACTGCTCTGA TGOAGAGCTC GAGTGTGAGT CTTACGGAAA CGGAGCCAC 300  
 CTGCAATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360  
 CAGAGAAGCC AGCCGATATG GATTGGCCTG CAGAACCCAC AGAAGAGGCA GCAGTGGCAG 420  
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGTGCTG GCAAGTCCAT GGGTGGGAAC 480  
 AAGCACTGTG GCGCATGAGC CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540  
 AACAGCGGCC AACACTCTCT GTGCAAGTAC OGACCATAGA GCAAGAAATCA AGATTCTGCT 600  
 AACTCTGCA CCAGCCCGCT CTCTCTCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660  
 TTCAGAGGGG AACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720

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GGCTTAGAGA CAGAAACTTT AGCAITGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG 780
CCCCGCCATC CCTTTCCACA GTATCCTTCT TCCCTCCTCC CTTGTCTCTG GCTGTCTCGA 840
GCAGTCTAGA AGAGTGCAATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
AAAGATTGA AGACAGAAGG AAGAAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCCCTCT GCCCTCTCTC CATTCCTGTC ACCCCACCCC AGCCACTCAA CTCTCGCTTG 1020
TTTTTCCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080
TACATTCCCT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

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**A143 Protein sequence:**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Protein Accession #: none found  
 Signal sequence: 1-22  
 Transmembrane domains: none found  
 C-type lectin domain: 47-156  
 Cellular Localization: secreted

**A144 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

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1 11 21 31 41 51
| | | | |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWPFYHKS N CYGYPRKLRN WSDAELEQCS 60
YNGGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSWG 120
KSMGNGKHCA EMSSNNFLT WSSNECNKRO HFLCKYRP

GGGGAACACC GGCCCGCCGT CGGGGAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCCTCTGTT ACCTCTCTGG TCTCTCTCTC TCTCTCTCTG TTGCTGGCTG CAGTGGCGCG 120
CCTCTCGAGCC GTCCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGGCGA ACAGTCCAGG 300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
GAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAAT GGCAAGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCTGT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTGTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
TCATCTGTAG CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
GTGTCTTACA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCATAGC CAAGAACCAC 840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
CCAGTGCCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAAATGCTC CATGTTTGA CCCCAGAAAT ACGAGGCCCA TGTGCTGAG AATGCAGTGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAGCG CCCCACCTCA CCAGCGTGGC 1140
GTGCCACCTA CCTTATCATG GCGGTGAGG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
CTGAGAGCAA CTTCCGATC CTGACAACCA GGAAGGGTGT GGATTTTGA GCGCAAAACC 1260
AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
CCACAGCCAC CATAGTGTGC CAGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGSCA TCCCCTCTGG GAGCCTGTG TGTGTCTACA 1440
CTGCAGAAAG CCTTGACAAG GAGAATCAAA AGATCAGCTA CGCATCCTG AGAGACCCAG 1500
CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTAC AGCTGTGGGC ACCCTGACC 1560
GTGAGGATGA CGATTTGTG AGGAACAACA TCTATGAAGT CATGCTCTG GCCATGGACA 1620
ATGGAAGCCC TCCCAACACT GGCACGGGAA CCTTCTGCT AACACTGATT GATGTCAACG 1680
ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAGC CTTGTGCGCC 1740
ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTC CAGGCCCAGC 1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
ATGTGAAAC CTGCCCCTGA CCTTGAAGAG GAGGTTTCAT CCTCCTGTG CTGGGGGCTG 2040
TCCTGGCTCT GCTGTTCTCT CTGCTGTGTC TGCTTTTGT GGTGAGAAAG AAGCGGAAGA 2100
TCAGAGGAGC CCTCTACTC CCAGAAGATG ACACCCGCTG CAACGTCTTC TACTATGGCG 2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGTCCAC CGAGGTCTGG 2220
AGGCCAGGCC GGAGGTGGTT TCCCGCAATG ACGTGGCAC AACCATCATC CCACACCCCA 2280
TGTACCGTCC TTAGCCAGCC AACCCAGATG AATOGGCAA CTTTATAATT GAGAACCTGA 2340
AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGT TTGACTATG 2400
AGGGCAGCGG CTCCAGCGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCGACCCAAG 2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520
ACGGTGGGCG GGAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AAGCTCAGG 2580
CACAGAGCAT CTCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTGG GAGCTTGTCA 2640
GGAAAGTGGC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
TCCTTAGCCT TFCAGGATGG AGGAATGTGG CGAGTTTGG TTCAGCACTG AAAACCTCTC 2760
CACCTGGGCC AGGGTTGCTC CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCGTAAAA 2820
TGCTCAACCC TGTGCTCTGG GCTGGGGCT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880
CTGGAATGGA ACCTCTCTAG GCCTCCTGCT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940

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TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG 3000  
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060  
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTGCGT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAACITTTT TATTAAGAA A

**Al45 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51  
 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV PREAEVTLA GGAQEPEGQA LGKVFMCPCG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDWV VAPISVPENG 120  
 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLIN KPLDRESIAK 180  
 YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMGDGSGTT TAVAVVEILD ANDNAPMFDP QKYBAHVPEP AVGHEVQRLT VTDLDAFNSP 360  
 AWRATYLLIM GDDGDHFTIT THPESNQGLL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMP DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540  
 VNDHGPVPEP RQITTCNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKFL KQPTYDVHLS LSDHGNKEQL TVIRATVCDG HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFL LVLLLVRKK RKIKEPLLLP EDDTRDNVY YGEEGGSEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTII PTPMYRPRPAN PDEIGNFIE NLKAAINTDPT APPYDTLLVF 780  
 DYEAGSGDAA SLSSLTSSAS DQDQDYDVLN EWGSRFKLA DMYGGEED

**Al46 DNA SEQUENCE:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Nucleic Acid Accession #: NM\_003318  
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGAATTCCTT TTTTTTTTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG 60  
 CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCCTCCCG GGTTCAGCG ATTCTCCTGC 120  
 CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180  
 CTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240  
 ACCTCAGGTG ATCCACTTGC CTGGCCTCC CAAAGTGCTA GGATTCACAG CGTGAAACTG 300  
 TGCTGGCTG ATCTTTTTT TGTGTGTGGA TTTTGAAGAC AGGGTCTCCC TTGGTCGCC 360  
 AGGCTGGAGT GCAAGTGGTG GATCTTGGCT CACTATAACC TCCACTCTCT GGTTCAGT 420  
 GATCCTCCCA CTTAGCCTCT CTGAGTAGCT GTGATTACAG CGCTGCACCA CCACACCCCG 480  
 CTAATTTTTT TATTTTTATT AGAGACAGGG TTTCAACATG TTGGCCAGGC TGTCTCTCAA 540  
 CTCTGGACT CAGGAGTACC GCCTGCCTCC ACTTCCCAAG GTCCCGAGAT TACAGGTGTG 600  
 AGTCACCATG CCTGACCTTA TAATCTTAA GTCAATTTTT CTGGTCCATT TCTTCTTAG 660  
 GGTCCCTACA ACAATCTGCG ATTAGGCGGT ACAATAATCT TTAATCTCAT GATTACAAA 720  
 AGGAAGATGA AGTGATTTCAT GATTTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCCT 780  
 GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA 840  
 TTTGGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA 900  
 ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG 960  
 TGCAATTTTC TGTAGAAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACRATTGATT 1020  
 CCATAATGAA CMAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080  
 AACTAAGCTT GAATAAAAT TCTGCTGATA CTACAGATAA CTGGGAACT GTTAACCAAA 1140  
 TTATGATGAT GGCAACAAC CCAGAGGACT GGTGAGTTT GTTGCTCAAA CTAGAGAAAA 1200  
 ACAGTGTCC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTGGTTAC AGTCAAGCAA 1260  
 TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGCTAGA ATTCAAGTGA 1320  
 GATTGTCTGA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAATGG 1380  
 CCAGAGCAAA CTGCAAGAAA TTGCTTTTGS TTCATATATC TTTTGACAAA TTGAACTGT 1440  
 CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG 1500  
 TACCAC TAGA AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560  
 TTTTCAGAGGA GGAAGAAGAG AATTATCAG CATCTACGGT ATTAAGTACC CAGAATCAT 1620  
 TTTCCGGTTC ACTTGGGCAT TTACAGAAATA GGAACAACAG TTGTGATTCC AGAGGACAG 1680  
 CTACTAAAGC CAGGTTTTTA TATOGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740  
 ACCGGAAATC ATGAGACAAA ACTAACAAAA CTAAACAGTC ATGCCCATTT GGAAGAGTCC 1800  
 CAGTTAACCT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGATACCT 1860  
 GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGTTGTG CCTGGATCTA 1920  
 AACCAAGTGG AATGAATTTC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT 1980  
 TCAAGGAACC TCTGGTGCA GATGAAGAAG GTTCTGAACT TATTATTACT GATTCAATAA 2040  
 CCCTGAAGAA TAAACCGGAA TCAAGTCTTC TAGCTAAATT AGAAGAACT AAAGAGTATC 2100  
 AAGAACCAGA GTTCCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160  
 GTATTAAACA GAATCCTGCT GCATCTTCAA ATCACTGGCA GATTCCGGAG TTAGCCCGAA 2220  
 AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAA 2280  
 AGTCAACACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTTGT AAGACACCAA 2340

5 GCAGCAATAC CTGGATGAT TACATGAGCT GTTTAGAAC TCCAGTTGTA AAGAATGACT 2400  
 TTCCACCTG TTGTGAGTTG TCAACACCTT ATGGCCCAACC TGCTGTGTT CAGCAGCAAC 2460  
 AGCATCAAT ACTTGCCTACT CCACCTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520  
 ATGAATGCAT TTCCGTTAAA GGAAGAATTT ATTCCATATT AAAGCAGATA GGAAGTGGAG 2580  
 GTTCAAGCAA GGTATTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640  
 TGAACCTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA CCGGAAOGAA ATAGCTTATT 2700  
 TGAATAAACT ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCACGG 2760  
 ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA 2820  
 AGAAAAATC CATTGATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG 2880  
 10 TTCAACAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACCAGCT AACTTTCTGA 2940  
 TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAAATG CAACCAAGATA 3000  
 CAACAAGTGT TGTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060  
 TCAAGATAT GTCTTCTCC AGAGAGAATG GGAATCTAA GTCAAAGATA AGCCCCAAAA 3120  
 GTGATGTTG GTCCTTAGGA TGTATTTGT ACTATATGAC TTACGGGAAA ACACCAITTC 3180  
 15 AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATG 3240  
 AATTTCCCGA TATTCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTGTT TTAATAAGGG 3300  
 ACCCAAAACA GAGGATATCC ATTCCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3360  
 CTCATCCAGT TAACCAAAATG GCCAAGGGAA CCACTGAAGA AATGAATAT GTTCGGGCC 3420  
 AACTTGTGG TCTGAATTCT CCTAACTCCA TTTTGAAAGC TGCTAAAACT TTATATGAAC 3480  
 20 ACTATAGTGG TGGTGAAGT CATAATTCTT CATCTCCAA GACTTTTGAA AAAAAAGGG 3540  
 GAAAAAATG ATTTGCGATT ATTCGTAATG TCAGATAGGA GGTATAAAT ATATTGGACT 3600  
 GTTAACTCT TGAATCCCTG TGGAAATCTA CATTGAAGA CAACATCACT CTGAAGTGT 3660  
 ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAC 3720  
 25 TTATGGCCT GTATATATG TAGACTTGT TTCTCTGTT TATGCTCTG TGTAATCTAC 3780  
 TTGACATCAT TTACTCTG GAATAGTGG TGGATAGCAA GTATATTCTA AAAAACTTG 3840  
 TAAATAAAGT TTGTGGCTA AATGA

# 30 A147 Protein sequence:

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 35 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

40 1 11 21 31 41 51  
 MNKVRDIKXK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDNL SLLKLEKYS 60  
 VPLSDALLNK LIGRYSQAIE ALPPDKYQGN ESPARIQVRP AELKAIQEPD DARDYFQMAR 120  
 ANCKKPAFVH ISFAQFELSQ GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKQKLLS 180  
 45 EEEKKNLSAS TVLTAAQSEFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR 240  
 NSLRQTNKTK QSCFPGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVGSGKP 300  
 SGNDSCLELN LKSVONSHEK EPLVSDEKSS ELIITDSITL KNTBESSLLA KLEETKEYQE 360  
 FEVPESNQKQ WQAKRKSECI NQNPAASENH WQIPELARKV NTEQKHTTPE QPVFVSQKQS 420  
 PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDPP PACQLSTPYG QPACFQQQOH 480  
 50 QILATPLQNL QVLASSSANE CISVKGRIYS ILKQIGSGGS SKVPQVLNEK KQIYAIKYVN 540  
 LEEADNQTLN SYRNEIAYLN KLQHSKDII RLYDYEITDQ YIYVMECCN IDLNSWLKXK 600  
 KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPANFLIV DGMKLIDFG IANQMOPDIT 660  
 SVVKSQVGT VNYMPPFAIK DMSSSRENGK SKSKI SPKSD VNSLGCILYY MTYKTPFQQ 720  
 IINQISKLHA IIDPNHEIEF PDIPKDLQD VLKCCLEKRP KQRISIPELL AHPYVQIQTH 780  
 55 PVNQMAKGT BEMKVLVQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKRGK 840  
 K

# 60 A148 DNA SEQUENCE

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51  
 CTCTTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60  
 GACAAGCACA TGGACTTTT TTATAATAGG AGCAACACTG ATACTGTGTA TGACTGGACA 120  
 70 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTT TCTGCCTGTT TATTTTCTAT 180  
 TCTAATCTTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATT CCCTTCTAC 240  
 TAAGTTTGG CTAATTAGC TGCTGCGGAT TTCTTGGCTG GAATGCGCTA TGTATCTCTG 300  
 ATGTTTAAACA CAGGCCAGT TTCAAAAATC TTGACTGTCA ACOGCTGGTT TCTCCGTCAG 360  
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGTTAT CGCGGTGGAG 420  
 75 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480  
 CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTATAGG GGGCGGTCCC CACACTGGGC 540  
 TGGAAATGCC TCTGCAACAT CTCTGCTGCG TCTTCCCTGG CCCCATTTA CAGCAGGAGT 600  
 TACCTTGTGTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGTT TGTGGTGATC 660  
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGCTCCGCA TACAAGTGGG 720  
 80 TCCATCAGCC CCGCGAGGAC ACCCATGAAG CTAATGAAGA OGGTATGATC TGTCTTAGGG 780  
 GCGTTTGTGG TATGCTGGAC CCGGGGCTG GTGGTTCTGC TCCTGACGG CCTGAACATGC 840  
 AGGCAGTGG TGTGAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900  
 GTCGTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGCGAC CATGAAGAAG 960  
 ATGATCTGCT GCTTCTCTCA GAGAAACCA GAGAGGCGTC CTCTCGCAT CCGCTCCACA 1020  
 GTCCTCAGCA GGAGTGACAG AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCACCCCA GGTGATGACT 1140  
GTCITTAGG

5

A149 Protein sequence:

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
Unigene number: Hs.258583  
Probeset Accession #: NM\_012152  
Protein Accession #: NP\_036284  
Signal sequence: none found  
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295  
Cellular Localization: plasma membrane

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1	11	21	31	41	51	
MNECHYDKHM	DFFYNRSTND	TVDDWTGTXL	VIVLCVGTFF	CLFIPFNSNL	VIAAVIKNRK	60
PHFPFYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIIVERHMS	IMRMVHSNL	TKKRVTLIL	LVNAIAIFMG	AVPTLGWNC	CNISACSSLA	180
PIYSRSLVF	WTVSNLMAFL	IMVVVYLRIY	VYVKRKTINV	SPHTSGSISR	RRTPMKIMKT	240
VMTVLGAFV	WTPGLVLL	LDGLNCRQCG	VQHVKNRFL	LALLNSVVP	IYYSYKDEDM	300
YGTMKRMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	ISQGAVCNK	STS	

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ProstateA150 DNA SEQUENCE

Gene name: ESTs  
Unigene number: Hs.293616  
Probeset Accession #: AW043782  
Nucleic Acid Accession #: none found  
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

30

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1	11	21	31	41	51	
AGCAACGACG	CGGGCGGCGG	GGAGCGGCGG	CGCGGCCATG	TGGCTGCTGG	GGCCGCTGTG	60
CCTGCTGCTG	AGCAGCGCGG	CGGAGAGCCA	GCTGCTCCCG	GGGAACAAC	TCACCAATGA	120
GTGCAACATA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	CGCCTGGCA	180
GTGTGACGGG	CTGCCTGACT	GCTTCGACAA	GAGTGTAGAG	AAGGAGTGCC	CCAGGCTAA	240
GTGAAATGT	GGCCCAACCT	TCCTCCCTCG	TGCCAGCGGC	ATCCATTGCA	TCATTGGTCG	300
CTTCGGGTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCCCTCG	CTTGTCTCCA	CGCCCGCTA	CCACTGCAG	AAACGGCTCT	GTATTGACAA	420
GAGCTTCATC	TGCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTTCTCAA	GAACCCGCGA	GTGGGCAGGT	GTTTGTGACT	TCAGAGAACC	AACTTGTGTA	540
TTACCCAGC	ATCACTATG	CCATCATCGG	CAGCTCCGTC	ATTTTGTGTC	TGGTGGTGGC	600
CCTGCTGGCA	CTGGTCTTGC	ACCACGAGCG	GAACGGGAAC	AACTCATGTA	CGCTGCCCGT	660
GCACCGGCTG	CAGCACCCCTG	TGCTGCTGTC	CGGCTGGTGG	GTCTTGAGCC	ACCCCAACCA	720
CTGCAACGTC	ACCTACAAAG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCGTGG	GAAGTAGGCT	CCCAACCTTC	CTACTCCGAG	GCCTTGCTGG	ACCAGAGGCC	840
TGCGTGGTAT	GACCTTCTTC	CACCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACCTGCCC	CCCTACCGCT	CCCGGTCCGG	GAGTGCCAAC	AGTGCCAGCT	CCCAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACCG	CCACAGCCCG	GGGCAGCCTG	GCCCCAGGA	1020
GGGCACTGCT	GAGCCGAGGG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTTATTCCA	AAGTCCATAT	GGGTTAATCT	GCTCTGACTT	GTTGCCATTC	TAACAATTTC	1140
TGCTCATGGG	AGGCTCTTTA	AGCACCTGTA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACTATCTCT	GCATTCCCTT	CCCTCCCGAG	ACTTCAGAGA	TGTTTTCTCT	GOGTCTCAGT	1260
TGACATGATC	TGTTGTGCGT	CTTTCTGTCT	AGGTCACTCT	TCCCTTGGGA	CCGAGATCA	1320
CACCCCTCAT	TTTCACTTA	TTCTGTTTCT	GTTGGAGAGA	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGCAGGAGA	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTTGCGGA	TTTGGGTTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCACTGGATG	GTCAACCCCG	CAAAAAAATT	CCATTGAGC	1560
ATCAAAACCT	GCTTTGACAA	ATCCTATTTC	ATGCCCCGAG	TTCAAGAGAG	TCAGTGGCCA	1620
AAGAAAACCT	TGGACGTGAG	TAACAACCTT	CAGCAGTCGC	AACGTTATTT	TGGTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATTCTGGCTT	TAGAAATTTC	CCCAAGAAATG	1740
CTCATCTCTG	GAGCTTTCTT	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCAGG	1800
GAGCCCTTCC	CATGAGTTTA	TCCAAGTTCT	CAGCTCCTAA	AATGCAGGCT	GCCAAGACCC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACTTAC	CTGGTTTCTG	GACTGTCAAC	CTCCAGCTGC	1920
ACCTGCCCGT	AGCCAGAGAA	TGAGGACCTA	ACTTGAGTTG	GCCCAAGTCT	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCCA	CCAGCCCTGT	CTTGCTCAAT	CATGCAGCCT	CAACACTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAGATC	CTTTTACCT	GTGCATTGAG	ACTTGAGGAC	2100
ACTGTGTTCT	ATCAGAGTGG	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCCTGGCTCC	2160
CTGCACTGTG	CAGGCTCTTC	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGCT	AGGCGCTTCC	CAACATCCCA	GTAGTTTCTC	CTCTGAGACA	CTAGGGCAAG	2280
AGACAATTTC	GAGTCAAGAT	TTTCCATTTC	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAAACAGTG	TGTTTGTGTT	TTCCCTTCTA	GTTAAGGGAC	TATTTATATG	TGTATAGGAA	2400
AGCTGTCTCT	TTTTTGTGTT	TTCCCTTAA	AAGGTCCAAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCCCTGC	CCGCTGAGC	CCCGTGATAA	CAAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTGTGTC	ATTGTTGCAC	TTTGAGGTTA	TTATTATATCA	AGTTCTTGAA	GGAAGCAGAA	2580
AGAGGGGACTC	CTCTCTCCCT	CCGTGTATAG	TCTCTATGTT	TGTGCTAGTT	TTTCTTTTTT	2640
TTCTCTGTGT	CCAGTCAGCC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAACCACTT	2700
AGGTGTTGTT	TGGCAAGAAA	CCACACTGAC	TGATGAGGGG	TAAAAAGGAA	CCAGGTAGAG	2760
CCACTCCGGG	CAGCTGTAC	CCATTGAGAA	CTTCTTTCCG	CAGCTGAGAA	AATGTTACAT	2820

AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTGAG 2880  
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940  
 AAGCTAGCCA CTGGTATTTT GTTTTGTGTT AAAAAAAGAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAAGAA CTTTTGATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTCATCT CCTGTAGTC AGAAGGGCTT TATTCTCTCC TTTGATGGGG CCCCTTCTTC 3180  
 TTCTCGTGC TCTGGAAGTT GTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCACTCTAG GAAAAACAAA TGGTTTATAGT 3300  
 AGATAAGGGA TGCCTACTAA TGCTTTTAA AACCAACAG GGACATTTTT ATTATAGATT 3360  
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCACCAACA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACAG 3540  
 AAAATAGTCT CATCTCTTTT TTCTCAAAAT GAGATCCGTG TTTTATTTTA GCATTAAAT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGAGC CTCAAAGTTA ATGTAAGCTG 3720  
 GAAAGGTGT GTGTGTTGTC TTTTGTGTTT TGGTTAGGC TTGGTTTGT TTTTAAATTT 3780  
 TTATACCTTC TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840  
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTGGAAGAAA GTTTTAAACA CCACTTCGGG 3900  
 TGGGCGGCG GGGCCCAOCT AGGTACGGCG ACCACGGCGG CCCAACGGG ACCCCAGAG 3960  
 GAAACCTCG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCGGG 4020  
 GGAAACGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

# **A151 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MWLLGPLCLL LSSAAESQLL PGNPTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFPKSD 60  
 EKECPKAKSK CGPTFPFCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSF ICDGQNNQD NSDEESSCESS QEPGSGQVFP TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHHQRKR NNLATLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240  
 YVASQAQNA SEVGSPPSYR BALDQRPAW YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT ABPRDSEPSQ GTEEV

# **A152 DNA SEQUENCE**

Gene name: Transmembrane protease, serine 2 (TMPRSS2)  
 Unigene number: Hs.105807  
 Probeset Accession #: T48536  
 Nucleic Acid Accession #: NM\_005656.1  
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGATAAC AGCAAGATGG 60  
 CTTTGAAGTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAGACCAT GGATACCAAC 120  
 CGGAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180  
 CTCAGTACTA CCGTCCCCC GTGCCCCAGT ACGCCCCGAG GGTCTGACG CAGGCTTCCA 240  
 ACCCGTCTGT CTGCAAGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAGACTA 300  
 AGAAAGCACT GTGCATCAC TTGACCTGGG GCACCTTCCT CGTGGGAGCT GCGCTGGCCG 360  
 CTGGCTTACT CTGGAAGTTC ATGGGCAGCA AGTGTCTCAA CTCTGGGATA GAGTGGGACT 420  
 CCTCAGGTAC CTGCATCAAC CCTCTAACT GGTGTGATGG CGTGTACAC TGCCCGCGCG 480  
 GGGAGGACGA GAATCGGTGT GTTGGCCTCT ACGGAACCAA CTTCATCCTT CAGATGTACT 540  
 CATCTCAGAG GAATCTCTGG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600  
 GGGCGGCTG CAGGACATG GGCTATAAGA ATAATTTTAA CTCTAGCCAA GGAATAGTGG 660  
 ATGACAGCGG ATCCACCAGT TTTATGAAAC TGAACACAAG TGCCGGCAAT GTGATATCT 720  
 ATAAAAAACT GTACCACAGT GATGCTGTCT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT 780  
 TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGCG GGTGAGAGCG 840  
 CGCTCCCGGG GGCCTGGCCC TGSCAGGTCA GCCTGCACGT CCAGAACGTC CAGCTGTGCG 900  
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCAGTGGTGG GAAAAACCTC 960  
 TTAACAATCC ATGGCATTGG ACGGCATTTG CGGGGATTTT GAGACAATCT TTCTATGTTCT 1020  
 ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080  
 AGAACATGA CATTGCGCTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA 1140  
 AACCAAGTGT TCTGCCCAAC CCAAGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200  
 CCGGGTGGGG GGCACCGAG AGACCTCAGA AGTGTGAAC GCTGCCAAGG 1260  
 TGCTTCTCAT TGAGACACAG AGATGCAACA CGAGATATGT CTATGACAAC CTGATCACAC 1320  
 CAGCCATGAT CTGTGCGGC TTCTGTCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG 1380  
 GAGGGCTCTT GGTCACTTGG AACACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440  
 GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTCAAGG 1500  
 ACTGGATTTA TCGACAATAG AAGGCAACCG GCTAATCCAC ATGGTCTTGG TCCTTGAAGT 1560  
 CGTTTACAAA GAAAACAATG GGGCTGTTTT TGCTTCCCGG TGCAATGATT ACTCTTAGAG 1620  
 ATGATTCAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGCTGGCTT TGGCACTCTC 1680  
 TGCCACTAGT TGCAGGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTTGT 1740



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COGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGGGG TCAATTGTGG AAGGAAGAGG 1800
GTTGGAGGCT GCCCCATTG AGATCTTCTT GCTGAGTCTT TTCCAGGGGC CAATTTTGGA 1860
TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920
GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGGTAGTGG 1980
TCCCAGCCTT ACTTCACAAG GGGATTITGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
GATGGTGGCC AGAAATAAAG GGACAGCCCT TTCATGGGTG GTGACGTGGT AGTCACCTGT 2100
AAGGGGAACA GAAACATTTT TGTCTTATG GGTGAGAAAT ATAGACAGTG CCCTTGGTGC 2160
GAGGGAAGCA ATTGAAAGG AACTTGGCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
CAITGGGTGG GGCTCCTGGG AGGAGAGCTC AGCCTTCTCT CTCATCCTCC CTGACCTGTC 2280
TCCTAGCACC CTGGAGAGTG AATGCCTCTT GGTCCCTGGC AGGGCCGCAA GTTTGGCACC 2340
ATGTGGCCTT CTTCAGGCCT GATAGTCATT GGAAATTGAG GTCCATGGGG GAAATCAAGG 2400
ATGCTCAGTT TAAAGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
CTGAGTTCAA AGCCATCTT

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A153 Protein sequence:

Gene name: Transmembrane protease, serine 2 (TMPRSS2)  
 Unigene number: Hs.105807  
 Probeset Accession #: T48536  
 Protein Accession #: NP\_005647.1  
 Signal sequence: none found  
 Transmembrane domains: 85-107  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MALNSGSPPA IGPYYENHGY QPENFYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60  
 SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFPMG SKCSNSGIEC 120  
 DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGFNFILQM YSSQRKSWHP VQDDWNENY 180  
 GRAACRDMGY KKNFYSSQGI VDDSGSTFSM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240  
 CLACGVNLNS SRQSRIVGGE SALPGAWPWQ VSLHVQNVHV CGGSIITPEW IYTAACHVEK 300  
 PLNNPWHHTA FAGILRQSPM FYGAGYQVQK VISHPNYDSK TKNDIALMK LQKPLTFNDL 360  
 VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNL 420  
 TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIHWLIGDTS WSGSCAKAYR PGVYGNVMVF 480  
 TDWIIRQMK NG

A154 DNA SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039  
 Unigene number: Hs.129179  
 Probeset Accession #: AI694767  
 Nucleic Acid Accession #: AI694767  
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
CAGAGAGGCT GTATTTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
GGGGTCACAC ATTCCCTTCCA TACGGTTGAG CCTCTACCTG CCTGGTGGTG GTCCACAGTTC 120
AGCTTCTTCA TGATGGTGGG TCCCAATGGC AATGAATCCA GTGCTACATA CTTCATCCTA 180
ATAGGCCTCC CTGGTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCOCATT GTGCTCCCTC 240
TACCTTATTG CTGTGCTAGG TAACCTGACA ATCATCTACA TTGTGCGGAC TGAGCACAGC 300
CTGCATGAGC CCATGTATAT ATTTCTTTGC ATGCTTTTCA GCATTGACAT CCTCATCTCC 360
ACCTCATCCA TGCCCAAAAT GCTGGGCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT 420
GATGCTGTGC TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480
CTGCTGGGCA TGCCCTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGGC CCATGCCACA 540
GTACTTACGT TGCTCTGTGT CACCAAAATT GGTGTGGCTG CTGTGGTGGG GGGGGCTGCA 600
CTGATGGGAC CCCTTCTGTG CTTCATCAAG CAGCTGCOCT TCTGCGCTC CAATATCCTT 660
TCCCATCCTT ATGCTCTACA CCAAGATGTC ATGAAGCTGG CCTGTATGTA TATCCGGGTC 720
AATGTCGTCT ATGGCCTTAT GGTCTATCCT TCCGCCATTG GCTTGGACTC ACTTCTCATC 780
TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTTGGGCT TGACACGTGA AGCCCAGGCC 840
AAGGCATTGG GCATCTGCGT CTCTCATGTG TGTGCTGTGT TCATATTCTA GTTACCTTTC 900
ATTGGATTGT CCATGGTGCA TCGCTTTAGC AAGGCGGGTG ACTCTCCACT GCCCGTCATC 960
TTGGCCATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
ACAAAGGAGA TTGACAGCG CATCCTTCGA CTTTTCATG TGGCCACACA CGCTTCAGAG 1080
CCCTAGTGTT CAGTGATCAA ACTTCTTTTC CATTCAGAGT CCTCTGATTC AGATTTTAAT 1140
GTTAATCATT TGGAAAGACG TATTCAGAAA AAAAATTTC TTAATAAAAA TACAACTCAG 1200
ATCCTTCAAA TATGAAACGT GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTTCTTT 1260
GTTTCTTGGC TACATATAAT TATTAATAAC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320
TTTTCAITTT ACCATGCAAT CCAATCTAA ACTGCTTCTA CTGATGGTTT ACAGCATTCT 1380
GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAAGGAAAA 1440
TAAACACAGA ATGATATAAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA 1500
ACTCCCAACC ACATGGATC TCAGAAAAAT ACTGCTTCA AAATGACTTC TACAGAGAAG 1560
AAATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680
ATGGACCCCT TTTTCTCTAT TTAATTTTCT TATCAACCOCT TTAATTAGGC AAAGATATTA 1740
TTAGTACCCT CATGTAGCC ATGGGAAAAAT TGATGTTTCA TGGGGATCAG TGAATTAAAT 1800
GGGGTCATAC AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860
GGAAGAACTG TTAAGAGAC CAACAGGGTA GTGGGTTAGA GATTTCCAGA GTCTTACATT 1920
TTCTARAGGA GGTATTAAAT TTCTTCTCAC TCATCCAGTG TTGATTTTAG GAATTCCTTG 1980
GCAACAGAAC TCATGGCTTT AATCCCACTA GCTATTGCTT ATTGTCTGG TCCAATTGCC 2040
AATTACCTGT GTCTTGAAG AAGTGATTTC TAGGTTCACC ATTATGGAAG ATTCTTATTC 2100
AGAAAGCTCG CATAGGGCTT ATAGCAAGTT ATTTATTTT AAAAGTTCCA TAGGTGTTTC 2160
TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220
TGAAGATAAC ATTGGCCTTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGGG AATCTTCAGG 2280

```

5 ACCATGCTTT ATTGGGGCT TTGTGCAGTA TGGAAACAGG ACTTTGAGAC CGGAAAGCA 2340  
 ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGCTATTA CCAAGGGTTA 2400  
 ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACTC AAATTACATA 2460  
 TACTAAACA TGTGATCATA TATGTGGTAA GTTCAITTT CTTTTCATC CCTCAGGTTT 2520  
 CCTGATATGG ATTCTATNA CATGCTTCA TCCCTTTTG TAATGGATAT CATATTGGGA 2580  
 AATGCCATTT TAATACTTGT ATTTGCTGCT GGACTGTAAG CCCATGAGGG CACTGTTTAT 2640  
 TATTGAATGT CATCTCTGTT CATCATTGAC TGCTCTTTC TCATCATTTGA ATCCCCAGC 2700  
 AAAGTGCTTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTCA TCAAACTGTA 2760  
 10 TCCCTTCTGT GCTGAACACA TAGCCAGGCA ATTTTCCAGC CTTCTTTGAG TTGGGTATTA 2820  
 TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAAAGTGC ATGTGCAATT TTTATACCTG 2880  
 GCTCATAAAA CCTCTCCATG TGCAGCCTTT CATGTTGACA TTAATGTGA CTTGGGAAGC 2940  
 TATGTGTTAC ACAGAGTTAA TTAACNGAA AGGCCTGGNA ATTTTGTNN AANNAAACTG 3000  
 TGGCCNAGG GCCCNCAACC CTTTTNNNA ATTTGGCAAN NTCCACTTT GTANTTTGGT 3060  
 15 AAGGAGGCCA GTTGGATAAG TGAATAATAA AGTACTATTG TGTC

**A155 PROTEIN SEQUENCE**

20 Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039  
 Unigene number: Hs.129179  
 Protein Accession #: not available  
 Signal sequence: none found  
 Pfam domain: 7tm\_1 [43-293]  
 Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295  
 25 Cellular Localization: not determined

30 1 11 21 31 41 51  
 | | | | |  
 MVDPNNGNESS ATYFILIGLP GLEBAQFWLA FPLCSLYLIA VIGNLTIIYI VRTEHSLHEP 60  
 MYIFLOMLSG IDILISTSSM PKMLAIPWPN STTIQFDACL LQMPAHSLS GMESTVLLAM 120  
 AFDRYVAICH PLRHATVLT PRVTKIGVAA VVRGAALMAP LEVFIKQLPF CRSNILSHSY 180  
 CLHQDVVKLA CDDIRVNVVY GLIVIIISAIG LLSLLISFSY LLILKTVLGL TREQAQAFG 240  
 TCVSHVCAVF IPYVPPFGLS MVRFRSKRRD SPLPVILANI YLLVPPVILNP IVYGVKTKEI 300  
 35 RQRILRLFHV ATHASEP

**A156 DNA SEQUENCE**

40 Gene name: vasoactive intestinal peptide receptor 1  
 Unigene number: Hs.198726  
 Probeset Accession #: X77777  
 Nucleic Acid Accession #: NM\_004624.1  
 Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

45 TCGGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTGCCCCGCC TCACTCATGC 60  
 CTCCTCCTCC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGGTGGCGG GTTAAGCGGC 120  
 TGGTGGTGGC GGGCGCGCGG GCTCGCTCTC GGGGAGGCGG GGGCGGATCT CGCGGCGCAG 180  
 GCGGCGCGCG CGGAGGTGGG GTGCGCGCGC GGAGGCGGCT CGAGCTTCGT GCTGCGCGCT 240  
 CGCTCTTGGG CTCCTGCGTG CAGGAGGAGT GTGACTATGT GCAGATGATL GAGGTGCAGC 300  
 ACAAGCAGTG CCTGAGGAGG GCCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360  
 50 GGGACAACCT CACCTGCTGG CAGCCACCC CTGGGGGCCA GGTAGTTGTC TTGGCCTGTC 420  
 CCTCATCTT CRAAGCTCTT TCCTCCATTC AAGGCGCGCA TGTAAGCCGC AGCTGCACCG 480  
 ACGAAGGCTG GACGCACTTC GAGCCTGGCC CGTACCCCAT TGCTGTGGT TTGGATGACA 540  
 AGGCAGCGAG TTGCGATGAG CAGCAGACCA TGTCTACGG TTCTGTGAAG ACGGCTACA 600  
 CCATTGGCTA CGGCTGTGCC CTGCGCAACC TTCTGTGTC CACAGCTATC CTGAGCCTGT 660  
 55 TCAGGAAGCT CCACTGCACG CGGAATACA TCCACATGCA CCTCTTCAZA TCCTTCATCC 720  
 TGAGGGCTGC CGCTGTCTTC ATCAAGACT TGGCCCTCTT CGACAGCGGG GAGTCGGACC 780  
 AGTGCTCCGA GGGCTGCGTG GGTGTGAAG CAGCCATGGT CTTTTCCTCA TATTGTGTCA 840  
 TGGCTAACTT CTTCTGCGTG CTGGTGGAGG GCCTCTACCT GTACACCTCT CTTGCGGTCT 900  
 60 CCTTCTCTC TGAGCGGAAG TACTTCTGGG GGTACATCT CATCGGCTGG GGGTACCCA 960  
 GCACATTAC CATGCTGTCG ACCATGCGCA GGATCCATTT TGAGGATTAT GGTCTGCTCA 1020  
 GGTGCTGGGA CACCATCAAC TCCTCACTGT GGTGATCAT AAGGGGCCCC ATCCTCACCT 1080  
 CCATCTTGGT AAACCTTCAT CTGTTTATTT GCATCATCG AATCCTGCTT CAGAACTGC 1140  
 GGCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATACT AAGGCTAGCC AGGTCCACAC 1200  
 65 TCCTGCTGAT CCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CGGACAATT 1260  
 TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTGTGGG GTCTTCCAG GGTTTTGTGG 1320  
 TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380  
 GGGCTGGCA CTTGCAAGGC GTCTGCGGCT GGAACCCCAA ATACCGGCAC CGTGGGAG 1440  
 GCAGCAACGG CGCCAGTGC AGCAAGCAGG TTTCCATGCT GACCGCGTC AGCCAGGTG 1500  
 70 CCGCGCGCTC CTCCAGCTTC CAAGCGAAG TCTCCCTGGT CTGACCACCA GATCCGAGC 1560  
 CCAAGCGGCC CCTCCGCCCC CTTCCTACTC GCAGCAGAG CGGGGAGAC AGGCCTGCC 1620  
 GGGCGCGCCA GCGCGGCCCC TGGGCTGGGA GGTCTGCCCC GGGCCCTGG TCTGTGTTC 1680  
 GGACACTCCT AGAAGACCA GGCCTAGAGC CTGCTGGAG CGTTTCTAGC AAGTGAGAGA 1740  
 GATGGAGCT CTTCTCTGG AGGATGCAGG TGGAACTCAG TCATTAGACT CCTCTCCA 1800  
 75 AGGCCCCCTA CGCCAATCAA GGGCAAAAAG TCTACATACT TTATCTCTGA CTCTGCCCCC 1860  
 TGCTGGCTCT TCTGCCCAAT TGGAGGAAAG CAACCGGTGG ATCTCTCAAC AACACTGGTG 1920  
 TGACCTGAGG GCAGAAAGGT TCTGCCCGGG AAGGTCAACA GCACCAACAC CACCGTAGTG 1980  
 OCTGAAATTT CACCATTGCT GTCAAGTTC TTTGGGTAA GCATTACCAC TCAGGCATT 2040  
 80 GACTGAAGAT GCAGCTCACT ACCCTATTCT CTCTTACGC TTAGTTATCA GCTTTTAAA 2100  
 GTGGGTATT CTGGAGTTT TGTTTGAGA GCACACCTAT CTAGTGGTT CCCCAAGGAA 2160  
 GTGGAAGTGC CCTTGGGTCA GTCTGGTGGG AGGACGGTGC AACCCAAGGA CTGAGGAGAT 2220  
 CTGAAGTGG TGGGAAATGA GAAGGCAGCC ACCAGCGAAT GCTAGGCTCT GGACTAAGCC 2280  
 TACCTGCTCT CCAAGTCTCA GTGGCTTCAT CTGTCAAGTG GGACTCTGTC ACACGAGCCA 2340  
 TTCTTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTTGTCCACC 2400  
 CACCTATGTG CCAACTGGTG TAACTAGGCT CAGAGATGTG CACCCATGGG CTCTGACAGA 2460

5 AAGCAGATCC TCACCTCTGCT ACACATACAG GATTTGAAC T CAGATCTGTC TGATAGGAAT 2520  
 GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT AACACGCCAG ATCCTCTTGG 2580  
 TTATTTGTTT ACCACTTGTA TTATTAATGC CATTATCCCT GAATTCCTCT TGCCACCCCA 2640  
 CCCTCCCTCG AGTGTGGCTC AGGAGGCTC CATCTCATGT ATCATCTGGA TAGGAGCTG 2700  
 CTGGTCAACAG CCTCTCTGT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA 2760  
 CCTCTGCCAG AAGATCCCTT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT 2820  
 GGAAAAAAA AAAA

10 A157 Protein sequence:  
 Gene name: vasoactive intestinal peptide receptor 1  
 Unigene number: Hs.198726  
 Probeset Accession #: X77777  
 Protein Accession #: JC2195  
 Signal sequence: none found  
 15 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430  
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51  
 | | | | | |  
 MPPPPILLSLR RLGGWSAVT RLVVAAAGAR SRGGRGSRG AGGGGRGVA RRRRLRLRAA 60  
 RSLLGSSLOE ECDYVQMI EV QHKQCLEEAQ LENETIGCSK MWDNLTCWPA TPRGVVLA 120  
 CPLIFKLFSS IQGRVSRSC TDEGWHLEP GPYPIACGLD DKAASLDLQQ TMFYGSVKTG 180  
 25 YTIYGLSLA TLLVATAILS LFRKLHCTRN YIHMHLFISF ILRAAAVPIK DLALFDSGES 240  
 DQCEGSGVGC KAAMVFFQYC VMANFFWLLV EGLYLYTLA VSFFSERKYF WGYILIGWGV 300  
 PSTFTMWVIT ARIHFEDYGL LRCWDITNSS LWIILKGPIL TSILVNFILF ICIIIRILLQK 360  
 LRPPDIRKSD SSPYRSLARS TLLLIPLFGV HYIMFAFFPD NFKPEVMKVF ELVVGSEFGF 420  
 VVAILYCPIN GEVQAELEPK WRRWHLQGV L GWNPKYRHPG GGSNGATCST QVSMLTRVSP 480  
 30 GARRSSSFQA EVSLV

A158 DNA SEQUENCE  
 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 35 Nucleic Acid Accession #: AL133619  
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 | | | | | |  
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCGCCCA GCTGCGCGAC CCCGGGCTCT 60  
 OGGCGCGGCG GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG 120  
 CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGAGATG GCTGGCCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240  
 45 GAAACAAGG GTAGCGCGGC GCGGGGCGCT AGGCCGCGCC TGCCCTCCCA GGCACTCA 300  
 ACACTGCGCG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360  
 GGGGGAACAC AGGACGGGGA GCCCCTCCAG ACTGTCCTTG CCCACCTGGC TGCACTGGCC 420  
 CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480  
 AGCCGTGGCT GGAAGATGTT ATGCAGCCAA GCACAGCAGC TGCTGCTCTC GGGAAAGCCCA 540  
 50 GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCGAGA CCTCCCTCT 600  
 CCAAGTAGAG CTGAATGGG AAGGAACCCC TGGGACAGCC CTTGCCCTGC TAGATCTTTG 660  
 CTCAGATTG CTGCTGTGGC CAGGCCCAAG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTCTG TTCTTGCCA CTTGTCCAAG 840  
 55 GCATTTCCCC ATCTCTACAG CGGCCCCAC CAGGCCAGG ATCTTGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATTAATCTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960  
 TGGAGCCAGC CTGGGAACAT GCGAGCTGGG GCGATGCGTA GGGCTCTCCC TTCCAGGGA 1020  
 GACATGAGGA AGGGGGTTGA GGGAGGGGCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080  
 CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CTTGCACTGC TGGGGAAGCT 1140  
 60 GACAGGACAC GGAAGAGGC CATGCTTCC CTGGGACCT GCTGTTCAT GTGTCCCAAG 1200  
 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCTTC TGCTCCCTTG 1260  
 GGGCTCTGCT GGGTCTGCAT CAACGAGTGG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320  
 AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGG 1380  
 GGGGCTAGCG CCGCACTGT GCGCTCTCT GCGACAGGCC TCTCCATGTC AAGCTTCCAG 1440  
 65 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500  
 TCCTTCAACA AGCAAGATTG AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560  
 CCCTACTTTC ACACAGCAA GCTGGACAAA GTTCTTGGGG TACAAGGSCA GGCCAGAAAG 1620  
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCAACAGGSC 1680  
 AGGCAGATGG GGGCGGGGGC ACACCCCOCA ATGATCTTGC CCTTCCCTCT GCGAAAGCCC 1740  
 70 ACCACACTTA GGCAGTGGGA AGTGTCTATC CCGAGCTGTG GGAATACCAA CCTCTGCAG 1800  
 ACCGAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860  
 CCGAGGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920  
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CTTGTGGCGG AGCGTGCCAT CTTGCCCGCA 1980  
 CTGAAGCAGA CCCCAGAGAA CAACCTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040  
 75 AAAGGGGCCG TGCATGCTC AGTGCTTTGA

A159 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 80 Protein Accession #: T43457  
 Signal sequence: none found  
 Transmembrane domains: 303-322  
 Cellular Localization: not determined

1 11 21 31 41 51  
 5 MSGAGVAA GT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQPL 60  
 QQQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAH S TLPLPQHRNT AINSSTRLGS 120  
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180  
 GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSPPCAPSL PQIAAVARPR ISSPMALSPH 240  
 10 MLGAQGIWTH SIQGSPLAIW AATMGTKGGS RVLFPCHLSK ALPHPDGSGPH PAQDPGLWSQ 300  
 AHFPLSLGLG L TSGGHLTG WSQPNIAAG AVPRALPSQG DMEKGVGGP FPSRCNSSE 360  
 LFWAKGQPSR QPQPCSGADA DRTREEMLS LGTCCSMCPK PSCFPDGPSP NHLSTRASAPL 420  
 GARWVCINGV WVEPPGGPSPA RLKEGSSRTH RFGGKRGRLA GGSADTVRSP ADSLSMSSFP 480  
 SVKSISNSAN SQGKARPOPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGOARK 540  
 15 EKAASNAGA ACMGNSQHQG RQMGAGAHFP MILPLPLRKP TTLRQCSEVLI RELWNTNLLQ 600  
 TQELRLKSL LEGSQRPQAA PEZASPPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660  
 LKQTPKNFA ERQKRLQAMQ KRRLHRSVL

## A160 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated

Unigene number: Hs.79136

Probeset Accession #: U41060

Nucleic Acid Accession #: NM\_012319.2

Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 30 CTGTCGCCGA ATTGGGCAG AGACCGCGTG TCGGCGCTG GTAGAGATTT CTGAAGACA 60  
 CCAATGGGCC CGTGTGGAA CAAACCTGCG CGCGTGGCG GCGCGTGGGA CAACGAGGCC 120  
 GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTGATCCTG ACCTTTGCC 180  
 TCTCTGTAC AAATCCCTTT CATGAACATA AAGCAGCTGC TTCCCCAG ACCACTGAGA 240  
 AAATTAGTCC GAATTGGGAA TCTGGCATT AATGTGACTT GGCATTTCC ACACGGCAAT 300  
 35 ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360  
 TCAGAAAAAT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420  
 ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480  
 AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATATCATG 540  
 CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCAGA CCATGACTCA GATAGTTTCA 600  
 40 GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660  
 GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720  
 TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTTCC 780  
 CCAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCAATC AAAGAGCCGG GTGAGCCGGC 840  
 TGGCTGGTAG GAAACAAAT GAATCTGTGA GTGAGCCCG AAAAGGCTTT ATGTATTCCA 900  
 45 GAAACACAAA TGAAATCTCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960  
 GCATGGGCTT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTG CCAGCCATCA 1020  
 TCAACCAAT TGATGCTAGA TCTGTCTGA TTCAACAAG TGAAAGAAG GCTGAAATCC 1080  
 CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTGGTGG TTTTATAGCC ATTTCCATCA 1140  
 TCAATTTCTT GTCTCTGCTG GGGGTATCT TAGTGCTCT CATGAATCGG GTGTTTTCA 1200  
 50 AATTTCTCCT GAGTTTCTCT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTT 1260  
 TACACCTTCT TCCACTTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320  
 CAATGGAAAT GAAAAGAGGA CCACCTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380  
 GTGCTTATTT TGATTCACG TGGAAGGGTC TAACAGCTCT AGGAGGCGTG TATTTTCATG 1440  
 55 TTCTTGTGTA ACATGTCTCT ACATTTGATC AACAAATTTA AGATAAGAAG AAAAAGAAATC 1500  
 AGAAGAAAC TGAAATGAT GATGATGTGG AGATTAAAG GCAATGTGTC AAGTATGAAT 1560  
 CTCACCTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC 1620  
 GAGCAGACTC ACAAGAGCCC TCCCCTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAAG 1680  
 AAGAGGTGAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740  
 60 GGTGCAAGAA TAAATGCCAT TCACATTTCC AGCATACT OGGCCAGTCA GACGATCTCA 1800  
 TTCACACCA TCATGACTAC CATCATATTC TCCATCATCA CCACACCAAA AACCAACATC 1860  
 CTCACGTCA CAGCCAGGCG TACTCTGGG AGGAGCTGAA AGATGCGGCG GTGCCACTT 1920  
 TGGCTGGAT GGTGATAATG GGTGATGGCC TGCACATTT CAGCGATGGC CTAGCAATTG 1980  
 65 GTGCTGCTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGCT GTGTTCTGTC 2040  
 ATGASTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100  
 AGCAGGCTGT CCTTTATAAT GCATTGTGAG CCAATGCTGGC GTATCTGGA ATGGCAACAG 2160  
 GAATTTTAT TGCTCATTAT GCTGAAAATG TTTCTATGTG GATATTGCA CTTACTGCTG 2220  
 GCTTATTCAT TGTGTTGCT CTGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280  
 70 GTGACCATGG ATGTAGCGCG TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340  
 GTTTTGAAT TATGTTACTT ATTCCATAT TTGAACATAA AATCGTGTTC CGTATAAAT 2400  
 TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT 2460  
 AGGGAGATGA GTTTGTATGC TGTACTATGC AGGTTTAAA GTTAGTGGGT TTTGTGATTT 2520  
 75 TTGTATTGAA TATTGCTGTC TGTACAAAG TCAGTTAAAG GTACGTTTAA ATATTTAAGT 2580  
 TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640  
 TAAACAAGAG AATTGGCATG ACATGTTCTG TATGTTTCAG GAAAAAATGT CTTTAATGCT 2700  
 TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGAATTTA GGTCTCTGAA GAACTGCTGG 2760  
 TGTTTAGGAA TAAGAAATGT CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820  
 80 AGCAAAGAAA TAAAGAGAAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880  
 AAAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAAGG 2940  
 CAGAATTAGT ATAGAGTACA TTCAATTAAC ATTTTGTGCA GGATTATTTT CCGTAAAAAC 3000  
 GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060  
 AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTTGAA TTTCAAAATG 3120  
 TTTGTCGGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180  
 TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGTTT ACCTGTTTAT 3240  
 CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAATACT ACATAAGTA 3300  
 TCATTTGATT OGATTACAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTGT 3360

GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGCTCTGTG GCATTCTCTA 3420  
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

5

**A161 PROTEIN SEQUENCE**

Gene name: LIV-1 protein, estrogen regulated  
Unigene number: Hs.79136  
Protein Accession #: NP\_036451  
Signal sequence: 1-21  
Pfam domain: Zip[591-743]  
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745  
Cellular Localization: plasma membrane

10

15

1	11	21	31	41	51	
MARKLSVILI	LTFALSVTNP	LHELKAAAF	QTTEKISFNW	ESGINVDLAI	STRQYHLQOL	60
FYRYGENNSL	SVGEFRKLLQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHER	HSDHEHSDH	120
EHHSDEHDS	HMNHAASGIV	KRKALCPDHD	SDSSGKDPN	SQKGAHRPE	HASGRNRVKD	180
SVSASEVTST	VYNTVSEGT	PLETIETPRP	GKLFPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
NESVSEPRKG	FMYSRMTNEN	PQECFNASKL	LTSHGMGIQV	PLNATEFNIL	CPAILNQIDA	300
RSCLIHTEK	KAEIPPKTYS	LQIAWVGPI	AISIISPLSL	LGVLVPLMN	RVFFKPLLSF	360
LVALAVGTL	GDAPLHLLPH	SHASHHSHS	HEEPAMEMKR	GPLFSLHSSQ	NIEESAYFDS	420
TRKGLTALG	LYPMFLVEHV	LTLIKQFKDK	KKKQKQKPN	DDDVEIKKQL	SKYESQLSTN	480
EKVDTDRT	EGVLRADSQ	PSHFDSSQPA	VLEEEVIMIA	HAHPQEVYNE	VVPRGCKNKC	540
HSHFDHTLQ	SDDLIHSHH	YHILHSHH	QNHHPHSHS	RYSREELKDA	GVATLAWMVI	600
MDGLHNFSD	GLAIGAAFT	GLSSGLSTV	AVFCHPELPE	LGDFAVLLKA	GMTVQKAVLY	660
NALSAMLAYL	GMATGIFIGH	YAEVSMWIP	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720
RMGYFFLQNA	GMLLPGFIML	LISIFEKIV	FRINF			

30

**A162 DNA sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.87223  
Probeset Accession #: AA250737  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

35

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1	11	21	31	41	51	
CGCGGGGCGC	GGAGTCGGCG	GGGCCTCGCG	GGACGCGGGC	AGTGCAGAGA	CGCGGGGCGT	60
GAGGACGCGG	GAGCGCGGAG	CGCACGCGCG	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
GTGAAAGGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180
CATAACCAT	TGGCTCTGAG	CTATGACAAG	AGAGGAAACA	AAAAGTTAAA	CTTACAAGCC	240
TGCCATAAGT	GAGAAGCAAA	CTTCCTTGAT	AACATGCTTT	TGCGAAGTGC	AGGAAAATTA	300
AATGTGGGCA	CCAGAAAGA	GGATGGTGAG	AGTACAGCCC	CCACCCCGCG	TCCAAAGGTC	360
TTGCGTGTGA	AATGCCACCA	CCATTGTCCA	GAAGACTCAG	TCAACAATAT	TTGCAGCACA	420
GACGGATATT	GTTCACGAT	GATAGAAGAG	GATGACTCTG	GGTTGCCTGT	GGTCACCTCT	480
GGTTGCCTAG	GACTAGAAGG	CTCAGATTTT	CAGTGTGCGG	ACACTCCCAT	TCCTCATCAA	540
AGAAGATCAA	TTGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAGACCTT	ACACCTTACA	600
CTGCCTCCAT	TGAAAAACAG	AGATTTTGT	GATGGACCTA	TACACCACAG	GGCTTTACTT	660
ATATCTGTGA	CTGTCTGTAG	TTTGCTCTTG	GTCTTATCA	TATTATTTTG	TTACTTCCGG	720
TATAAAAGAC	AAGAAACAG	ACCTCGATAC	AGCATTGGGT	TAGAACAGGA	TGAAACTTAC	780
ATTCTCTCTG	GAGAAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGGA	840
TCAGGCTCC	CTCTGCTGGT	CCAAAGGACT	ATAGCTAAGC	AGATTGAGAT	GGTGAACAG	900
ATTGGAAGAG	GTGCTATGG	GGAAGTTTGG	ATGGGAAAGT	GGCGTGCGGA	AAAGGTAGCT	960
GTGAAAGTGT	TCTTCACAC	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
ACAGTGTGTA	TGAGGCATGA	AAACATTCTG	GGTTTCATTG	CTGCAGATAT	CAAAGGGACA	1080
GGGTCTCGGA	CCAGTTGTGA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
TATCTGAAGT	CCACCAACCT	AGACGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
AGTGGCTTAT	GTCATTACA	CACAGAAATC	TTTAGTACTC	AAGSCAAACC	AGCAATTGCC	1260
CATCGAGATC	TGAAAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAACCTG	CTGTATTGCT	1320
GACCTGGGCC	TGGCTGTATA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
ACTCGAGTTG	GCACCAAAAG	CTATATGCCT	CCAGAAAGTGT	TGGACGAGAG	CTTGAACAGA	1440
AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCCTCAT	CCTTTGGGAG	1500
GTGCTAGGA	GATGTGTATC	AGGAGGTATA	GTGGAAGAA	ACCAGCTTCC	TTATCATGAC	1560
CTAGTGCCCA	GTGACCCCTC	TTATGAGGAC	ATGAGGGAGA	TTGTGTGCAT	CAAGAAGTTA	1620
CGCCCTCAT	TCCCAAAACG	GTGGAGCAGT	GATGAGTGTC	TAAGGCAGAT	GGGAAAACCTC	1680
ATGACAGAA	GCTGGGCTCA	CAATCCTGCA	TCAAGGCTGA	CAGCCCTGCG	GGTTAAGAAA	1740
ACACTTGCCA	AAATGTGAGA	GTCCAGGAC	ATTAAACTCT	GATAGGAGAG	GAAAAGTAAG	1800
CATCTCTGCA	GAAAGCCAAC	AGGTACTCTT	CTGTTTGTGG	GCAGAGCAAA	AGACATCAAA	1860
TAAGCATCCA	CAGTACAAGC	CTTGAACATC	GTCTGCTTTC	CCAGTGGGTT	CAGACCTCAC	1920
CTTTCAGGGA	GCGACCTGGG	CAAGACAGAG	GAAGCTCCCA	GAAGGAGAGA	TTGATCCGTC	1980
TCTGTTGTGA	GGCGAGAGAA	CGTTGGGTA	ACTTGTTCAA	GATATGATGC	AT	

75

**A163 Protein sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.72472 / Hs.87223  
Probeset Accession #: AA250737 / U89326  
Protein Accession #: NP\_001194  
Signal sequence: 1-13  
Transmembrane domains: 128-144  
PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
Cellular Localization: plasma membrane

80

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1      11      21      31      41      51
|      |      |      |      |      |
5  MLLRSAGKLN VGTKKEDGES TAFTPRPKVL RCKCHHCPE DSVNNICSTD GYCFTMIEED 60
   DSGLPVVTSG CIGLEGSDFQ CRDTPIPHQR RSEECCTERN ECKNDLHPTL PPLKNRDFVD 120
   GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQSTRPRYS IGLEQDETYI PPGBSLRDLI 180
   EQSQSSSGSGS GLPLLQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVPFTTEAS 240
   WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
10  MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSRNIV KKNGTCCIAD LGLAVKFISD 360
   TNEVDIPNPT RVGTIKRYMPP EVLDESINRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420
   EBYQLPHYDL VPSDPSYEDM REIVCIKCLR PSFPNRNSSD ECLRQMGKLM TECHAHNPAS 480
   RLTAIRVVKCT LAKMSESQDI KL

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## A164 DNA sequence

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15  Gene name: ESTs
   Unigene number: Hs.157601
   Probeset Accession #: W07459
   Nucleic Acid Accession #: AC005383
20  Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
25  GACAGTGTTC GCGGCTGCAC GCTCGGAGS CTGGGTGACC GCGGTAGAAG TGAAGTACTT 60
   TTTTATTGCG AGACCTGGGC OGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
   CCTGGCGGTA GTTCTCCGGA CCTCAGCCGG GTCCGGTGGT GCCGCCCTCT CCCAGGAGAG 180
   ACAAACAGGT GTCCACGTG GCAGCCGGCG CCCGGGCGCC CCTCCTGTGA TCCCGTAGCG 240
   CCCCTGCGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGCAC CGAGCGCTGG 300
   TGCGCGCTCT CCTTCGGTTA TATCAACATG CCCCTTTTCC TGTGCTGGA GGCCGTCTGT 360
30  GTTTTCCTGT TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAACAAA 420
   GAAACCATCT GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
   ATCATGTTTC TGTATAGTGG GTCTAACAGC GTCCGGAAAG GGAGCTTTGA AAGGTCCAG 540
   CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CGAGAGAGGT CAGAGTGGGA 600
   GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCTCT TGAATTCATT TTCAACCCAA 660
35  CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
   CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC 780
   CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAAGGGG ATGTGGCACT GCCATCCAG 840
   CAGCTGAAGG AAGGGGTGTG CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900
   GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGC TGCTGTGGGC TGAGCAGGTG 960
40  GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
   ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGCTCCGG 1080
   GAGTTGCTCG GCAATGCCCC ATGCTGGAGA GGATGCGGCG GGACCTTTGC GGTGCTGGCT 1140
   GCACACTGTG CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGTC CACCTGCTAC 1200
   AGGACCACTT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
45  CCAGAAGGAC TGGACGGCTA CCAAGTGCCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
   TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCCGACTCT TCTTCTGCTT GGACAGCTCT 1380
   GCGGGCACC A CTCTGGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
   GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
   CTGGTGGCGG TGCTGTGGGG GGAGTACCAG GATGTGCTG ACCTGGTCTG GAGCCTCGAT 1560
50  GGCAATCCCT TCCGTGGTGG CCCACCTCTG ACGGCGAGTG CCTTGCAGCA GCGGCGAGAG 1620
   CGTGGCTTGG GAGAGGCCAC CAGGACCGGC CAGGTAGAGT GGTGTTTGTG 1680
   CTCACCTGAT CACACTCCGA GGATGAGGTT GCGGGCCGAG CGGCTCAGCG AAGGGCGCGA 1740
   GAGCTGCTCC TCTGGGTGTG AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800
   GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATTCCT 1860
55  GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGTT GCCGACACA AGCCCTGGAC 1920
   CTCGTCTTGA TGTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
   AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGC 2040
   CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCCAACCGG 2100
   GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGTGGG CTGAGCCGGC 2160
60  ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220
   GTCGCCAAGG CTGTGGTGGT GCTCAGAGG GGGAGAGGCG CAGAGGATGC AGCCGTCTCT 2280
   GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGCGTGGG GCCTGTCTTA 2340
   AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CGGATTCCC TGATCCAGST GGCAGCTTAC 2400
65  GCCGACCTGC GGTACCAACA GGACGTGCTC ATTGATGGC TGTGTGAGAG AGCCAAGCAG 2460
   CCACTCAACC TCTGCRAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CTGACAGAAT 2520
   GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC OCCACTGCGA GAACCGTGAG 2580
   TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GATGGATTTC TTGAGACGCC CTGAGGCAC 2640
   ATGGCTCCCG TGCAGGAGGG CAGCAGCGGT ACCCTCCCA GCAACTACAG AGAAGGCGCTG 2700
70  GGCAGTAAA TGGTGCCTAC CTCTGGAAT GTCTGTGCC CAGGTCCTTA GAATGTCTGC 2760
   TTCCCGCGGT GGCAGGAGCC ACTATTCTCA CTGAGGAGG AGGATGTCCC AACTGCAGCC 2820
   ATGCTGCTTA GGCACAAGAA AGCAGCTGAT GTCAOCCACA AAGATGTTTG TTGAAAAGTT 2880
   TTGATGTGTA AGTAATACCC CACTTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940
   CTGCCACCTT CCCTTTGAGG ATAAACAAGG GGTCTGAAAG ACTTAAATTT AGCGGCTGGA 3000
75  GGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCGAGCAG 3060
   AGGCTTTTAC TAGAGCATCC TTTGAGCGGC GAAGGCCAAG GCCTTTCAAG ATGGAAGACA 3120
   GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAGGGGG 3180
   CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCTTTTGT GTGTGGAAGA GACTTGGAAA 3240
   GGTCTCAGAG TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGCGGA GGGCTGAGT 3300
80  TGTGCATGGG CCCAGGCTCG GAGGGCCAGG TAAATTCGTT CTGAGTCGTG AGCAGTGTC 3360
   ACCTTGAAGG TCTTC

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A165 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLEAV CVPLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSPERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEPLDLSFST QQEVKARIKR 120
MVFKGGRITET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRPFRN EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVPLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVVFVRKFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVNSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVS 480
EAVRAELSEI TGSPKHMVYV SDPQDLFNQI PELQGLCSR QRPGRTOAL DLVFMLDISA 540
SVGPENFAQM QSEVRSICALQ FEVNPQVTVV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRRNGI 660
SVLVVGVGPV LSEGLRRLAG PRDSLIVAA YADLRYHQDV LIENLGEAK QPVNLCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAVPQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

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A166 DNA sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR  
 Unigene number: Hs.37744  
 Probeset Accession #: AA011176  
 Nucleic Acid Accession #: AF272890  
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
TGCTACCCCG GCCCGGGCTT CTGGGGTGTG CCCCAACCA C GCGCCAGCCC TGCCACACCC 60
CCGCGCCCGC GCCTCCGCG C TC GCGCATGG GCGCGGGGT GCTGCTCTG GCGGCTCTCG 120
AGCCCGGTAA CCTGTGCTCG CCGCACCOC TCCCGCAOCG CGCGGCCACC GCGCGCGCGC 180
TGCTGTGTGC CGCGTGGCG CCGGCTCTGT TGCTGCTTCC CGCCAGCGAA AGCCCGGAGC 240
CGCTGTCTCA GCACTGGACA GCGGCGATGG GTCTGCTGAT GCGGCTCATC GTGCTGTCTA 300
TCGTGGCGGG CAATGTGCTG GTGATCTGG CCACTGCCAA GACGCGCGGG CTGCAGACGC 360
TCACCAACCT CTTCATCATG TCCCTGGCCA GCGCGGACCT GGTATGCGGG CTGCTGGTGG 420
TGCCGTTTCGG GGCACCATC GTGGTGTGGG CCGGCTGGGA GTACGGCTCC TTCTTCTGG 480
AGCTGTGGAC CTGAGTGGAC GTGCTGTGCG TGAOGGCCAG CATCGAGACC CTGTGTGTCA 540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCAAGAG CTGCTGACGC 600
GCGCGCGGGC GCGGGGCTCT GTGTGCAOCG TGTGGGCCAT CTGCGGCTGT GTGTCTTCC 660
TGCCCATCTC CATGCACTGG TGGCGGGCGG AGAGCGAOGA GCGCGCGCGC TGCTACAACG 720
ACCCCAAGTG CTGCGACTTC GTACCAACCC GGGCCTACGC CATCGGCTCG TCCGTAGTCT 780
CCTTCTAOGT GCCCCTGTGC ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCGAGGCC 840
AGAAGCAGGT GAAGAAGATG GACAGCTGCG AGCGCGGTTT CCTCGGCGGC CCAGCGCGGC 900
CGCCCTCGCC CTGCGCTCGC CCGCTCCCGC GCGCGCGGCC CCGCGCGGCC 960
CGCGCGCGGC CGCGGCCACC GCCCGGCTGG CCAACGGGCG TCGGGTAAAG CGGCGGCCCT 1020
CGCGGCTCGT GGCCTTACGC GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
TCTTCAOGCT CTGCTGGGCT CCGTCTTCTC TGGCCAAAGT GGTGAAGGCG TTCCACCGCG 1140
AGCTGTGTGC CGACCGGCTC TTGCTCTTCT TCAACTGGCT GGGCTAAGCC AACTCGGCTC 1200
TCAACCCATC CATCTACTGC CGCAGCCCGC ACTTCGCAA GGCCTTCCAG GACTGCTCT 1260
GCTGCGCGCG CAGGCTGTGC CGCGGGGCGC ACGCGACCCA CGGAGACCGG CGCGCGGCTC 1320
CGGCTGTCTT GCGCGGGGCC GACCCCGCGC CATCGCCCGG GCGCGGCTCG GACGACGAG 1380
ACGAAGATGT CGTGGGGGCC ACGCGCGCGC CGCGGCTGCT GGAGCCCTGG GCGGCTGCA 1440
ACGCGGGGCG GCGGGCGGAC AGCGACTCGA GCCTGGAGCA GCGGTGCGCG CCGGCTTGG 1500
CCTCGGAATC CAAGGTGTAG GGCCTGCGCG GGGCGCGCGA CTCCGGGCAC GCTTCCAG 1560
GGGAACGAGG AGATCTGTGT TTAATTAAAG COGATAGCAG GTGAACCGA AGCCCAACAT 1620
CCTGCTCTGA ATCATCCGAG GCAAAGAGAA AAGCCACGGA CCGTTGCACA AAAAGGAAAG 1680
TTTGGGAAGG GATGGAGAG TGGCTTGTG ATGTTCTTGT TTG

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A167 Protein sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR  
 Unigene number: Hs.37744  
 Protein Accession #: AA011176  
 Signal sequence: none found  
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248  
 Pfam domain: 7tm\_1 [75-377]  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MGAGVLVLGA SEPNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQWTAG 60
MGLMALIVL LTVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMGLL VVPPGATIVV 120

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5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

WGRWEYGSFF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLL TRARARGLVC 180  
 TWVAISALVS<sup>~</sup> FLPIIMHWMR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSPYVPLCIM 240  
 AFVYLVRVFE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAAATAP 300  
 LANGRAGRKR PSRLVALREQ KALKTLGIIM GVFTLCNLFP FLANVVIKAPH RELVPDRLFV 360  
 PFNWLGYANS AFNPPIIYCRS PDKRAPOQL LCCARRAARR RHATHGDRPR ASGCLARPGP 420  
 PPSPGAASDD DDDDVVGATP PARLLEPWAG CNGGAASD SSLDEPCRPG FASESKV

Al68 DNA sequence

Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GGCGTCCGCG CACACCTCCC CGGCGCGCGG CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60  
 CGGCAACCGC TGAGCCATCC ATGGGGGTGG CGGGCCGCAA CCGTCCCGGG GCGGCCTGGG 120  
 CGGTGCTGCT GCTGCTGCTG CTGCTGCCGC CACTGCTGCT GCTGGCGGGG GCCGTCCCGC 180  
 CGGTGCGGGG CCGTGCCCGG GGGCCGCGAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240  
 ATGACTGCCA TGCCGACGCG CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA 300  
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360  
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACCTGTT 420  
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGCTT TGATGTGGAC GAGTGCCTGG 480  
 AGAACAAATG CCGCTGCCAG CATACCTGTG TCAAGTTCAT GGGGAGCTAT GAGTGTCTGT 540  
 GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG 600  
 GCCTGAGCTG CATGAATAAG GATCAGCGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660  
 GCAGCGTCGG CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780  
 GCGGAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840  
 AGCGAGAGGG CACTGTCTCG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900  
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAT GGAGGCTGTG 960  
 ACAGCACTG TAAGATACT TCGACAGGTG TCCACTGCAG TTGCTCTGTT GGATTCACTC 1020  
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080  
 GTGATCATTT TGCAAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAAGGATTTA 1140  
 AATTATTAAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200  
 GTGACCAACG CTGCATCAAC CACCCTGGCA CATTTGCTTG TGCTTGCAAC CGAGGCTACA 1260  
 CCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320  
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCGGGTACA 1380  
 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT 1440  
 CACCCCGGTG GTCCCTGCAC TGGGTAAGA GTGGTGGAGG AGACGGGTGC TTCTCAGAT 1500  
 GTCACTCTGG CATTCACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA 1560  
 AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTTCCCGAG GGTCTGCGAC 1620  
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680  
 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT 1740  
 TTATCACTGT TGAGTTTGA CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTTGTGACC 1800  
 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860  
 AGGCGGTCCA CAGGAGGACG TTTCACTCC AGCTCTCAGG CATGAACCTC GACCTGGCTA 1920  
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCGT TGGAGTGGGG CAGGCTCATG 1980  
 CAGAAAAACA ATGTGTGAGT TGCAGGCTG GGACCTATTA TGATGGAGCA CGAGAAOCTG 2040  
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TTGGAACCAT 2100  
 GCCCAAGACC AGGAAATTTCT GGGGCCCTGA AGACCCGAGA AGCTTGGAAT ATGTCTGAAT 2160  
 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGACCTT TGCCAGCTCT 2220  
 GTGCCCTGGG CACGTTCGAG CCGTGAAGCTG GTCGAACTTC CTGCTTCCCT TGTGGAGGAG 2280  
 GCCTTGCCAC CAACATCTAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340  
 GTTCACCTGG ACATTTCTAC AACACCCACA CTCACCGATG TATTCGTTGC CCAGTGGGAA 2400  
 CATACCAGCC TGAATTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTAOGACTG 2460  
 ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520  
 GAGATTTCAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACCCG 2580  
 AGTGTACGTG GACCATCAAC CCACCCCCCA AGGCGCGCAT CCTGATCGTG GTCCCTGAGA 2640  
 TCTTCTGCCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGGGAAA ACCTCTTCAT 2700  
 CCATTTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCATCT GCCTTCACCT 2760  
 CCAGGTCAA GAAGCTGTGG ATTCAATTCA AGTCCAATGA AGGGAACAGC GCTAGAGGCT 2820  
 TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCGAGA ACTCATTGAA GACATAGTTT 2880  
 GAGATGGCAG GCTCTATGCA TCTGAGAAC ATCAGGAAAT ACTTAAGGAT AAGAACTTTA 2940  
 TCAAGGCTCT GTTGTATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCGAGG 3000  
 AGTCCCGAGA GATCGTTTCA AGATCGTTCA TCOGATTGCT ACGTTCCAAA TGTGCCAGGT 3060  
 TTTTGAGACC TTACAAATGA CTCAGCCACG GTGCCACTCA ATACAAATGT TCTGCTATAG 3120  
 GGTGGTGGGG ACAGAGCTGT CTTCTCTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCTCT 3180  
 CGGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATAAT TTGGTAAATT 3240  
 GAATCTGGTT TTCTTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300  
 GACTCTTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CCGGCTGGCT GAGCTGCACT 3360  
 TTGGTCAGCC TAGGTGAGAC TCACTGTGCC TTCTGGGGTC TTAATCTTCC TCAAGGAGTC 3420  
 TGATGTGAAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCTCTAGC 3480  
 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGACGG CTCTGACCG GCAGAACAGG 3540  
 CAAGAGGGGA GGAAGGAGA CCCCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG 3600  
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660  
 AGTTCTAAGC AGTGTCTGTG AAAAAAATA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720  
 AGCACTTCTG GAGACAT

Al69 Protein sequence

Gene name: CEGP1  
 Unigene number: Hs.222399



Probeset Accession #: AA256485  
 Protein Accession #: CAB92285  
 Signal sequence: 1-31  
 Transmembrane domains: none  
 PFAM domains: EGF-like\_domains [49-84,132-167,177-213,286-321,407-442] CUB\_domain [809-918]  
 Cellular Localization: may be secreted

10 1 11 21 31 41 51  
 MGVAGNRNRP AANAVLLLLL LPPPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60  
 LCQNTPTSYK CSCRPYQGE GRQCEDIDEC GNEINGGCVH DCLNIPGNVYR CTCFDGFMLA 120  
 HDGHNCLDVD ECLENNNGCQ HTCVNVMSY ECCCCKEGFPL SDNQHTCIHR SEEGLSCHMK 180  
 DHGCSHICKE APRGSVACBE RPFELAKNQ RDCILTCNHG NGGQCHSCDD TADGPECSCH 240  
 15 PQYKMGHTDGR SCLEREDTVL SVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCTCKDT 300  
 STGVHCSCFPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360  
 SQQDVDECSL DRPCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGQQQVCVN 420  
 TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480  
 20 SSDVTIRTIS VTFKLNEGKC SLKNAELFPE GLRPALEPKH SSVKESPRYV NLTCSSGQKV 540  
 PGAPGRPSTP KEMFITVSEF LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600  
 FHLQLSGMNL DVAKKPPRPS ERQAESCQVG QGAENQCQVS CRAGTYVDGA RERCILCPNG 660  
 TFFNEGGQMT CEPCKPRPGNS GALKTPRAWN MSECGLCQP GEYSADGFAP CQLCALGTFO 720  
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC FVGTYQPEFG 780  
 25 KNNCVSCPGN TTDFDGSIN ITQCKNRRCS GELGDFGTGYI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRILIV VPEIFLPIED DGDYLVMRK TSSNSVTTY ETCQTYERPI AFTSRSKKLW 900  
 IQFKSNEGNS ARGFQVFPYT YDEYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960  
 LAHPQNYFYKY TAQESREMPF RSFIRLLRSK VSRFLRPYK

30 A170 DNA sequence  
 Gene name: DEME-6 protein (KIAA0452)  
 Unigene number: Hs.125783  
 Probeset Accession #: AL039402  
 Nucleic Acid Accession #: AF007170  
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

35 1 11 21 31 41 51  
 AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60  
 CTGGACCACT GCATGACCGC CTGGACCTC TTCTCTACCA ACCAGTCTCT AGAAGCACTC 120  
 40 AGCTACTCTA AGCCCAAGAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180  
 CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240  
 ATGAAGGAGG CACAGATGCT GTGTCAAGG CACCGAGGA AGTCTTCTGT AACAGATTCC 300  
 TTCAGCAGCG TGGTGAACCG CCCCACTCTG GGCCTAATTCA CTGAAGAAGA AATCCACGCT 360  
 GAGGTCTGCT ATGCAGAGTG CCTGCTGCAG CGAGCAGCCC TGACCTTCTT GCAGGACGAG 420  
 45 AACATCTGCA GCTTCAATCAA AGGCGGCATC AAAGTTCGAA ACAGCTACCA GACCTACAAG 480  
 GAGCTGGACA GCCTTGTTCA GTCTCACAA TACTGCAAGG GTGAGAACCA CCGCACTTTT 540  
 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTACT 600  
 AGGATCCTGA GGCCTGTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660  
 CAGCTGGAGG AGGGAGCGTG AGGGCAGAGC TTCCGCTCTG TGCTCTGTGT CATGCTCTCTG 720  
 50 CTGTGCTACC ACCTTCTCCT CACCTTCGTG CTGGTACTG GGAACGTCAA CATCGAGGAG 780  
 GCGGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCTTA AGGGTGCCAT CTCTCTGTTC 840  
 TTTGCAAGGA GGATTGAAGT CATTAAAGGC AACATTGATG CAGCCATCG GCGTTTCGAG 900  
 GAGTGTCTGT AGGCCAGGCA GCACTGGAAG CAGTTTCAAC ACATGTGCTA CTGGGAGCTG 960  
 55 ATGTGTGTCT TCACCTACAA GGGCCAGTGG AAGATGTCTT ACTTCTACGC CGACCTGTCT 1020  
 AGCAAGGAGA CTGCTGTGTC CAAGGCCACC TACATTACCA TGAAGGCCGC CTACCTCAGC 1080  
 ATGTTTGGGA AGGAGGACCA CAAGCCGTTT GGGGACGACG AAGTGAANTT ATTTGAGGCT 1140  
 GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200  
 CGGAAGTCCC GGCGTACTT CTCTCTCAAC CCTATCTGCG TGCCAGTGCC TGCTCTGGAA 1260  
 60 ATGATGTACA TCTGGAACGG CTACGCGGTG ATTGGGAAGC AGCGGAACT CACGGATGGG 1320  
 ATACTTGAGA TTATCACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCGAGA GAACGAGTAC 1380  
 TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440  
 CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500  
 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCCTGCTGCT TATGGAGCAA 1560  
 65 GACAGAAAGC AAGAGGCCAT CAACTTTTG GAATCTGCCA AGCAAACTA CAAGAATTAC 1620  
 TCCATGGAGT CAAGGACACA CTTTCAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680  
 CTAGAGAACA GCAGCAGATC CATGCTCTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGTT 1740  
 CGGGCTGGA AGACAGAGAG AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCTT 1800  
 CCCCTGCCCC TGCCCTGCTT TTGGGGTCCA CGGCACTCC AGTTGGATGG CACAACATAG 1860  
 70 TGTATCCGTG CAGAAGCGGA GCTGGCATT TCAACAGTGT AGCCAAGGGC CTTTGCCAAG 1920  
 GGCAGAGCAG GTGGAGCCCT CTGCTGCCCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980  
 GTGATGTTTA AGAAGATGTA TGAACAGTTT ACATTTTCTT TAGAATAACA TTGATGGGAT 2040  
 CACAGTTGGC TTTAAAAACC AACAAACATC AACCACTGT AAGTCTTTGT CTTCACCTAT 2100  
 75 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAAATG CTTTTCAAAT 2160  
 TCAGCAAGTT CTCAGCTTGT GTGAAGGAAG GTCTTCTAGA GGACCTGAGG AATGCCTGGG 2220  
 AGAGGCTAAG CCTCAGGCTT CATGCTTCTT GGGGTGAGG ATGAGGATGT ACACAGACAC 2280  
 CCCTACTCTT ACTACTCACA CTTCAATTCA CTCCTTTTGT AAATTTCCAA TTTAAAAATC 2340  
 AAGCAAGTCT TTTTAGTGAG ATAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400  
 AGTAGAAAT GCCAGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460  
 80 AAATTTGGGG GGCAGGAGGA GGTCTCTAGA ATCCAGTCTG TATCTTGTCT GTATGCCAAA 2520  
 CTGAAACCACT TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTCCAAGGTA 2580  
 CATTGTCTTA CTGACAGCAT TTTTGTAAAA ACTGTTATTC TTGAAAAAAA AAAAAAATAA 2640  
 AA

A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)  
 Unigene number: Hs.125783  
 Probeset Accession #: AL039402  
 Protein Accession #: AAC39582  
 Signal sequence: none  
 Transmembrane domains: 210-226  
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51  
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 MTALDLFLTN QFSEALSYLK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMKEA 60  
 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEBIHAEVCY AECLLQRAAL TFLQDENMVS 120  
 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHPEGGV KLGVGAFNLT LSMPLPTRILR 180  
 15 LLEFVFGSGN KDYGLQLLEE GASGHSFRSV LCVMLLLCYH TFLTFLVLGTG NVNIEEAERL 240  
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEECC E AQHWKQFHH MCYWELMWCF 300  
 TYKGQWMSY FYADLLSKEN CWSKATYIYM KAAYLMSFGK EDHKPFQDDE VELFRAVPG 360  
 KLKIAGKSLP TEKPAIRKSR RYFSSNPISL PVPALMMYI WNGYAVIGKQ PKLTDGILEI 420  
 ITKAEEMLEK GPENYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480  
 20 LIPNALLELA LLLMEQDRNE EAIKLLESAK QNYKYNYSMB RTHFRIQAAT LQAKSSLENS 540  
 SRSMVSSVSL

25 A172 DNA sequence  
 Gene name: EST  
 Unigene number: Hs.200102  
 Probeset Accession #: AL117406  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51  
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ATGACTAGGA AGAGGACATA CTGGGTGCCC AACTCTTCTG GTGGCCTCGT GAATCGTGCC 60  
 ATGACATAG GCGATGACAT GGTTCAGGA CTTATTATATA AAACCTATAC TCTCCAAGAT 120  
 35 GGCCCTCGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCACCG 180  
 TGGGGGAAGT ATGATGCTGC CTTGAGAAAC ATGATTCCTT TCGTCCCAA GCCGAGGTTT 240  
 CCTGCCCCCC AGCCCTCGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC 300  
 ACCCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCTCCACTG 360  
 TCAGTCCATG ATGCCTCAGA CAAAAATGTC CAAAGGCTTC ACCTCCTTTG GGAAGAAGAA 420  
 40 GTCTCAAGGC GAGGGATGGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480  
 ACAAGGTGGA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATGTCAGG TGTACTCGGG 540  
 CCAATATTGA TTATACCAA GATCCTGGAA TATTAGAAG AGCAGTGGG GAATGTTGTC 600  
 CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC 660  
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 45 TTTGACCTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780  
 ATCAGCTTCT TCACCGGTGA TGTAACTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840  
 GTACTGATCA CTTGCGCATC GCTGGTCATC TGCAGCATTT CTCTCTACTT CATTATTGGA 900  
 TACACTGCAT TTATTGCCAT CTTATGCTAT CTCTGCTTCT TCCACTGGC GGTATTCTAG 960  
 50 ACAAGATGAG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGGACCA GGCATCCGT 1020  
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 ATGGCCTTCA GCATGCTGGC CTCTTGAAT CTCTTGGC TGTCAGTGT CTTGTGCTCT 1200  
 ATTGCAATGA AAGCTCTCAC GAATTCAGG TCTGCAATGA TGAGGTTCAA GAAGTTTTC 1260  
 CTCACGAGA GCCCTGTTT CTATGTCCAG ACATTAACA ACCCCAGCAA AGCTCTGGTC 1320  
 55 TTTGAGGAGG CCACCTTGTG ATGGCAACAG ACCGTGCTCG GGATGCTCAA TGGGGCACTG 1380  
 GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCCTAGAGA TGCCCTCGGG 1440  
 CCAGAGGAAG AAGGGAACAG CCTGGGCCA GAGTTGCACA AGATCAACCT GGTGTGTGCC 1500  
 AAGGGATGTA TGTTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAGAGCAG CCTGTGTGTA 1560  
 60 GCCATCCTGG AGGAGATGCA CTGTCTGAG GGTCTGGTGG GGGTGCAGGG AAGCCTGGCC 1620  
 TATGTCCCC AGCAGGCCCTG GATCGTCAGC GGAACATCA GGGAGAACAT CCTCATGGGA 1680  
 GGCATATAT ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCTT GAATGGGGAC 1740  
 CTGGAACCTC TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCTT CAACCTCTCT 1800  
 GGGGGGCAGA AACAGAGGAT CAGCCTGGCC CGCGCGTCT ATTCCGACCG TCAGATCTAC 1860  
 65 CTGCTGGAGC ACCCCTGTGC TGCTGTGGAC GCCACGTTGG GGAAGCATAT TTTTGAGGAG 1920  
 TGCAATTAAGA AGACACTCAG GGGGAAGACG GTGCTCTCGG TGACCCACCA GCTGCAGTAC 1980  
 TTAGAATTTT GTGGCCAGAT CATTTTGTG GAAAATGGGA AAATCTGTGA AAATGGAAC 2040  
 CACAGTGAGT TAATGCAGAA AAAGGGGAAA TATGCCAAC TTATCCAGAA GATGCACAA 2100  
 GAAGCCACTT CGGACATGTT GCAGGACACA GCAAAGATAG CAGAGAAGCC AAAGGTAGAA 2160  
 70 AGTCAGGCTC TGGCCACCTC CTGGAAGAG TCTCTCAACG GAATGCTGT GCGGAGCAT 2220  
 CAGCTCACAC AGGAGGAGGA GATGGAAGAA GGCTCCTTGA GTTGGAGGGT CTACCAACAC 2280  
 TACATCCAGG CAGCTGAGG TTACATGGTC TCTTGCAATA TTTTCTTCT CGTGGTGTG 2340  
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 GGGACCAATA GCAGCCGAGA GAGCAATGGA ACCATGGCAG ACCTGGSCAA CATTGCAGAC 2460  
 75 AATCCTCAAC TGTCCTTCTA CCAGCTGGTG TACGGGCTCA ACGCCCTGCT CCTCATCTGT 2520  
 GTGGGGGTCT GCTCCTCAGG GATTTTCACC AAAGTCAAGA GGAAGGCATC CAGGGCCCTG 2580  
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 TATTATATGA TGTTCAGAA GGCCATCGGT GTGTTCAAGA GACTGGAGAA CTATAGCCGG 2880  
 TCTCCTTTAT TCTCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGTCTAT 2940  
 GGAAGAACTG AAGACTTCAT CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC 3000  
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 CTTGTGACCT TGGCTGTGTC CCGTGTCTG GCTTTTGGCA TTTCTCCAC CCCCTACTCC 3120

5 TTTAAAGTCA TGGCTGTCAA CATCGTGTCTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC 3180  
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 AAGATGTGTG TCTCGGAAGC TCCTTTACAC ATGGAAGGCA CAAGTTGTCC CCAGGGGTGG 3300  
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 ACOGTGCTTC ACGGCATCAA CCTGACCATC GCGGCGCAAG AAGTGGTGGG CATCGTGGGA 3420  
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 GCAGGCCGGA TTCTCATTTGA CGGOGTGGAC ATTTGCAGCA TCGGCTTGA GGACTTGGCG 3540  
 TCCAAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC 3600  
 10 CTAGATCCCT TTGACCGTCA CACTGACCAG CAGATCTGGG ATGCTTGGG GAGGACATTC 3660  
 CTGACCAAGG CCATCTCAAA GTTCCCAAA AAGCTGCATA CAGATGTGGT GGAAAAAGGT 3720  
 GGAAACTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGGCTGT GCTTCGCAAC 3780  
 TCCAAGATCA TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCCCTG 3840  
 ATCCAGCGCA CAATCGTGA AGCCTTCCAG GGCTGCACCG TGCTCGTCAT TGCCACCCGT 3900  
 15 GTCACCACTG TGCTGAAGTG TGACACATC CTGGTTATGG GCAATGGGAA GGTGGTAGAA 3960  
 TTTGATCGGC CGGAGGTACT GCGGAAGAAG CCTGGTCTAT TGTTCGCAGC CCTCATGGCC 4020  
 ACAGCCACTT CTTCCTGAG ATAAGGAGAT GTGGAGACTT CATGGAGGCT GGCAGCTGAG 4080  
 CTCAGAGGTT CACACAGGTG CAGCTTOGAG GCCCAGATC TGCGACCTTC TTGTTTGGAG 4140  
 ATGAGAACTT CTCTGGAAG CAGGGGTAAA TGTAGGGGGG GTGGGGATTG CTGGATGGAA 4200  
 20 ACCCTGGAAT AGGCTACTTG ATGGCTCTCA AGACCTTAGA ACCCCAGAAC CATCTAAGAC 4260  
 ATGGGATTCA GTGATCATGT GGTTCCTCTT TTAACITACA TGCTGAATAA TTTTATAATA 4320  
 AGGTAAAAGC TTATAGTTT CTGATCTGTG TTAGAAGTGY TGCAATGTCT GTACTGACTT 4380  
 TGTAAATAT AAAACTAAGG AAAACTCAAA AAAAAA AAAAAA

25 A173 Protein sequence  
 Gene name: EST  
 Unigene number: Hs.200102  
 Probeset Accession #: AL117406  
 Protein Accession #: none found  
 Signal sequence: none found  
 30 Transmembrane domains: 169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034  
 PFAM domains: ABC transporter [502-673], ABC\_membrane\_region [163-432, 771-1060]  
 ATP-binding\_domains [508-516, 1139-1147]  
 Cellular Localization: plasma membrane

35  
 1 11 21 31 41 51  
 MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKITYLQD GPMSQQRNP EAPGRAAVPP 60  
 40 WKGYDAALRT MIFPRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLIDENTIPPL 120  
 SVHDASDNV QRLHRLWEEB VRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFCIASVLG 180  
 PILIIPKILE YSEBQLGNV HGVGLCFALF LSECVKSLSP SSSWIINQRT AIRFRAAVSS 240  
 FAFELKIQFK SVIHITSGEA ISFFTGDVNY LFEVGYGGL VLITCASLVI CSISSYFIIG 300  
 YTAFAIILCY LLVFPLAVFM TRMAVKAQHH TSEVSDQRIK VTSEVLTCIK LIKMYTWEKP 360  
 45 FAKIIEGMES LTPCSKPGDG MAPSMLASLN LLRLSVFFVP IAVGLTNSK SAVMRFKKFP 420  
 LQESPVFFVQ TLQDPKALV FEEATLSWQQ TPCGIVNGAL ELERNHASE GMRPRDALG 480  
 PEEEGNSLGF ELHKINLVVS KGMMLGVCGN TSGKSSLLS AILEEMHLE GSVGVQGSLS 540  
 YVPQANIVS GNIRENLMG GAYDKARYLQ VLHCCSLNRD LELLFPFGDMT EIGERGLNLS 600  
 GGQKQRISLA RAVYSRQIY LLDDPLSAVD AHVGHIFEE CIKKTLRGKT VVLVTHQLQY 660  
 LEFCQIILL ENKICENGT HSELQKQKQK YAQLIQKMHK EATSDMLQDT AKIAEKPKVE 720  
 50 SQALATSLBE SLANGAVPEH QLTQBEEMEE GSLSWRVYHH YIQAGGYMV SCIIFFPVVL 780  
 IVFLTIPFSP WLSYMLEQGS GTNSSRESNG TMADLGNAD NPQLSFYQLV YGLNALLLIC 840  
 VGVCSSGIPT KVRKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLLP 900  
 IFSEQPLVLS LMVIAVLIV SVLSPYILLM GAIMVICPI YTMFKAIG VFKLENYSR 960  
 SPLFPHILNS LQGLSIIHYV GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALREIMTN 1020  
 55 LVTLAVALFV AFGISSTFYS PKVMANIVL QLASSPQATA RIGLETEAQF TAVERILQYM 1080  
 KMCVSEAPLH MBGTSCFPQGW PQHGEIIPQD YHMKYRDNTV TVLHGINTLI RGHVVGIVG 1140  
 RTGSGKSSLG MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRFN 1200  
 LDFFDRHTDQ QIWDALERTF LTKAISKFPK KLEHTDVVENG GNFSVGERQL LCIARAVLRN 1260  
 60 SKIILIDEAT ASIDMETDTL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMNGKRVVE 1320  
 FDRPEVLRK PGSLFAALMA TATSSLR

65 A174 DNA sequence  
 Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51  
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 75 GACCGGAGGA GGGAGAGCCG GCGGAGGCT GCGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
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 CGCTCGCTC CTGGAAGTTC CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360  
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 GCTCCTGGAC CTAGGGCCCG GGTGTGTGCG CTCTGGGGCG TCGCGGCAGA GGGAGTGGC 540  
 CGCGCGGAA AGCGCGCGCG GACAGTCAGT GACGAGGCC GGGGTGCGC GGGGCCACGA 600  
 CTCTCGGAG ACCGTCTGCG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660  
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5 TGGCTGGAGC CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTGACGGC 840  
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 10 CTGGTGGCAG CGTCTGCTG CAGATGTCTC CGGCTAAGC AGGATCCCA GCAGAGCGA 1320  
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 20 CATCCAGGTT ATCATGTATT TATGATGGA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
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 25 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220  
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 35 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAAAACAT CATCCCCTTC 2820  
 TTGATTGTAT CTTAATTTTC TGGCTTAAAG GTGACATCTG AGAGGTAATG CATCTTTTT 2880  
 TATATTGAAA TCATAAACTA TCAC00GCTG CTCTCTGAG TTACTTTTAA TTTTGCCTG 2940  
 TGGTATGTT TGGG0TTTC CTCTCTGTTG GTTTTCAGAG C00CATGTCT ATATAGTCT 3000  
 GAGTGCAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCTA GATCTGATA 3060  
 40 AAAAAATTTT TTGCTTATG TATAAAATT CAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCTCA G0CATAACT GAGACTGGG ATGAAATTTA AACAGATAC GATTACTTT 3180  
 GCAGATCATA AGGCTTTTT TACTCTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240  
 GATTGTAAG AGAAAAGCTT TTCAACGAA GATTGCTTT CTCTCCAC ACTGTTCTG 3300  
 ATTTCTCTC TCCTTCAGGC CTCACAGGC ACTGTATTCA TTGCCAATGT TCCAAATAT 3360  
 45 CAATTCAG TGAATTTAT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACAGTATT TTGTAATTA ACAATCGCT 3480  
 GTATGATAG GTCTCTTACA CATTTATGTC TATAGATAT TATGATCAT CTTTCTATC 3540  
 TGTTCATGA CTGAATAATG TAAAAACAG GTTGCAATT GGTATCATCA ATGATACTCA 3600  
 50 TTTTAAATA ACCAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660  
 TGA0000000 AAAAA0000 AAAAA0000

**A175 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MLSGFLMSPS TQHQRAYTPG GKQLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEA0KGNRGE PPAWIRAQQQ PRPPPAGQAP GTAAGGAQDP RL0PGRSRGR VRLPVKPP0A 120  
 65 SGRQPRG0SD CIPRFP0ASA THKAVPK0TG PPAEDGD0LG APGPRARRRR LLGVA0EGSG 180  
 PRGRRRTVS DEAR0SPGR LLD0RPALSG DAL0APRVVP CGALAAR0SP HP0TPLR0CS 240  
 CCWLRCWRRG R0P0GBYCHG WLD0QGVWRI GFQCP0RFDG GDATIC0GSC ALRYCC0SAE 300  
 ARLDQ0GCDN DRQ0GAG0PG RADK0GPRRL GRASCL0GTQ GD0GAP0PV RAWQ0CS0EG 360  
 70 SPKGRQLLRA FPGLLPRARR RGFP0SPRGG PSPLQR0PALP IYV0FLIVGS VFVAFI0LGS 420  
 LVAAC0CRCL RPKQDPQ0SR AP0GNRLMET IPWIP0S0ST RGSSSRQ0ST AASSSS0ANS 480  
 GARAPPTR0Q TNCLLP0GTH NN0VYNMPTN PSVLN0CQAT QIVP0GQYL HP0YVGYTVQ 540  
 HDSVPMTAVP PFM0GLQPGY RQIQSP0FHT NSEQMYPAV TV

**A176 DNA SEQUENCE**

Gene name: ESTs, Weakly similar to CGH07L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GCCCTTGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60

5 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCGCGGGGCC GGGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGCCCC CCTGCCCTGC CTGACGTGCC 360  
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTAGG CGCATCACGC AGCTGGAGCA GGAGAACTCG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540  
 10 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCC CCAGGGCCAG CCTGGCACTC 600  
 AGCCCTTCGA GGGTGGGGCG CCCATCGCAC CCACTCTCT TGGCTGGAGA CCCCAGGCG 660  
 GCCCAGGCAC AGTCCCGGAG TGGGGGCCCTT CTTGCCGCC TFGCCAGATG GGCTCCCCAG 720  
 GCCTGCCCCC AGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCG CTACTACTGG CCGCTGTCTG 840  
 15 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCGCC TTTCCAGCGG TGCCGCCCTG 900  
 GGTCCCATCT TCAGGAAAAG GCCTGCCCA CGCCAGGCTG CACTTCCAC AACGGGCAGC 960  
 AGAGGGCGCG GGGCGGCTCC GACGCGGCTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCTCTGC TGGCTGGGGA GCCCCAGGGA TAGCGGTGG ACTTCAGGTT 1140  
 CTGGCCAGCG CTGAGGGACC CTGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200  
 20 GGCTGTCATG TGCTCCAC AGACCTGGG GTGATGGCTT TCCCCCTCTT GCGCGGACG 1260  
 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCGAG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCACTCCA TAGGCAAGC CTGTTTCCCC CGACTCAGGA TTTCGAAGGC 1380  
 CTGGGGTCTT GCTCACCCCC CTTTGTCTCT ACGCCAGCC TGTCCCGAGG TTTCAGCTGG 1440  
 25 GAGAGGCGAG CTCCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500  
 GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT 1560  
 GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACTT GGAGGGTCCC AGTGTACCA 1620  
 GAACAGGGGG CAGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGCGCAG GGCTCCGAT GCGGGGTGAG TGCGTGGGGG GCGCAGGGCC 1740  
 30 CCGGATGCGG GGTCACTGCG TGGGGGGCGC AGGGCCCCCTT CGTGTCCAGG GCATTTGGT 1800  
 ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCACTC 1860  
 CCTTCCGAGG CCGAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTTCC 1920  
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980  
 GCCCTCCTAC CTTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAGGATG TCAGGCTTGG 2040  
 35 ACCTCCTGGG CAGGAAAGGG TGCAGGTCTT GAGGGCTGTG GCCCCACAGC CCCAGCACCC 2100  
 AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAAGCC CCGTGCAGCA 2160  
 GGCTGGGCTC TGCCCAACAG GGCTCCCCA CGTCTGCTT TGAGGGTGCC TGCCATGCC 2220  
 TGGGGGATTC TGGCATCTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCG 2280  
 GGTGACTTCA TCAGGAGACC GCCACATAG AGCTGGAGCC CGCAGCTGAA GCGAAATGT 2340  
 40 GAGACAGGCT GGCACCTCCG GAAAACTGC CTTTCAGCCT TGGTGTCCG TGCAAGGTGA 2400  
 AAAGAATAAG GTCTCCAGG TTTACAGCTT GAAATCAGGC TAGTGATGG CCTGGAGAC 2460  
 CAGAGGGGGA GAATTTAAG GCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520  
 GCAGACCTCG CTTGGAGCCT GCCCTAGGAC GCTGGGGGG TCACTCTCCG TGCAGGATG 2580  
 GAGCAGCGTC CTTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGAGGT ACATACAGT 2640  
 45 GCGTGACAC TGATGTGACA CCGGAAAATG TCTCAGGATG TTGAAATGT TCTTTGGGGG 2700  
 CAGAAGTGTG CCGAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACCA GGCCTCAGGA 2760  
 TTTGTGTGTG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTACGC 2820  
 TTGGAATCCC AGCACTTGA GCGAGGAGT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCCTCTCT ACARAAGAA AAAAAAGATG AGAGATCCAG GTTTAAAAAT 2940  
 50 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAACAC AGATTGACTC 3000  
 TAGACCCAC TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

## A177 DNA SEQUENCE

55 Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51  
 | | | | |  
 GCGGAACACC GGGCCGCGGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60  
 TCCCTGTGTG ACCTCTCGOG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120  
 65 CCTCCGAGCC GTGCCGGGGG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCTT GGGCTGCCCT GGCAGAGGC 240  
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACGTGTGG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCAATCCAAA CGTATCTTAC 360  
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAT GGCAGGGGTC 420  
 70 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGCGCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540  
 AGACAGGCTG GTTGTGTGTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600  
 TCTTTGGCCA CGCTGTGTCA GAGAAATGGT CTTCACTGGA GGACCCCATG AACATCTCCA 660  
 TCATCGTGAC CGACCAAGAT GACCAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720  
 75 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840  
 AGGACCCACA GCACTCATG TTCACAATT CCGGAGCAGC AGGCACCATC AGCGTCATCT 900  
 CCAGTGGCCT GGAACCGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
 TGGATGGGGA GGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCTTT GATGCCAATG 1020  
 80 ACAATGCTCC CATGTTTGAC CCCAGAAAT ACAGGGCCCA TGTGCTGAG AATGCACTGG 1080  
 GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAGCC CCCCAACTCA CCAGCGTGGC 1140  
 GTGCCACCTA CTTTATCATG GCGGTGACG ACGGGGACCA CTTTACCCTC ACCACCCACC 1200  
 CTGAGAGCAA CCAGGGCATC CTGACAAACA GGAAGGGTTT GGATTTTGAAG GCCAAAAACC 1260  
 AGCACCCCT TACGTTGAA GTGACCAACG AGGCCCTTT TGTGCTGAAG CTCCCAACCT 1320  
 CCACAGCCAC CATAGTGTGC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380

5 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440  
 CTGCAGAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA COGCATCCTG AGAGACCCAG 1500  
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTAC AGCTGTGGGC ACCCTCGACC 1560  
 GTAGGAATGA GCAATTGTGT AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCCACTACT GGCAAGGAA CCCTTCTGCT AACACTGATT GATGTCAAAG 1680  
 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740  
 ACGTGCTGAA CATCAOGGAC AAGGACCTGT CTCCCCACAC CTCCCCTTTC CAGGCCACGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 10 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTGGAAGC CTGCCCTGGA CCGTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT CTGTGTTCTC CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 15 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGCTAA CACAGACCCC ACAGCCCGGC CCTACGACAC CCTCTGGTGG TCGACTATG 2400  
 AGGGCAGCGG TCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCGACCAAG 2460  
 20 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGCATGT 2520  
 ACGTGGCGG GAGGAGCGAC TAGGGCGCCT GCGTGCAGGG CTGGGGACCA AACGTGAGG 2580  
 CACAGAGCAT CTCGAAGGGG TCTCAGTTCC CCTCTCAGCT GAGGACTTCG GAGCTGTGTA 2640  
 GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760  
 25 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCGGTAAAA 2820  
 TGCTCAACCC TGTGTCTCTG GCGTGGGCTC GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA ACCTCTCTAG GCGTCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940  
 TCAAAAGGTT AGAGAAAGTT CTTCAAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCCG 3000  
 TCCTGCAATT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060  
 30 ATACTGAGTG TGCCTAGGTT GCGCCTTATT TTTTATTTTC CCGTGTGCGT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCTGT TATATGTACT AGAAGCTTTT TATTAAAGAA A

**A178 Protein sequence:**

35 Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675  
 40 Cellular localization: plasma membrane

45 1 11 21 31 41 51  
 MGLPRGPLAS LLLLQVCHLQ CAASEPCRAV FREAEVILEA GGAEQEPGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDWV VAPISVPENG 120  
 KGFPPQRLNQ LKSNKDRDTK IPYSITGPGA DSPPEGVFAV EKETGMLLIN KPLDREBIK 180  
 YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKPTQDTF RGSVLEGVLF GTSVMQVAT 240  
 50 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMGDGSGTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEV AVGHEVQRLT VTDLDAFNPS 360  
 AWRATYLYMG GDDGDHFTIT THPESNQOIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMPD DSGQVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLLTLD 540  
 55 VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPTSPFP AQLTDDSDIY WTAEVNNEGD 600  
 TVVLSLKKFL KQDTYDVHLS LSDHGKNEQL TVIRATVDCD HGHVETCPGP WKGGFILFVL 660  
 GAVLALLPLL LVLLLLVREK RKIKEPLLLP EDDTRDNVPY YGEBGGGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEAGSGDAA SLSSLTSSAS DQDQDYDYLA EWGSRPFKLA DMYGGGEDD

**A179 DNA SEQUENCE**

60 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 65 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51  
 CTCTTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60  
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGGA TGACTGGACA 120  
 GGAACAAGAC TTGTGATTGT TTGTGTGTTT GGCAGTITTT TCTGCTGTT TATTTTTTTT 180  
 TCTAATTCTC TGGTCATGCG GGCAGTGATC AAAAACAGAA AATTTCATTT CCGCTTCTAC 240  
 75 TACCTGTTGG CTAATTTAGC TGCTGCGGAT TTCTTGCTG GAATTGCCCTA TGTATTCTCG 300  
 ATGTTTAAAC CAGGCCACGT TTCAAAAACT TTAGCTGTCA ACCGCTGGTT TCTCCGTCAG 360  
 GGCCTCTCTG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCGGTGGAG 420  
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480  
 CTGCTCATTT CTCTTGCTG GGCCATGCGC ATTTTATGAG GGGCGGTCCC CACACTGGGC 540  
 80 TGGAAATGCC TCTGCAACAT CTCTGCGCTG TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600  
 TACCTTGTTT TCTGGACAGT GTCCAACTTC ATGGCTTCC TCATCATGGT TGTGGTGTAC 660  
 CTGCGGATCT CCGGTATACG CAAGAGGAAA ACCAACTGCT TGTCTCCGCA TACAAGTGGG 720  
 TCCATCAGCC GCGCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

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CGGTTTGTGG TATGCTGGAC CCGGGGCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840  
AGGCAGTGTG GCGTGCAGCA TGTGAAAAG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900  
GTGCGTAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960  
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGGGTC CCTCTCGCAT CCGCTCCACA 1020  
GTCTCGACA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080  
GTCTGCAATA AAAGCACITC CTAAACTCTG GATGCTCTCT GCGCCACCCA GGTGATGACT 1140  
GTCTTAGG

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A180 Protein sequence:  
Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
Unigene number: Hs.258583  
Probeset Accession #: NM\_012152  
Protein Accession #: NP\_036284  
Signal sequence: none found  
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295  
Cellular Localization: plasma membrane

15

1 11 21 31 41 51  
MNECHYDKHM DFPYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNSL VIAAVIKNRK 60  
FHFPPFYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120  
LVIAVERHMS IMRMVRHNSL TKKRVTLIL LVWAIAlFMG AVPTLGWNCL CNISACSSLA 180  
PIYSRSYLVF WTVSNLMAFL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT 240  
VMTVLGAFVV CWTPGLVLL LDGLNCRQCG VQHVKNRFL LALLNSVVNP IISYKDEDM 300  
YGTMKIMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

20

A181 DNA SEQUENCE  
Gene name: ESTs  
Unigene number: Hs.162859  
Probeset Accession #: AA569531  
Nucleic Acid Accession #: AA569531  
Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

25

1 11 21 31 41 51  
ATGACCTACA GTTACTCATT TTTCAGGCCT GAGTTGATCG TTAATCATCT TAATTATGTT 60  
CATTCTGAAG CCACAGGAG AACCAAGACC AAAACCTTAT TGCTCTGCT TTCATTTCTT 120  
GATGAACCT CTGGACTAAG CACACATCTT CCTTGTATT CTCTCTCAAA GGAGTGTGGA 180  
GTGCTTCATC TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC 240  
CAGCTATACC TGTGGACAT GGGTGGTTT ACAATATTTA AGAACCCTGTG GATGAGCCTC 300  
ATACCCAGAG GGAACAAACG CTCCCCAAAA AGAGTTACAG AAACCATCCT GAGAGATTTT 360  
AAGCAGAAGC AAAGTTCAAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420  
CTCTCTTAT TCTGGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTTGGGCA 480  
GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTTCTTCA 540  
GCTACGTTGT CCCAGCATT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC 600  
AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTATC TACTGAGCTG CTACCATATC 660  
CCAGCTACTC CTGCAATGT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT 720  
TATGTAATAT CACAGACAAG GAAACTGAAC GCAGAAATGT TTTATTCTCT GCCAAACATC 780  
ACATGAGGAT GAACAATGAA ACCGATTGAA AACCAAGATT GTCTGATTCC AACATCTCTG 840  
GGTCCTTTT CACTCTGATA TGCTGCAATT AAAAAGCCAT TTCTAAGACT GT

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A182 Protein sequence:  
Gene name: ESTs  
Unigene number: Hs.162859  
Probeset Accession #: AA569531  
Protein Accession #: none found  
Signal sequence: 1-46  
Transmembrane domains: none found  
Cellular Localization: not determined

35

1 11 21 31 41 51  
MTYSYSFFRP ELIVNHLNYV HSEANRRTKT KTLISLLSFL DETSGLSTHL PCLSLSKECG 60  
VLHLDIHGKK EDMRITQSS QLYLWDMGGF TIFKNLWMSL IPRGNKRSPK RVTETILRDF 120  
KQKQSSKIQE ERRRESAGFN LSSFVFWGNA GRGDRPQIWA GSKQPSG

40

A183 DNA SEQUENCE  
Gene name: ESTs  
Unigene number: Hs.179809  
Probeset Accession #: N95796  
Nucleic Acid Accession #: XM\_050197  
Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

45

1 11 21 31 41 51  
TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCGGGTGAC 60  
AGCCGCGCGC CTCGCCAGG ATCTGAGTGA TGAGACGTGT CCGCACTGAG GTGCCCCACA 120  
GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAAGGGCT GGCAGAAATG 180  
GGCGCTGGC TGATTCTCTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCGG CAGCTTCTGG 240  
AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCCTGAGC CACTACCGCC 300

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5 TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCGCTGCG TGCGGCACCG GAAAGCCACG 360  
 CTCCTGTGCTG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCCG AGGCATCACC 420  
 TATGTGCCCG CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGTCTG 480  
 GGCATTGGTC CAGTGTGGGG CTGGTCTGTG GTCCCGCTCC TAGGCTCAGC CAGTGACCCAC 540  
 TGGCGTGGAC GCTATGGCCG CCGCGGGCCC TTCACTCTGG CACTGTCTCT GGGCATCCTG 600  
 CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGCTGTG CCGGATCC 660  
 AGGCCCTGAG AGCTGGCACT GCTCATCTCG GCGTGGGGC TGCTGGACTT CTGTGGCCAG 720  
 GTGTGCTTCA CTCCACTGGA GGCCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780  
 10 CGCCAGGCTC ACTCTGTCTA TGCCCTTCAT ATCAGTCTTG GGGGCTGCTT GGGCTACCTC 840  
 CTGCTCTGCA TTAGCTGGGA CACCACTGCT CTGGCCCTCT ACCTGGGCAC CCAGGAGGAG 900  
 TGCCCTCTTG GCTGCTCAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGCTGGTG 960  
 GCTGAGGAGG CAGGCTGGG CCCCACCGAG CCAGCAGAAG GGCTGTGCGC CCCCTCCTTG 1020  
 TGCCGCCACT GCTGTCCATG CCGGGCCCGC TTGGCTTTCC GGAACCTGGG GCGCTGCTT 1080  
 15 CCGCGGCTGC ACCAGCTGTG CTGCCGCTAG CCGCGCACCC TGCGCGGCTT CTGCTGGCT 1140  
 GAGCTGTGCA GCTGGATGGC ACTCATGACC TTCACTGTGT TTTACACGGA TTTCTGGGGC 1200  
 GAGGGGCTGT ACCAGGGCGT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCC GAGACACTAT 1260  
 GATGAAGGCG TCGCATGGA GAGCCTGGGG CTGTTCTTGC AGTGCGCCAT CTCCCTGGTC 1320  
 TTCTCTCTGG TCATGGACCG GCTGGTGCAG CGATTGCGCA CTCGAGCAGT CTATTGGGCC 1380  
 20 AGTGTGGCTG GTTCCCTGTG GGCTGCGGTG GCCACATGCC TGTCCACAG TGTGGCCGTG 1440  
 GTGACAGCTT CAGCGCCCTT CACCGGGTTC ACCTTCTCAG CCCTGCAGAT CCTGCCCTAC 1500  
 ACACCTGGCT CCTCTACCA CCGGAGAAAG CAGGTGTTCC TGCCCAATA CCGAGGGGAC 1560  
 ACTGGAGGTG CTAGCATGGA GGACAGCCTG ATGACCACTG TCCTGCCAGG CCTAAGCCT 1620  
 GGAGCTCCTT TCCTTAATGG ACACTGGGTG GCTGGAGGCA GTGGCCTGCT CCCACCTCCA 1680  
 25 CCGCGCTCTC GCGGGGCTC TGCCCTGTAT GTCTCCGTAC GTGTGGTGGT GGGTGGAGCC 1740  
 ACGAGGCCA GGGTGGTTC GGGCCGGGCG ATCTGCTGCG ACCTGCCAT CTGGAATAGT 1800  
 GCCTTCTGCG TGTCGCCAGT GGGCCCATCC CTGTTTATGG GCTCCATTGT CCAGCTCAGC 1860  
 CAGTCTGTCA CTGCTATAT GGTGTCTGCC GCAGGCTGCG GTCTGTGCGC CATTTACTTT 1920  
 GCTACACAGG TAGTATTGGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAACCTTCC 1980  
 30 AGCACAATGG GGTGGAGGCG CTGCTCACT GGGTCCAGC TCCCGCTCC TGTTAGCCCC 2040  
 ATGGGGCTGC CCGGCTGGCC GCCAGTTTCT GTTGTGCCA AAGTAATGTG GCTCTCTGCT 2100  
 GCCACCTGCT GCTGTGAGG TGCGTAGCTG CACAGCTGGG GGCTGGGGCG TCCCTCTCCT 2160  
 CTCTCCCGAG TCTCTAGGCG TGCCCTGACT GAGGCTTCC AAGGGGTTT CAGTCTGGAC 2220  
 TTATACAGGG AGGCCAGAG GGTCCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT 2280  
 35 ACCAGGCTC AAGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTTT 2340  
 GGGAGCTGAA TAACTCAGT CACTGGTGT CCATCTCTA AGCCCTTAA CCGTCACTT 2400  
 CGTTTAATGT AGCTCTTGA TGGAGTTTC TAGGATGAAA CACTCTCCA TGGGATTGGA 2460  
 ACATATGAAA GTTATTGTA GGGGAAGAGT CCGAGGGGCG AACACACAAG AACCAGTCC 2520  
 40 CCTAGCCCC ACAGGCACTG GTCTTTTTTG CTNAGNTCCA CCCCCCCTT CTTTACCCTT 2580  
 TT

**A184 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.179809  
 45 Probeset Accession #: N95796  
 Protein Accession #: XP\_050197  
 Signal sequence: none  
 Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401  
 50 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 55 MVQLWVSR LRRHKAQLLL VLLTFGLEV CLAAGITYVP PLLLEVGVVE KFMTMVLGIG 60  
 PVLGLVCPPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDFRPL 120  
 ELALLILGVG LLDPCGVQCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180  
 IDWDTSALAP YLGTQBECLF GLTLTIFLTC VAATLLVASE AALOPTPEAP GLSAPSLSPH 240  
 CPCRRLARL RNLGALLPRL HQLCCRPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL 300  
 60 YQGVFRAEPG TBRARHYDEG VRMGSGLFL QCAISLVFSL VMDRLVQRFQ TRAVYLASVA 360  
 AFPVAAGATC LSHSVAVVTA SAALTGTFPS ALQILPYTLA SLYHREKQVF LFKYRGDTGG 420  
 ASSEDSLATS FLPGPKPGAP FPNHVGAGG SGLLPPFPAL CGASACDVSF RVVVGEPTEA 480  
 RVVPGRGICL DLAILDSAPL LSQVAPSLFM GSVIQLSQSV TAYMVAAGL GLVAIYPATQ 540  
 VVFDKSLIAK YSA

**A185 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.11260  
 Probeset Accession #: R73640  
 70 Nucleic Acid Accession #: AK002126  
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 75 ATGGTTGCCG GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60  
 TGCTGTGCTA TCTCTGTCTT GTACATGTTG GCCTGCACCC CAAAGGTGA CGAGGAGCAG 120  
 CTGGCACTGC CCAGGGCCAA CAGCCCCACG GGGAGGAGG GGTACAGGC CGTCTTCTAG 180  
 GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240  
 80 AAGGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT 300  
 GCTGCTGGCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAAA CCCAGGCCGA CCTCCTGGCC 360  
 TTCTGCACT CGCAGGTGGA CAAGGCAGAG GTGAATGCTG GCGTCAAGCT GCCACAGAG 420  
 TATGACAGCA TGCCCTTCCA TAGCTTTACT CTACAGAAGG TGTACAGCT GGAGACTGGC 480  
 CTTACCGCC AGCCCGAGGA GAAGCCTGTG AGGAAGGACA AGCGGAGTGA GTTGTGGGAA 540  
 GCCATTGAAT CAGCCTTGA GACCCTGAAC AATCTGCAG AGAACAGCC CAATCACCGT 600



5 CCTTACACGG CCTCTGATT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660  
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACACGAAT TCAACCGCT CATCTTATTT 720  
 CGACCATTCG GCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT 780  
 ATCAATGTTA TCGTGCTCT AGCAAAAAGG GTGGACAAGT TCCGGCAGTT CATGCAGAAAT 840  
 TTCAGGAGGA TGTGCATTGA GCAGGATGGG AGAGTCCATC TCACTGTGTG TTACTTTGGG 900  
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTGAAAACA CTCCAAAGC TGCCAACTTC 960  
 AGGAACCTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAGGG ACTTGATGTT 1020  
 GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTCTCTTTT TCTGTGATGT GGACATCTAC 1080  
 10 TTACATCTG AATTCCTCAA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140  
 TATCCAGTTC TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGATGCAGTC 1200  
 CCTCCCTTGG AACAGCAGCT GGTCAATAAG AAGGAACTG GATTTTGGAG AGACTTTGGA 1260  
 TTTGGGATGA CGTGTCACTA TCGGTACAGC TTCATCAATA TAGGTGGGTT TGATCTGGAC 1320  
 ATCAAAGGCT GGGGCGGAGA GGATGTGCAC CTTTATGCGA AGTATCTCCA CAGCAACCTC 1380  
 15 ATAGTGGTAC GGACGCTGT GCGAGGACTC TTCCACTCT GGCATGAGAA GCGCTGCATG 1440  
 GACGAGCTGA CCCCGAGCA GTACAAGATG TGCATGCAGT CCAAGGCCAT GAACGAGGCA 1500  
 TCCCACGGCC AGCTGGGCAT GCTGGTGTTC AGGCACGAGA TAGAGGCTCA CCTTCGCAAA 1560  
 CAGAACAGA AGACAAGTAG CAAAAAACA TGA

# 20 A186 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.11260  
 Probeset Accession #: R73640  
 Protein Accession #: NP\_060841  
 25 Signal sequence: 1-26  
 Transmembrane domains: none found  
 Cellular Localization: not determined

30 1 11 21 31 41 51  
 | | | | |  
 MVRRGLLAWI SRVVLVLL CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ 60  
 EWEEQHRYNV SSLKRQIAQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTQADLLA 120  
 FLHSQVDKAE VNAGVKLATE YAAVPFDSFT LQKVYQLETG LTRHEPEKPV RDKRDELVE 180  
 35 AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILF 240  
 RPFPIMKVK NEKLANMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG 300  
 KEELNEVKG I LENTSKAAMF RNFTFIQLNG EFSRGRGLDV GARFWKGSNV LLFFCDVDIY 360  
 FTSEPLNCR LNTQPGKKVF YPVLFSQYNP GIIFYGHDAV FPLEQLVLK KETGFWRDFG 420  
 FGMTQYRSD FINIGGFDD IKGWGGEDVH LYRKYLSHNL IIVRTIPVRGL PHLWHEKRCM 480  
 40 DELTPEQYKM CMQSKAMNEA SHGQLGMLVF RHEIEAHLRK QRQKTSKGT

## A187 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 45 Nucleic Acid Accession #: AF189723  
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 | | | | |  
 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 TTTCAATGCTT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 55 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTGGCTT CTGCAGTCAT CAGTGTITTA 240  
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTACAGTT 300  
 GCCTTTGTTT AGGAATATCG TTCAAGAAAA TCTCTGAAG AATTGAGTAA ACTTGTGCCA 360  
 CCAGAATGCC ATTGTGTGGG TGAAGGAAAA TTGGAGCATA CACTTGGCCG AGACTTGGTT 420  
 CCAGGTGATCA CAGTTTGCTT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTGTGTT 480  
 60 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCGTGTGTTT 540  
 AAGGTGACAG CTCTCAGCC AGCTGCAACT AATGAGATC TTGCATCGAG AAGTAACATT 600  
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTAT TGGAACAGGA 660  
 GAAATTCCTG AATTGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTACTC CTTTGGTATA 780  
 65 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCTCTGA AATGTTTACT 840  
 ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCGAAGGTC TCCCATTTGT GGTCAAGTGT 900  
 ACGTAGCTC TTGGTGTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960  
 ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTCG AACACTGAOG 1020  
 AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCAATG TGAGGTTACT 1080  
 70 GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTGATG GTGATGTTGT TCATGGATTC 1140  
 TATAACCCAG CTGTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200  
 AGAAACATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260  
 ATGGGCTCTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320  
 GAGCAAAAGT GGAATGGCTG TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380  
 75 TGTTTATAGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
 GGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACCG 1500  
 ATGGGCTCAG CCGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGTAAGT GGCACAGCTG 1560  
 ACATTTCTTG GCTTGTGGG AATCATGTAT CCACETAGAA CTGCTGTGAA AGAAGCTGTT 1620  
 80 ACACACACTT TTGCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTG ACAGGAGACT 1680  
 GCAGTTGCAG TCGCAGTCT TCTGGGATG TATTCCAAAA CTTCAGATC AGTCTCAGGA 1740  
 GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTCACAAA TAGTACCAAA GGTTCAGTA 1800  
 TTTTACAGAG CTGCCCCAAG GCACAAGATG AAAATTATTA AGTCCTACA GAAGAACGGT 1860  
 TCAGTTGTAG CCATGACAGG AGATGGAATA AATGATGCAG TTGCTCTGAA GGTGACAGC 1920  
 ATTGAGATTG OGATGGGCGA GACTGGTACA GATGTTTGA AAGAGGCAGC AGACATGATC 1980  
 CTAGTGGATG ATGATTTTCA AACCAATAAT TCTGCAATG AAGAGGTTAA AGGGATTAT 2040

5 AATAACATTA AAAATTCGT TAGATTCCAG CTGAGCAGCA GTATAGCAGC ATTAACCTTA 2100  
 ATCTCATTGG CTACATTAAT GAACCTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160  
 ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220  
 GATGTCAATT GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTTGATA 2280  
 CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340  
 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400  
 TTTTGTGACA TGTTCATGTC ACTAAGTTC AGATCCAGA CCAAGTCTGT GTTTGAGATT 2460  
 GGACTCTGCA GTAATAGAAT GTTTGTCTAT GCAGTTCCTG GATCCATCAT GGGACAATTA 2520  
 10 CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTCAGA CTGAGAGCCT AAGCATACTG 2580  
 GATCTGTGTT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640  
 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700  
 CTTGAAGTAT GA

15 **A188 Protein sequence:**  
 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Protein Accession #: AAF27813  
 Signal sequence: none found  
 20 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
 Cellular Localization: not determined

25 1 11 21 31 41 51  
 MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI 60  
 SQFKNPLIML LLASAVISVL MQQFDDAVSI TVAILIVTV AFVQEYRSEK SLEELSKLVP 120  
 30 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSDIES SLTGETTPCS 180  
 KVTAPQPAAT NGDLASRSNI AFMGTLVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAPKT 240  
 PLQKSMOLLG KQLSFYSFGI IGIIMLVGWL LGKDILEMPT ISVSLAVALI PEGPLIVTV 300  
 TLALGVNRMV KIRAIIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAETV 360  
 GVGYNQFGEV IVDGIVVHGF YNPAVSRIE AGCVNDVAI RNNTLMGKPT EGALIALAMK 420  
 35 MGLDGLQDDY IRKAEYPPSS EQKMAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480  
 GQTLTLTQQQ RDVYQEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTGVKEAV 540  
 TTLIASGVSI KMITGDSQET AVAIALSRLGL YKTSQSQSVS ESDIDAMDVQQ LSQIVPKVAV 600  
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGTGT DVCKEADMI 660  
 LVDDDFQTIM SAIEEGGIY NNINKFVRPQ LSTSIALLTL ISLATLMNFP NPLNAMQILW 720  
 40 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFNW 780  
 ELRDNVITPR DTTMTFTCFV FDFMNFALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840  
 LVIYFPPLQK VFQTESLSIL DLLFLGLTSL SVCIVAEIHK KVEREREKIQ KHSSTSSSF 900  
 LEV

45 **A189 DNA SEQUENCE**  
 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 50 Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 ATGGGCTACC AGAGGCAGGA GCGTGTATC COGCCGAGA GAGGATGCC TTAITCAATG 60  
 AAGCAAGCTG GGTTCCTTTT GGAATATTG CTTTATCTT GGGTTTCATA TGTTACAGAC 120  
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCAGTCT 180  
 TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTITG 240  
 TATCCTTTTA TAGCAATGAT AAGTTACAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300  
 60 TTTCAAAGAA TCCAGAGAGT TGATCTTGAA AACGTGTTTA TTGGTCGCCA CTTTATTATT 360  
 GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCTTGT ACOGAAATAT AGCAAAGCTT 420  
 GGAAAGGTCT CCTCATCTC TACAGTTTA ACAACTCTGA TTCTTGGAT TGTAATGGCA 480  
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGTGTGGT ATTTGCAAGG 540  
 CCCAATGCCA TTCAAGCGGT CGGGGTATG TCTTTTGCAT TTATTGGCA CCATAACTCC 600  
 65 TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCG CCTATCCAT 660  
 ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATCTTTG CTACATGCG ATACTTGACA 720  
 TTTACTGGCT TCAOCCAAAG GAGCTTATTT GAAATTTACT GCAGAAATGA TGACCTGGTA 780  
 ACATTTGGAA GATTTTGTTA TGGTGTCACT GTCAATTTGA CATACCTAT GGAATGCTTT 840  
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTTCATC GGTTTTCCAC 900  
 70 ATTGTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC 960  
 CTGGGATAG TTCTAGAACT CAATGGGTG CTCTGTGCAA CTCCCTCAT TTTTATCATT 1020  
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACTCTCGA TAAGATTATG 1080  
 TCTTGTGTCA TGCTTCCAT TGGTGTCTGT GTGATGGTTT TTGGATTGCT CATGGCTATT 1140  
 ACAAAATCTC AAGACTGCAC CCATGGGCAG GAAATGTCT ACTGCTTCC TGACAATTTT 1200  
 75 TCTCTCAAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CAACTTTC TACTTTAAAT 1260  
 ATTAGTATCT TTCAACTCGA GTAA

80 **A190 Protein sequence:**  
 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

5  
1 11 21 31 41 51  
| | | | |  
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVSIVTD FSLVLLIKGG ALSGTDITYQS 60  
LVNKTFFGPPG YLLLSVQLFL YPFIAMISYN IIAGDTLSKV FQRIPGVDPE NVFIGRHFII 120  
GLSTVTFTLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGHPIH KTEDAWVPAK 180  
10 FNAIQAVGVM SFAFICHENS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240  
FTGFTQGDLF ENYCRNDDLIV TFGRFCYGVV VILTYPMCEP VTREIVANVF FGGNLSVVFH 300  
IVVTVMVITV ATLVSLLLDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360  
SCVMLPIGAV VMVFGFVMAI TNTQDCTHQ EMPYCFPDNF SLTNTSESHV QQTQLSTLN 420  
ISIFQLE

15 A191 DNA SEQUENCE  
Gene name: ESTs  
Unigene number: Hs.293185  
Probeset Accession #: N62096  
Nucleic Acid Accession #: N62096  
20 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
| | | | |  
ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CGCGCGCAGT TTTCCCTTGT TTTATTGATA 60  
AAAGGAGGGG CCCTCTCTCG AACAGATACC TACCACTCTT TGCTCAATAA AACTTTCCGGC 120  
TTTCCAGGGT ATCTGTCTCT CTCTGTCTCT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180  
AGTTACAATA TAATAGCTCG AGATACTTTG AGCAAAGTTT TCAAGAAGAT CCCAGGAGTT 240  
30 GATCCTGAAA ACGTGTTTAT TGGTCGCCAC TTCATTATTG GACTTTCCAC AGTTACCTTT 300  
ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360  
ACAGGTTTAA CAATCTGAT TCTTGGGAAT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420  
CACATACCAA AACAGAAGA CGCTTGGGTA TTGCAAAGC CCAATGCCAT TCAAGCGGTC 480  
GGGGTTATGT CTTTGTGCA TATTGTGCCAC CATAACTCCT TCTTAGTTTA CAGTCTCTTA 540  
35 GAAGAACCAC CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCATCGT GATTTCGTGA 600  
TTTATCTGTA TATCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660  
GACTTATTGG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTTGTATT 720  
GGTGTCACTG TCATTTTGAC ATACCCTATG GAATGCTTTG TGACAAGAGA GGTAATTGCC 780  
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC 840  
ATCAGCTGAG CCAGCTCTGT GTCACTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900  
40 AATGGTGTGC TCTGTGCAAC TCCCTCAATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960  
CTGTCTGAAG AACCAAGGAC ACACCTCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020  
GGTGTCTGTC TGATGGTTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080  
CATGGGCAGG AAATGTTCTA CTGCTTTCTT GACAAATTTT CTCTCACAAA TACCTCAGAG 1140  
45 TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200  
TAA

50 A192 Protein sequence:  
Gene name: ESTs  
Unigene number: Hs.293185  
Probeset Accession #: N62096  
Protein Accession #: none found  
Signal sequence: 1-26  
55 Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351  
Cellular Localization: plasma membrane

60 1 11 21 31 41 51  
| | | | |  
MGYQRQEPVI PPQPSLVLLI KGGALSGTDT YQSLVNKTFFG FPGYLLLSVL QFLYPFIAMI 60  
SYNIIAGDTL SKVPQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGRVSLIS 120  
TGLTTLILGI VMARAISLGP HIPKTEDAWV FAKPNAIQAV GVMSPAFICH HNSFLVYSSL 180  
EEPTVAKWSR LIHMSIVISV PICIFFATOG YLFTGTGFTQG DLFPENYCRND DLVTFGRFCY 240  
65 GVTVILTYPM ECFVTREIVIA NVFPNGNLSS VPHIVVTVMV ITVATLVSLI IDCLGIVLEL 300  
NGVLCATPLI PIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360  
HGQEMFYCFP DNPSLTNTSE SHVQQTQLS TLNISIFQLE

70 A193 DNA SEQUENCE  
Gene name: ESTs  
Unigene number: Hs.293185  
Probeset Accession #: N62096  
Nucleic Acid Accession #: N62096  
75 Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
| | | | |  
ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CGCGCGCAGG TCAATAAAAC TTTCCGCTTT 60  
CCAGGCTATC TGCTCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120  
TACAATATA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180  
CTGAAAACG TGTTTATTGG TGGCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240  
CTGCCCTTAT CCTGTATCCG AAATATAGCA AAGCTTGGAA AGGCTCCCT CATCTCTACA 300  
GGTTTAAACA CTCTGATTCT TGGAAATGTA ATGGCAAGG CAATTTCAT GGGTCCACAC 360  
ATACCAAAAA CAGAAGACGC TTGGGTATTG GCAAAGCCCA ATGCCATTCA AGCGGTGGGG 420

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GTATGCTCTT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480  
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540  
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600  
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660  
GTCACGTGCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720  
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATG TTGTAACAGT GATGGTCATC 780  
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840  
GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCAT CAGCCTGITA TCTGAAACTG 900  
TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGCTT GTGTCATGCT TCCCATTGGT 960  
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15 A194 Protein sequence:

Gene name: ESTs  
Unigene number: Hs.293185  
Probeset Accession #: N62096  
Protein Accession #: none found  
Signal sequence: none found  
Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330  
Cellular Localization: plasma membrane

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GFPLGILLIF WVSVYTFDSL VLLIKGGALS GTDTYQSLVN KTFGPPGVLL LSVLQFLYFF 120  
 IAMISYNIIA GDTLSKVQQR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIARKLKV 180  
 SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVPKFNIA IQAVGVMSFA FICHNSFLV 240  
 YSSLEPTVA KWSRLIHMSI VISVPICIFF ATCGYLTFTG FTQGDLFENY CRNDDLVTFG 300  
 RFCYGVTVIL TYRMECFVTR EVIANVFFGG NLSSVPHIVV TUMVITVATL VSLLDICLGI 360  
 VLELNGVLCA TPLIFIIPSA CYLKLSEPR THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420  
 QDCTHGQEMF YCFPDNFSLT NTSESHVQQT TQLSTLNISI FQ

# A197 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.31608  
 Probeset Accession #: H18836  
 Nucleic Acid Accession #: NM\_017636  
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 20 ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCACG 60  
 GAGAAGCCCA CGATGCTCA CGAGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC 120  
 AATTTCCTCC GGCTCTCTGA CGGAACGGAT CCAGCTGCAG TTTATAGTCT GGTTCACACG 180  
 ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGCCCC 240  
 GTCTCCAGA CCTGGCTGCA GGACCTGCTG CGTCTGGGGC TGGTGGCGGC TGCCACAGAGC 300  
 ACAGGAGCCT GGATTGTAC TGGGGGTCTG CACACGGGCA TCGGCGGCA TGTGGTGTG 360  
 GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGCACC AAGTGGTGGC CATGGGTGTG 420  
 GCCCCTGGG GTGTGTCCG GAATAGAGAC ACCCTCATCA ACCCCAAGGG CTGTTCCCT 480  
 GCGAGGTACC GGTGGCGGG TGACCCGGAG GACGGGTCC AGTTTCCCT GGACTACAAC 540  
 TACTCGCCT TCTTCTGTG GAGCAGCGC ACACACGGCT GCCTGGGGG CAGAACCCG 600  
 TTCCGCTTGC GGCTGGAGTC CTACATCTCA CAGCAGAGA CGGCGGTGG AGGGACTGGA 660  
 ATTGACATCC CTGTCTGTG CTCTCTGATT GATGGTGTG AGAAGATGTT GACGCGAATA 720  
 GAGAACGCCA CCGAGGCTCA GCTCCATGT CTCTCTGTG CTGGCTCAGG GGGAGCTGCG 780  
 GACTGCTGG CCGAGACCTT GGAAGACACT CTGGCCCCG GAGATGGGG AGCCAGGCAA 840  
 GGCGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCCAAG GGGACCTTGA GGTCTGCGAG 900  
 GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTGTA CAGTCTATT TCTGAGGAT 960  
 GGGTCTGAG AATTCTGAG CATAGTTTTC AAGGCCCTTG TGAAGCCCTG TGGGAGCTCG 1020  
 GAGGCTCAG CTACCTGGA TGAGCTGCTG TTGGCTGTGG CTGGGAACCG CGTGGACATT 1080  
 GCCCAGAGTG AACTCTTTG GGGGACATC CAATGGCGGT CCTTCCATCT CAGAGCTTCC 1140  
 CTCATGGAGC CCTCTGTAAG TGACCGGCTT GAGTTGTGTC GCTTGTCTAT TTTCCAGGCG 1200  
 CTCAGCCTGG GCCATCTCT GACCCCGATG GGCCTGGCCC AACTCTACAG CGCGGCGCCC 1260  
 TCCAACTGCG TACTCCGCAA CTTTGTGAC CAGCGCTCC ACAGCGCAGG CACCAAGGCC 1320  
 CCAGCCCTAA AAGGGGAGC TGCGGAGCTC CGGCCCTCG ACCTGGGCA TGTGCTGAGG 1380  
 ATGTCTGTGG GGAAGATGTG CGCGCGAGG TACCCCTCG GGGCGGCTG GGAACCTCAC 1440  
 CAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTGG ACAAGGCCAC CTCGCGGCTC 1500  
 TCGCTGATG CTGGCTCGG GCAGGCCCC TGGAGCGACC TGCTTCTTT GGCACGTGTG 1560  
 CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTA 1620  
 GCTCTTGGG CCTGTTTGTG GCTCCGGGTG ATGGCACGCC TGGAGCTTGA CGCTGAGGAG 1680  
 GCAGCACGGA GGAAGACCTT GCGTTTCAAG TTTGAGGGGA TGGGCGTTGA CCTCTTTGGC 1740  
 GAGTGTATC GCAGCAGTGA GGTGAGGGCT GCCGCGCTCC TCCTCGCTG CTCGCGGCTC 1800  
 TGGGGGATG CCACTTGCTT CCAGCTGGCC ATGCAAGCTG ACGCCGCTG CTCTTTGCC 1860  
 CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGG GAGATATGG CAGCATACA 1920  
 CCCATCTGG CCTGGTTCT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CGGCTCATC 1980  
 ACCTTCAGGA AATCAGAAGA GGAGCCCA CAAGGAGAGC TAGAGTTGA CATGGATAGT 2040  
 GTCATTAATG GGGAAAGGCC GTTCGGGAGC GCGGACCCAG CCGAGAAGAC GCCGCTGGGG 2100  
 GTCCCGGCC AGTCGGGCGG TCCGGGTTGC TGCGGGGCC GCTGCGGGG GCGCGGCTG 2160  
 CTAAGCCGCT GGTTCACATT CTGGGGCGCG CCGGTGACCA TCTTCATGG CAACGTGGTC 2220  
 AGCTACCTGC TGTCTCTGCT GCTTTCTCG CGGTGTCTG TCGTGGATT CCAGCCGGCG 2280  
 CGCGCCGCT CCTTGAGCT GCTGCTCTAT TTCTGGCTT TCACTGCTG GTGCGAGGAA 2340  
 CTGCGCCAGG GCTCTAGCGG AGCGGGGGG AGCCTGSCCA GCGGGGGCCC CGGCTTGGC 2400  
 CATGCTCAC TGAGCCAGCG CCTGCGCTC TACCTGCGG ACAGCTGGA CAGTGGGAC 2460  
 CTAGTGGCTC TCACCTGCTT CCTCTGGG GTGGGCTGCC GGCTGACCCC GGGTTTGTAC 2520  
 CACCTGGGCC GCACTGTCT CTGCATGAC TTCATGGTTT TCAGGTCGG GCTGCTTAC 2580  
 ATCTTCAAGG TCAACAAACA GCTGGGCCC AAGATCTGTA TCGTGAGCAA GATGATGAG 2640  
 GACGTGTCT TCTTCTCTT CTCTCTGGG GTGTGGCTGG TAGCCTATG GGTGGCCACG 2700  
 GAGGGGCTCC TGAGGCCACG GACAGTGAC TTCCCAAGTA TCCTGCGCGG CTTCTTCTAC 2760  
 CGTCCCTACC TGAGATCTT CGGCGAGAT CCGCAGGAGG ACATGAGAGT GGGCTCATG 2820  
 GAGCACAGCA ACTGTGTG TGAGCCCGGC TTCTGGSCAC ACCCTCTGG GGGCCAGCG 2880  
 GGCACTGCG CTCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTG CATCTTCTG 2940  
 CTGCTGGCCA ACATCTGCT GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTGGC 3000  
 AAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCGCTT CATCGGGAA 3060  
 TTCCACTCTC GGGCCGCGCT GGGCCCGCCC TTTATGCTCA TCTCCACTT GGGCTCTCT 3120  
 CTCAGGCAAT TGTGCAAGGG ACCCGGAGC CCGCAGCGGT CCTCCCGGC CTCGAGCAT 3180  
 TTCCGGTTT ACCTTTCTAA GGAAGCGAG CGGAAGCTGC TAACTGGGA ATCGGTGCAT 3240  
 AAGGAGAACT TTCTGCTGGC ACGCGCTAGG GACAAGCGG AGAGCGACTC CGAGCGTCTG 3300  
 AAGCGCAGT CCGAGAGGT GGACTTGGCA CTGAAACAGC TGGGACACAT CGCGAGTAC 3360  
 GAACAGCGCC TGAAGTGTCT GGAGCGGAG GTCCAGCAGT GTAGCGCGT CTTGGGGTGG 3420  
 GTGGCCGAGG CCTGAGCG CTCTGCTTG CTGCCCCAG GTGGGCGCC ACCCCCTGAC 3480  
 CTGCTGGGT CCAAGACTG A

## A198 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.31608  
 Probeset Accession #: H18836  
 Protein Accession #: none found

Signal sequence: none found  
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995  
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MEDAFGAAVV TVWDSDAHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
TWGFRAPNLV VSVLGGSGGP VLQTLWLQDLL RRLGLVRAQS TGAWIVTGGL HTGIGRHVGV 120
AVRDHQMAST GGTQKVAMGV APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVQPFLLDYN 180
YSAPFLVDDG THGCLGGENR FRLRLLESYIS QQKTGVGGTG IDIPVLLLI DGDEKMLTRI 240
ENATQAQLPC LLVAGSGGAA DCLABTLEDL LAPGSGGARQ GEARDRIRRP FPKGLLEVLQ 300
AQVERIMTRK ELLTVYSSSD GSEEFETIVL KALVKAOGSS EASAYLDELRL LAVAMNRVDI 360
AQSELFRGDI QWRSFHLEAS LADALLNDRP EFVRLISHQ LSLGHFLTFM RLAQLYSAAP 420
SNSLIRNLDD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
PGQFGESMY LLSKATSPSL SLDAGLGQAP WSDLLWALL LNRAQMAMYF WEMGSNAVSS 540
ALGACLLLRV MARLEPDABE AARRKDLAFK FEGMGVDLFG ECVRSSEVRA ARLLLRRCPL 600
WGATCLQLA MQADARAFFA QDGVQSLLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI 660
TFRKSEEEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCGRRRC 720
LRRWFHFWGA PVTIPMGNVV SYLLFLLLFPS RVLLVDFQPA PPGSLLELLY FWAFTLLCEE 780
LRQLSGGGG SLASGGGPGP HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
HLGRITVLCD FMVPTVRLHL IFTVNKQLGP KIVIVSKMMK DVEFFLFFLG VMLVAYGVAT 900
EGLLRPRDSD PFSILRRVVFY RPYLQIFCQI PQEDMDVALM EHSNCSSEFG FWAHPGAQA 960
GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMPSYTFG KVQGNSDLYW KAQRYRLIRE 1020
PHSRPALAPP FIVISHLRLL LRQLCRRPRS PQPSSPALEH FRVYLSKEAE RKLLTWESVH 1080
KENFLARAR DKRESDSERL KRTSQKVDLA LRQLGHIREY EQRLKVLERE VQCCSRVLGW 1140
VAELSRSLAL LPPGGPPPPD LPSGKD

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**A199 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.40808  
 Probeset Accession #: AA054237  
 Nucleic Acid Accession #: AA054237  
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCGCG GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCCTGGGG 60
CTGCTCGTCA CGGCCATCTT CACCGACACC TGGTACGAGA CCGACCCCGG GCGCCACAAG 120
GAGAGCTGGG AGCGCAGCGG CGCGGGCGCC GACCCCCCGG ACCAGAAGAA CCGCCTGATG 180
CCGCTGTGCG ACCTGCGGCT GCGGGACTCG CCCCCTGCGG GCGGCCGCGT GCTCCCGGGC 240
GGCCCGGGGG GCGCGGACCC CGAGTCTCTG CGCTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
GCCGAGTGGG GCCCGGCCCT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCTATG ACCCGGACAT OGACACCCCT ATCTGAAAG GTATTGCGCA GCGATGCACG 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCAGG ACATTCCTTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTATA GAAGAATCAC TGCTGGCTTC 540
CTGGGATAGG CCGTAGCCGT CCTTCTCTGC GGCTGCATGG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
TGACACCATTT CCTCTGTAC TTATGCGGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCTGCCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCCTGCTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATGCG TTATCCGTTT 840
ATTACCGGGA CCAAGATTGC ACAGCTAAGG TCTGGCAGAG ACTCCACGGT ATGA

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**A200 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.40808  
 Probeset Accession #: AA054237  
 Protein Accession #: none found  
 Signal sequence: 1-18  
 Transmembrane domains: 179-201, 209-231, 257-279  
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DFPDQKNRLM 60
PLSHLPLRDS PPLGRRLLPF GPGRADPESW RSLGLGLGLD AEOGRPLPAT YSGLWRKCYF 120
LGIDRDIDTL ILKGIAQRCT AIKYHFSQPI RLERNIPENLT RTIQQDEWHL LHLRRITAGF 180
LGMNAVAVLC GCIVATVSFP WEESLTQHVA GLLPLMTGIF CTISLCTYAA SISYDINRLP 240
KLILYSLPADV EHGYSWSIFC ANCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

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**A201 DNA SEQUENCE**

Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Nucleic Acid Accession #: NM\_016570  
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGAGGCGGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60
AAGGTTCCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120

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5 TTTACAACCTA TGGCTTTATT AACCATAATG GAATTCCTCAG TATATCAAGA TACATGGATG 180  
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATAAT 240  
 ACTGTTGCCA TGAAGTGTC AATATGTGGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300  
 GTTGCACTCG CAGATGGGTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360  
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACCT 420  
 CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480  
 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540  
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCTCTG TGGTCATGCA 600  
 10 CATTGGGCAG CATTGTGCAA CCATGAATCT TACAAATTTT CTCATAGAAT AGATCATTGT 660  
 TCTTTGGAG AGCTGTGTCC AGCAATTAIT AATCCTTTAG ATGGAACCTGA AAAAATTGCT 720  
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780  
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840  
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTTCTCTT 900  
 15 ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTGAAG ACTCTGTGGT 960  
 ATTGTTGGAG GAATCTTTTC AACACAGGC ATGTTACATG GAATTGGAAG ATTTATAGTT 1020  
 GAAATAATTT GCTGTGTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080  
 GAGGATGGCC ACACAGACAA CCACCTACCT CTTTGTAGAA ATAATACACA TTGA

20 A202 Protein sequence:  
 Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Protein Accession #: NP\_057654  
 25 Signal sequence: none found  
 Transmembrane domains: none found  
 Cellular Localization: nuclear

30 1 11 21 31 41 51  
 | | | | |  
 MRRILNRKKTLL SLVKELDAFF KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60  
 KYEYEVVDKDF SSKLRINIDI TVAMKCOYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120  
 35 KEWQRLQLQL QSRLEQEHSL QDVIPKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180  
 VAGNFHITVG KATPHPRGHA HLAALVNHEH YNFSHRIDHL SFGLVPAII NPLDGTEDIA 240  
 IDHNMQFYF ITVVPKLTHT YKISADTHQF SVTERERIIIN HAAGSHGVSG IFMKYDLSSL 300  
 MVTVTEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKPIV EIICCRFLRG SYKPVNSVFP 360  
 EDGHTDENHLP LLENNTHT

40 A203 DNA SEQUENCE  
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)  
 Unigene number: Hs.44926  
 Probeset Accession #: S79876  
 45 Nucleic Acid Accession #: NM\_001935.1  
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 | | | | |  
 CGCGGCTCTC GCGCGCCGCG GTGACTTCTG CCTGCGCTCC TTCTCTGAAC GCTCACTTCC 60  
 GAGGAGACGC GACACATGAA GACACCGTGG AAGATTCTTC TGGAGCTGCT GGGTCTGCTC 120  
 GCGCTTGCTA CCATCATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180  
 ACAGCTGACA GTGCGAAAC TTACACTCTA ACTGATTACT TAAAAATAC TTATAGACTG 240  
 55 AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAACA AGAAAAATAAT 300  
 ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGAGAA CAGTACATTT 360  
 GATGAGTTTG GACATCTTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420  
 TTAGAAATACA ACTAAGTGAA GCAATGGAGG CATTCCTACA CAGCTTCATA TGACATTTAT 480  
 GATTTAAATA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540  
 60 ACATGGTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGA ACAATGACAT TTATGTTAAA 600  
 ATTGAACCAA ATTACCAAG TTACAGAAATC ACATGGACGG GGAAGAAGA TATAATATAT 660  
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCITCA GTGCCACTC TGCTCTGTGG 720  
 TGGTCTCCAA ACGGCACCTT TTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT 780  
 65 ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCA 840  
 TATCCAAAGG CAGGAGCTGT GAATCCAACT GTAAAGTTCT TTGTTGTAAT TACAGACTCT 900  
 CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCTGCTTTC TATGTTGATA 960  
 GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAAGAATTTT TTTGCACTGG 1020  
 CTCAGGAGGA TTCAGAACTA TTCGGTCATG GATATTGTG ACTATGATGA ATCCAGTGGG 1080  
 70 AGATGGAATC GCTTAGTGCC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140  
 AGATTTAGGC CTTCAGAACC TCATTTTACC CTTGATGGTA ATAGCTTCTA CAAGATCATC 1200  
 AGCAATGAAG AAGGTTACAG ACACATTTCG TATTTCCAAA TAGATAAAAA AGACTGCACA 1260  
 TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACCAAG TGATATCTA 1320  
 TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAAAATCAA 1380  
 75 CTTATTGACT ATACAAAAGT GACATGCCTC AGTGTGTAGC TGAATCCGGA AAGGTGTGAG 1440  
 TACTATTCTG TGTCATTTCG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500  
 GGTCGCCCCC TCTATACTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCTCGGAA 1560  
 GACAATTCTG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAAACTGGAC 1620  
 80 TTCAATTATT TGAATGAAAC AAAATTTTGG TATCAGATGA TCTTGCTCTC TCATTTTGAT 1680  
 AAATCCAGA AATATCTCTT ACTATTAGAT GTGTATGCAG GCCCATGTAG TCAAAAAGCA 1740  
 GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800  
 GCTAGCTTTT GTAGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860  
 AGAAGACTCG GAACATTGGA AGTGAAGAT CAAATTGAAG CAGCCAGACA ATTTTCAAAA 1920  
 ATGGGATTCT TGGACAACAA ACGAATTGCA ATTTGGGGCT GTTCATATGG AGGGTACGTA 1980  
 ACCTCAATGG TCCTGGGATC GGGAAAGTGG GTGTTCAGT GTGGAATAGC CGTGGCGCCT 2040

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 20  
 25

```

GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100
CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAATAATTTT 2160
AAACAAGTTG AGTACCTCCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
AGCCACTTCA TAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400
AAGCTTATTA AAACCTATT TGTGTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520
ATACCTTACA TCTTAAGTAG GGACTTCTGT CTTCAACAAC GATTATTACC TTACAGAAGT 2580
TTGAATTATC CGGTCGGGTT TATTGTTTA AAATCATTTT TGCATCAGCT GCTGAAACAA 2640
CAAAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700
TTTCTAACTG GACTGGTTCA AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760
AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAG CTCCCTCGG 2880
AGAAGAGCTG TTCACCAAGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAACAGTCT 2940
CAGGAAATCA AATATCGAAA GCACGTGACT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
AAAGAAATGT AAGGGAATCT GCCAGCAACG CAGCCCCAG GTGCCAGTTA TGGCTATAGG 3060
TGCTACAAAA ACACAGCAAG GGTGATGGGA AAGCATTTGA AATGTGCTTT TAAAAAATAA 3120
TACTGATGTT CCTAGTGAAG GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
CTGTTAAAG ATGAAAATAT TTGTATCACA AATCTTAACT TGAAGGACTC CTGTCATCAA 3240
TTTTTCTTAT TTCAATTTCT TGAGTGCTTT AATTAAAGA ATATTTTAACT TTCCTGGAC 3300
TCATTTTAAA AATGGAACA TAAATACAA TGTATGTAT TATTATCCCT ATTCTACATA 3360
CTATGGAATT TCTCCAGTC ATTTAATAAA TGTGCCTTCA TTTTTC
  
```

**A204 Protein sequence:**

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)  
 Unigene number: Hs.44926  
 Probeset Accession #: S79876  
 Protein Accession #: NP\_001926.1  
 Signal sequence: none found  
 Transmembrane domains: 6-28  
 DPPIV\_N\_term domain: 43-557  
 Peptidase\_S9 domain: 558-635  
 Cellular Localization: plasma membrane

40  
 45  
 50

```

1 11 21 31 41 51
| | | | |
MKTFWKILLG LLGAALVTI ITVPVVLINK GTDDATADSR KTYTLTDYLK NTYRLKLYSL 60
RWISDHEYLY QENNILVFN AEYGNSSVFL ENSTFDEFHG SINDYSISPD GQFILLEVNY 120
VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSPV GHKLAYVMNN DIYVKIEPNL 180
PSYRITWTGK EDIIYNGITD WVYEEVFPFA YSALWNSPNG TFLAYAQFND TEVPLIEYSF 240
YSDLSLYPK TVRPVYPRAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
CDVTWATQER ISLQWLRIQ NYSVMDICDY DESSGRMNCL VARQHIEHST TGWVGRFRPS 360
EPHFTLDGNS FYKIIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420
EYKGMPPGGRN LYKIQILIDYT KVTCLSCLEN PERQVYVSFS FSKEAKYVQL RCGSPGLPLY 480
TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDPIILN ETKFWYQML PPHFDKSKKY 540
PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RSGSYQGDKI MHAINRRLGT 600
FEVEDQIEAA RQFSTMGFVD NKRIALINGWS YGGYVTSNVL GSGSGVFKCG IAVAFVSRWE 660
YYDSVYTERY MGLPTFPEDNL DHYRNTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720
KALVDVGVD FQAMWYTEDH GIASSTARQH IYTHMSHPK QCPSLP
  
```

**A205 DNA SEQUENCE**

Gene name: predicted exon  
 Unigene number: none found  
 Probeset Accession #: none found  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

65  
 70

```

1 11 21 31 41 51
| | | | |
ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAAATGACA ATGCCATCAG AGTTGACAAC 60
AGAAAGTGTA TTAAGGTGCG TGCTAACCGA TGTTCCCTGC ATGAGGCAGA AAGTGAATCC 120
AGAAACCCTC AGGAGCTCTG GATGGGCTCG CTCTCTCTGA TGGGGGTCCT AGAAGCATGT 180
GTGGAATAGA GGCCTCTGTC AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCAC 240
CAGCCACAC TGGATGTCTA A
  
```

**A206 Protein sequence:**

Gene name: predicted exon  
 Unigene number: none found  
 Probeset Accession #: none found  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 46-68  
 Cellular Localization: not determined

80

```

1 11 21 31 41 51
| | | | |
MALAKVREFN ANDNAIRVDN RSVIKVRANQ CSLHEAESES RNPQELNMGL LLLMGVLEAC 60
VEMRPLSVWS LRDDKEQSPH QPTLDV
  
```



A207 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.222886  
 Probeset Accession #: AI672225  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

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10      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAACTGCT 60
      CTCATACTTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
      ATTGATGTAT CTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
15      ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
      TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTCATGTGGG ATTCCCAGAA 300
      AACCTGACTA ATGGTGCCGC TGCTGGCAAT GGTGATGATG GATTAATTCC TCCAAGGAAG 360
      AGCAGAACAC CTGAAAGCCA GCAATTTCCT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
      GTCAAAGATC AGATAGTTGT AGATATGCGG CGTTATTCTT GA
  
```

A208 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.222886  
 Probeset Accession #: AI672225  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 16-38  
 Cellular Localization: not determined

```

30      1      11      21      31      41      51
      |      |      |      |      |      |
      MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPILLEQN IDVSSQDLDR RPESMLFLVI 60
      IMWTSFVEDN LSMGWGKLED FMAIBEEMKK HGSTHVGFPE NLINGAAAGN GDDGLIPPRK 120
35      SRTPEQQFP DTENEYHRF VKDQIVVDMR RYF
  
```

A209 DNA SEQUENCE

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1  
 Unigene number: Hs.23796  
 Probeset Accession #: NM\_014253  
 Nucleic Acid Accession #: NM\_014253  
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

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45      1      11      21      31      41      51
      |      |      |      |      |      |
      GACTGCTTGC ATTTAAAGGAC TTCCTCATCC TTTTTCATCAT GAAACTGAGC TTGCTTAATC 60
      AGAGATGGAG CAAACTGACT GCAAACCCCTA CCAGCCTCTA CCAAAGTCA AGCATGAAAT 120
      GGATCTAGCT TACACAGTTT CTCTGATGTA GAGTGAAGAT GGAGAGAAAC CAAGACAGTC 180
50      ATACAATGCC AGGGAGACCC TGCAACGAGTA TAACCCAGGAG CTGAGGATGA ATTACAATAG 240
      CCAGAGTAGA AAGAGGAAAG AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAC 300
      CTCTCACACT CTGTGCTCTG GCTACCAAAC AGACATGCAC AGCGTTTCTC GGCATGGCTA 360
      CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA 420
      TGCACTAAGA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCTCTGT TGTCCAGCCG 480
55      GGCCAACTCT GCATTATCCT TGACTGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA 540
      TGGTTTCAAA TTCTCTCTGT TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 600
      TGTGCAGAGC AGCCACACCA ACCAGTTCAC CTTCAGACCC CTCGCCACGC CACCTCGGCC 660
      TCTCATGCC TGCACTGTG CCAGGAAGCC ACCCCCTGCA GCGGACTCTC TTCAGAGGAG 720
      ATCAATGACT ACCCGAGCC AGCCAGCCC AGCTGCTCCA GCTCCCCCAA CCAGCAAGCA 780
60      GGATTCACTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCAG 840
      GCATTCCCTG TTCAACATG GATCTGGTTC CTCTGCGATC TTCAGTGAG CCACTCAGAA 900
      CTACCCCTCTG ACATCCAATA CCGTGTACTC GCCCCCTGCC AGGCTCTCTC CTCGAAGCAC 960
      CTTTCCCGA CCGCTCTTGA CCTTTAACAA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
      AGCATTTAGC GCCACTGCAA TCACAGTGAC TTTGGCCTTG TACTAGCCT ATGTGATTGC 1080
65      AGTGCAATTG TTGGGCTGTA CTGGCAGTT GCAACCAATT GAAGGAGAGC TGATGCAAAA 1140
      TGGAGTTAGC AAAGGGAACA GGGGAGACGA GTCCATGGAC ACTACTTACT CTCCAATTGG 1200
      AGGAAAAGTT TCTGATAAAT CAGAGAAAAA AGTGTTCAG AAGGAGCGG CGATAGACAC 1260
      TGGAGAAGTT GACATTGGTG CACAGGTGAT GCAGACCAAT CCACCTGGTT TATTCTGGOG 1320
      TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTCTT TAGCCAAAGGA 1380
70      CTCTCTGCTG GGAATTTATG GCAGAGAAAA CATTCACCT ACACATACTC AGTTTGATTT 1440
      TGTAAAACCTA ATGGATGGCA AACAGCTGGT CAAGCAGGAC TCCAAGGGCT CTGATGATAC 1500
      ACAGCACTCC CCTCGGAAAC TGATCTTAAC TTGCTTCAG GAGACAGGTT TCATAGAGTA 1560
      TATGGATCAA GGAACCTTGT ATCTGGGCTT TTACAATGAT GGAAAAAGA TGGAGCAAGT 1620
      ATTGCTGTGA ACTACAGCAA TTGAAATAT GGTGACTGT TCAACCAAT GCAATGGAAA 1680
75      TGGAGAGTGT ATCTCTGGCC ATTGTCATTG TTTCCAGGA TTCTTGGAC CTGACTGTGC 1740
      TAGAGATTCC TGCCCTGTGC TGTGTGTG TGATGGAGAA TACGAGAAAG GACACTGTGT 1800
      CTGCGGCAAT GGTGGAAGG GGCCAGAGTG TGACGTTCCG GAAGAACAAT GCATTGATCC 1860
      AACATGCTTT GGCCAGGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA 1920
      AGGAGAAAAA TGGAGGAAG AGGACTGCCT AGACCCCAAT TGTTCCAACC ATGGCATCTG 1980
      TGTAAAGAGA GAATGTCACT GTTCTACTGG CTGGGGAGGA GTTAACTGTG AAACACCACT 2040
      TCCTGTATGT CAAGAGCAGT GCTCAGGACA CGGAACCTTT CTCTGGAGAC CTGGAGTATG 2100
      CAGCTGTGAT CCCAAGTGGG CAGGATCTGA CTGCTCAACA GAGCTGTGTA CCATGGAGTG 2160
      TGGTAGCCAT GAGTCTGTCT CAAGAGGAAT TTGCCAGTGT GAAGAAGGCT GGGTAGGACC 2220
80      AACATGTGAG GAACGCTCCT GTCAATTCTCA TTGTACTGAG CATGGCCAAAT GCAAAGATGG 2280
  
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	AAAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAAATTGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
	AAATGGTTGG	CACGTGTGTG	GTGAGGTGGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTCTAT	2460
5	GGAAATGCTT	TGTGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTTAAACG	ACTGTGTGGA	2520
	TCCTGACTGT	TGTCACAAAA	GCAACTGTGA	TATAAGTCCT	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCATTCAGC	AAAGCCAAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAAATCC	TCATTGGCAA	GGACAGTACT	CATGTCAATC	CTCCTGAGGT	2700
	GTCAATTTGAC	AGCAGGCGTG	CCTGTGTGAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAAC	2760
10	TCCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACCCAGAT	GATTATGGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAGCTTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CCTTTCCTGC	CTGAGAAGAG	AACACTCTGG	TGCGCTTGGA	ATCAGTTTAT	2940
	TGTGTGTAGG	AAAGTCACCA	TGCAGAGAGT	TGTATCAGAC	CCGCCATCCT	GCGATATCTC	3000
	CAACTTTATC	AGCCCAAAAC	CTATTGTGCT	TCCTTCACCG	CTCACATCAT	TTGGAGGGTC	3060
	CTGTCCAGAG	AGGGGAACCTA	TTGTTCTTGA	GCTGCAGGTT	GTACAGGAGG	AAATTCOCAT	3120
15	TCCTCCAGC	TTTGTGAGCG	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAAACCT	3180
	GCTACGGATC	CTTCTGACAC	ATTCAACGAT	TCCCGTAGGC	ATGATAAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAC	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTTGCTTA	3300
	CACATTTGCT	TGGAACAAGA	CCGATATCTA	TGGACAGAAG	GTTTGGGGCC	TGGCAGAGGC	3360
20	TTTGGTATCT	GTGGGATATG	AATATGAAAC	GTGCCCTGAC	TTTATTTCTCT	GGGAGCAAGG	3420
	GACAGTGTGT	TTACAAGGTT	TTGAGATGGA	TGCTTCTAAG	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAGTGG	AATCATACAT	AAAGGGAATG	GAGAAAATAT	3540
	GTTCATTTCC	CAGCAGCCCC	CAGTCATATC	AACCATTAATG	GGTAATGGAC	ACCAAAGGAG	3600
	TGTAGCTGCG	ACCAACTGCA	ATGGCCGAGC	CCACAACAAC	AAACTCTTTG	CTCCTGTGCG	3660
	CTTAGCTTCT	GGCCCTGATG	GCAGTGTGTA	TGTTGGCGAC	TTCAATTTTG	TAAGGAGAAAT	3720
25	ATTTCCTCG	GGAAACTCG	TTAGTATTTT	GGAATTAAGC	ACCAAGTCTG	CTCACAATAA	3780
	CTATCTGGCT	ATGACCCCTG	TGCTGGAATC	ACTCTATCTA	TCAGACACCA	ATACTCGCAA	3840
	AGTCTACAAG	TGTAATCTCT	TTGTGGAGAC	GAAAGATCTG	TCCAAGAAAT	TTGAAGTGGT	3900
	GGCAGGAATC	GGTGTACAGT	GCCTTCCCTT	TGACCAGAGT	CATTGTGGAG	ATGGTGGGAG	3960
30	AGCATCGGAA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTGATAGGCG	ATGGATTTAT	4020
	TTACTTTGTG	GATGGGACTA	GATTTGCGAA	AATTGATGAG	AATGCTGTGA	TCACAACGTG	4080
	AATCGGCTCA	AATGGTCTGA	CTTCCACACA	ACCACTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACCTAGGTT	CGATTAGAGT	GGCCCAACAGA	CCTTGCAGTA	AATCTATATG	ACAATTCATT	4200
	GTATGTTCTG	GATACCAACA	TTGTGCTGCA	AATTTCTGAG	AACAGGCGTG	TTCCGATCAT	4260
35	CGCAGGACCG	CCCATTCACT	GCCAGGTGCG	AGGCATCGAT	CATTTCCTGG	TCAGCAAGGT	4320
	AGCAATTCAC	TCCACTCTAG	AGTCAGCGAG	GGCCATCAGT	GTCTCCCAAC	GCGGGCTGCT	4380
	CTTCATAGCT	GAAACAGACG	AGAGGAAAGT	AAACCGCATT	CAGCAAGTAA	CCACCAATGG	4440
	GGAGATCTAC	ATCATGCTCG	GTGCCCCACG	TGACTGTGAC	TGCAAAATTTG	ATCCAAACTG	4500
	TGACTGTGTT	TCAAGTGTATG	GTGGCTATGC	CAAAGATGCA	AAGATGAAAG	CCCTTCTCTG	4560
40	CTTAGCAGTG	TGCGCTGATG	GAACCCCTCTA	TGTGGCAGAC	CTCGGAAATG	TTGGAATTCG	4620
	TACCATCAGC	AGGAACCAAG	CCCACCTGAA	TGACATGAAC	ATTTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAACCTGTACC	AGTTCACTGT	AAATGGAACC	CACCTACACA	CCCTGAACTT	4740
	GATAACCAAG	GACTATGTTT	ATAACTTCAC	CTACAATTCT	GAAGGTGACT	TGGGCGCGAT	4800
	TACCAGCAGC	AATGGCAATT	CAGTGCACAT	TGCGGTGAT	GCAGGCGGAA	TGCCGCTATG	4860
45	GCTTGTGGTG	CCTGGCGGAC	AAGTATACTG	GCTGACTATA	AGCAGCAATG	GAGTCTGTAA	4920
	AAGAGTGTCA	GCCCAAGGCT	ATAATCCCGG	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCTGGCTACC	AAAGGTAAAG	AAAATGGATG	GACAACCGTT	TATGAGTATG	ACCCCGAGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGGTGACG	AGCTTCCACA	GTGACCTGGA	5100
50	GAAGCTGAGA	AAAGTGGAGC	TAGATACTTC	CAACCGTGAA	AATGTCCTCA	TGTCAACCAA	5160
	CTTGACGGCA	ACTAGTACCA	TATATATTTT	AAAACAAGAA	AATACTCAAA	GTACCTATCG	5220
	GGTGAATCCA	GATGTTTCCC	TGCGTGTGAC	TTTTTGCCAGC	GGGATGGAGA	TGGGCTCTAG	5280
	CTCAGAGCCC	CACATCCCTGG	CAGGGGCGAGT	CAACCCCTACC	CTGGGCAAAAT	GCAACATCTC	5340
	ATTGCGCGGA	GAGCACAATG	CAAACTCAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
	AGGCAATGTT	TGCGCTTTTG	AAAGGAGGCT	GAGGGCCAC	AACAGAAACC	TACTCTCCAT	5460
55	AGATTTTGAT	CATATAACCC	GCACAGGAAA	GATCTATGAT	GACCATCGAA	AATTCACCCCT	5520
	TGGAATCTTT	TATGACCAGA	CTGGGCGACC	CATTCTGTGG	TCTCTGTGAA	GCAGATATAA	5580
	TGAAGTGAAC	ATCACAATTT	CACCTTCGGG	ATTGGTGACG	TTTATTCAAA	GAGGAACGTG	5640
	GAATGAATAA	ATGGAATATG	ACCAAGTGGG	GAAATTAATT	TCAAGAACTT	GGGCTGATGG	5700
	GAAAATTTGG	AGCTATACCT	ACTTAGAAAA	ATCTGTGATG	CTTCTCTTAC	ACAGCCAGCG	5760
60	GGTTACATCT	TTTGAATATG	ACCAATCAGA	TTGCCCTGCTG	TCAGTTACCA	TGCCTAGCAT	5820
	GGTGCGCCAC	AGCTTACAAA	CCATGCTTTC	AGTGGGCTAC	TACCGTAATA	TCTACACCCC	5880
	ACCGGACAGT	AGCACTTCTT	TTATCCAAGA	CTATAGTCTG	GATGGCCGAT	TGCTACAGAC	5940
	CCTGCATCTG	GGACAGGGC	GCAGAGTCTT	ATACAAGTAC	ACCAAGCAAG	CAAGGCTTTC	6000
	TGAGGTTCTC	TATGATACCA	CTCAGGTAC	ATTAACATAT	GAAGAGTCTT	CTGGAGTGAT	6060
65	TAAGACAATA	CACCTGATGC	ATGACGGATT	CATCTGCACA	ATCAGATACA	GGCAAAACAGG	6120
	ACCTCTTATT	GGACGCCAGA	TTTTTCAGATT	CAGTGAAGAA	GGCCTTGTGA	ATGCACGGTT	6180
	CGACTACAGC	TACAAACATT	TCCGAGTCAC	AAGCATGCAA	GCTGTAATCA	ATGAAAACCCC	6240
	TTTGCCCTATA	GATCTTTACC	GATATGTTGA	TGCTCTGTGC	AGAACAGAGC	AGTTTGGAAT	6300
	ATTCAGTGTA	ATTAATTACG	ATTTAAATCA	GGTCATAACT	ACTACAGTGA	TGAAAACACAC	6360
70	CAAAATCTTC	AGTGCCAATG	GACAAGTCAT	TGAAGTCCAA	TATGAAATCC	TAAAGGCAAT	6420
	TGCTACTGCG	ATGACCATTC	AATATGATAA	TGTGGGCGCA	CATGGTAATA	TGTGCATAAG	6480
	GGTAGGAGTA	GATGCCAATA	TAACAAGGTA	CTTCTATGAA	TACGATGCTG	ATGGGCAACT	6540
	TCAGACTGTT	TCGTAAATG	ACAAAACCCA	GTGGCGTTAT	AGTTACGATC	TGAATGGAGA	6600
	CATCAACCTC	TTAAGCCATG	GGAAGAGTGC	TGCTCTTACT	CCTCTCCGAT	ATGACCTCCG	6660
	AGACCGCATC	ACCAAGTTAG	GAGAAATTCA	GTATAAAATG	GATGAAGATG	GCTTTCTGAG	6720
75	GCAGAGGGGA	AATGATATTT	TTGAATATAA	TTCTAATGGC	CTGCTGCAGA	AAGCCTACAA	6780
	TAAGGCTTCT	GGCTGGAGTG	TGCAGTATTA	CTATGATGGG	CTTGGGCGAC	GTGTGCGGAG	6840
	TAAGTCCAGC	CTAGGGGAGC	ACCTTCAGTT	CTTTGTGAC	GCGACCGCGA	ACCCCATAGG	6900
	AGTTACTCAT	TTGTACAACC	ACACAAGCTC	GGAGATTACA	TCTCTGTATT	ATGATCTCCA	6960
80	AGGTACCTTT	ATTGCCATGG	AGTTAAGCAG	TGTTGAAGAA	TATTATGTAG	CCTGTGATAA	7020
	TACAGGTACC	CCACTAGCTG	TGTTTACGAG	CCGAGGTGAG	GTCAATAAAG	AGATACTATA	7080
	CACACCTTAT	GGCGATATCT	ATCATGACAC	TTACCCCTGAC	TTTCAGGTCA	TAATTGGTTT	7140
	TCATGGAGGA	CTCTATGATT	TCCTTACTAA	ATTAGTGCAC	CTGGGGCAAA	GGGATTATGA	7200
	TGTTGTGTCT	GGCAGATGGA	CAACGGCCTA	TCATCACATA	TGGAAACAGT	TGAACCTCCT	7260
	TCCTAAACCA	TTCAACCTCT	ACTCCTTTGA	AAATAACTAC	CCAGTTGGCA	AAATTCAGAA	7320

	TGTTGCAAG	TATACCACAG	ACATCAGAAG	TTGGTTGGAG	CTATTTGGTT	TCCAATTACA	7380
	CAATGTACTA	CCTGGATTTC	CCAAACCTGA	ATTAGAAAAT	TTAGAATTAA	CTTACGAGCT	7440
	TCTACGGCTT	CAGACAAAAA	CTCAAGAGTG	GGATCCTGGA	AAGACTATCC	TGGGCATTCA	7500
	GTGTGAACCTC	CAGAAACAGC	TCAGGAATTT	CATTTCCCTG	GACCACTAC	CTATGACTCC	7560
5	CCGATACAAT	GATGGACGGT	GCCTTGAAGG	AGGGAAGCAA	CCAGGTTTG	CTGCTGTCCC	7620
	TTCTGTTTTT	GGGAAGGTA	TAAATTTTGC	CATCAAGGAT	GGCATTAGTA	CAGCTGATAT	7680
	TATAGGAGTA	GCCAATGAAG	ATAGCAGGCG	GCTTGCTGCC	ATTCTCAATA	ATGCCCATTA	7740
	CTGGGAAAC	CTACATTTTA	CCATAGAGGG	GAGGGACACT	CACTACTTCA	TTAAGCTTGG	7800
10	GTCTCTGGAG	GAAGACCTGG	TGCTCATCGG	TAACTCTGGG	GGGAGGCGGA	TTCTGGAGAA	7860
	TGGTGTCAAT	GTCACTGTGT	CCCAGATGAC	TTCTCTGTGG	AATGGGAGGA	CTAGACGGTT	7920
	TGCAGATATT	CAGCTCCAGC	ATGGAGCCCT	GTGCTTCAAC	ATCCGGTATG	GGACAACTGT	7980
	CGAAGAGGAA	AAGAATCAOG	TGTTGGAGAT	TGCCAGACAG	CGCGCAGTGG	CCCAGGCCGT	8040
	GACTAAGGAA	CAAGAAGGC	TGCAAGAGGG	GGAAGAGGGG	ATTAGGGCAT	GGACAGAAGG	8100
	GGAAAAGCAG	CAGCTTTTGA	GCACTGGGCG	GGTACAAGGT	TACGATGGGT	ATTTGTTTTT	8160
15	GTCTGTTGAG	CAGTATTTAG	AACTTTCTGA	CAGTGCCAAT	AATATTCAC	TTATGAGACA	8220
	GAGCGAAATA	GGCAGGAGGT	AAACAAAATA	TCTCTGCCTT	TGCGTCACCA	AAGACTGCCT	8280
	GTTTTTAAAA	CAATAAATGG	TTTATTGTAT	TGGTTTTCTA	GATCAGAACT	CTGTATATGT	8340
	AAATATGGAG	GA AAAACATA	TCCAACCTGCC	TTTCAATGTG	ACGGAAGATG	GTATTTTAAT	8400
	ATTGTTTGT	TAAACTCTTT	AAGAAATGAC	AGAGATTTTT	AGTTCTTGTG	TGGCAGTATT	8460
20	CAAAATAACA	CAAGTAGAAC	TCAACACAGT	AAAAACAGTT	TTCAGAAAGC	ACCACTTTCA	8520
	ATTTGCCGAG	CCATGCAAT	GTTCCAAAT	CCAGAAAGAA	CCCAAGGTTT	TCTATCTCTA	8580
	TTGTGAGAAG	CAGTTTTCAT	CTTAACTGTT	GGCAGAACTT	ACGGGCTATT	TGAATAGGTG	8640
	GTGCAATAGT	ATCTGAACT	TGCCCTTCSA	AAGACTGCCA	GCCCTTGTAC	GTTTTCCAGA	8700
25	TCTGTATAG	GAAACTTAAA	AACAGGTGTA	AAATGTCTTC	AGCCACCATC	TCCTAGAGTG	8760
	AGGACCCAAT	TGCCCTTCCT	TCTTGATTAT	TCTCTCTTGC	TTGTTAAAGT	AAATGCCATA	8820
	TTGTTGTGCT	GTGTTTGGC	GTGTGGTGGC	TGGGTTCTGT	CTACCATGCT	TCCTGTGGG	8880
	TGTGGTAACC	AGACTGTATA	GCCGCTATTT	GCTCGTGTGT	ACATGATACC	AAAGCAGCTG	8940
	GCCAGCGTGA	CCTCTCTCAC	ACGACCTGTT	TTGACTCAAT	TTTTTACTAA	AAGTTGTTCA	9000
30	GCTGTATTGG	TATCATGTAA	ACATAGCTTT	TATTAACCTG	GGTAGGAATT	TCTCATTTAT	9060
	ATATAGAGTA	GTGTTTGGCT	ATAGTTTCAC	ATTAGTGATT	CAGTATCTAT	ACACTGACCC	9120
	AATGGTTTTG	TGCACATGAA	CGGTAATTTA	CTTAAAGATA	TGATTCTGGT	ACAAAACAA	9180
	ACAAAGGCTT	TAGCAGGCAT	ACGTGTCTGG	GATGCCGATA	CATACATTAA	CTACTACTGC	9240
	AGAAATTCAT	AAGAGCCAAA	ACCTTAAAAA	AATAGACCTG	GTACTTAAAT	GAAAGTACTA	9300
	AAGGGAAGAC	CAGACCAAC	ATCAGACGAG	TTGCTGCCAC	ATTGTTTCAG	CCCCTTAGA	9360
35	TTTATCTTTC	AAATGTACAA	TTCTGTATIG	AACATCTCCC	AGCCATCTTC	AGGAAATCGA	9420
	ATCAAGTAAA	TCCTTTCCAA	CCGAAAACAT	TTCAACTAAC	TATAGAGAGG	CAGACTCATT	9480
	TTTACTAAAA	TAATTTATAC	AGTTAGTTAT	TTTCGTTCTC	CGTACTTACC	CATTATCTTT	9540
	TATTTAATCG	CTCTACTGTC	CTAGGAAAAT	AACATTTTTT	CAGGACGGGT	TATTTGTTCT	9600
40	GCGATCATTT	AAATTTGGA	GAAAGGTGAG	GATTAGTGTT	AATATCAGCT	GCACTTTCTC	9660
	AATCTCTAGG	AATCTCTGAG	TAAACCAAGC	CCCTGGGTGA	GCTGGAAGAT	TTGTGCCCAT	9720
	TGACAAAGAG	ATAGTTTGTG	AAATGCTGTG	TAATTTGTAAG	TTACCAACAA	TGAAAATACA	9780
	TGACAGCACA	ATGTGGCCCG	TAGAAAATTC	CCCTGAGCCA	GCTTCTGCAC	TTTCATCACC	9840
	GAATCTGAAC	ATTTGCTATG	TCTGAAGGCA	AATTTATGAT	GGAATGTTAG	TTTGATTGCT	9900
45	TTCCAGATGC	TACCTAAATG	CAGTGTGGGG	TCATTGCCTT	GCTTTGCGAT	GACAGTTTCT	9960
	TTGAAAATAT	GCNAAATCAT	AAGCTCATGT	TAAGGTTTTT	CAAGAGTCTG	CCCTCTACTA	10020
	CACAAAGGAA	AGCAAGGGAA	AGGAAATGAC	CCCTGSCAAC	AGTAGGGAAG	GGTGATTCCA	10080
	AACATTTTCAT	TTTCAAAACC	TTGGGGTTAG	AATACCACCT	ACACATGTAT	TCTGAGAGAC	10140
50	AGAAATTCAG	AGGAACCTGC	CTCTCTTTAT	AACCTGGAAC	ACACCGAGCT	GATATATTGC	10200
	TAATCCATAC	TAAATATATA	TTATTGGGTT	TTTTCTGAAT	CAGGCTCTGA	TTAATGGTAC	10260
	AGTATTTATT	CAGATGGAA	TTCTAAAATT	ACTAACAAAC	TTGTTGAAAA	TTTGAATAOC	10320
	TCCACACCAA	CCATAAATG	GACCTTAAGT	TCTAGAAC	TCTGATGTTT	TTTTAAATTA	10380
	ATGGAATAAT	AATTTGTGAA	CTGTATATAG	AGAGTGCAAT	CATAAATGTG	ATTATGTATT	10440
	TTATACAAAA	TCCAAATGAT	CAATATTAGA	GTCTATTTTG	CTTATATTTT	AAGCAATTAT	10500
55	ACGTTTTTGC	AATTCATGTA	TGATGTATCA	TTTTCAAACT	GCTTTAAATA	TCCATTAGAA	10560
	ACAAATATTT	GAAGCTTTTA	CTTAATAGTG	ATTACCTTGA	ACTGTGCAAT	TCTAGTTTGT	10620
	AATACGTATT	TGTTTGGTTC	GTGCTTTTAG	TTGTTAAAG	TTACATTTGT	ATTATATTCA	10680
	GGAAATGCAC	TTTTTATTAC	TTACAGCTGT	GGTTTTAATA	CTGCCTTGAA	CTATTATTAT	10740
	TCCTTTTACA	ACTCCTAAAG	CTTGAGGGAG	GAAAGAAAAA	AAAAACAAAA	CTACTAATCA	10800
60	GTAGTAAATC	GAAGAGAAAC	ATTTTGGCAT	TTCTTAAGAA	GAAGATGGAG	ATATTGAGTA	10860
	TATCACTTCC	TATTCAGCTG	AATAGAAAGA	ATGCTTTCAT	TGACTTGCAG	TTCTGCACTT	10920
	TAAATTTATT	AAAGAACAAT	TCGTTTGCAT	TTCTGTATGA	AAGTAAAGAC	ATTTTTCAGA	10980
	GAAACATATG	AATTTCTCAT	ACCCAGCAGA	CAGATGGCTG	ACACTGCACA	GCCACACACC	11040
	ATTGAGATGA	GTTAAAGTGA	GAGCATAGTA	GTTGGACTCT	CCTATGAAGA	ACATTCTGGG	11100
65	CTGGAGGCAG	GGAATACTCC	ATGTTTGTGT	CTTTTCTCTA	CTTAAGCCCA	TTTTGTTTGT	11160
	GCTTTTCTGT	TTTGTTTTGT	TTTCACTCTT	GCATACAGT	CTAGAGATCC	AAATGAACTG	11220
	AAAAGTTCAA	AGTTTAAAC	ATTTAAATAT	GTTTACTTTT	AGTTGTCAAT	CTAATCGTTA	11280
	TTGATTAGAA	GCATGACTCC	TGAAGGAAAG	GGAATATAAT	CTCAATTCAT	ACTAATCTGC	11340
	AACAAAACAC	TTTTACATA	TAAATAAGTA	TATGATTTAT	TTTTAACCCA	AAAAATGTAT	11400
70	AAAATAAGTG	TGTCCTTTAC	TGTCAATTIA	TCGAGAAGAT	CTATAATATA	TAGACTACAT	11460
	ATATATAATA	TATACAACT	AGCCAAATGT	ATGAAAACCT	GACAAATGAT	AATTTGGAA	11520
	TCACATGCTA	CCATATGAGA	CAGGTATGAA	ATTAAGTTAT	AATTTTCATG	AGACATTTTC	11580
	ATCACTGTTG	ACACAGTTTC	AAGGCATTC	ATCATGTTAT	TTTGACTCTT	TTTCTTTTTT	11640
	TTTTCTTTAA	AAATATATTT	TTAACTAGAC	CAGGCCCCAC	TATAATATCA	CTTAAGAGAG	11700
75	TCAGGGCAAA	GTTTTTGCAT	TTATGAAGAT	GTGTTCAATG	AAGGGTGATT	GTAATGGAGT	11760
	TCATTGGTAA	TAGAAGCAAA	AGTACAGTAA	CGAAGTATTG	AAAAGAAAAT	TTTGGAGACA	11820
	TTGGAGCATTA	TTATATATAG	CTTGTGGAAA	GACATAAGGC	TACAGATGGA	ATGGAACATT	11880
	CCTGTTTTCT	TGAAGAAATT	CACATACACA	TAGCTGACCT	GACTAGTACT	TCAGCTCTTC	11940
	CACAGCCTTC	TATAAAGGTT	CTTCTCTCTG	CAAGAAAAAC	AAAAACAAAC	AAAAACAAAC	12000
80	AAAAAATAAC	AAAAAAGCG	CAAAAAACAA	AAAAACAAA	AAAAACAAAG	TAAAAATTA	12060
	AAATACAGAA	AACAAACAC	AAAAAAGAA	TCAACCAATA	ATAGTGACTA	TTATTTTCAG	12120
	TGTTCTCTTC	ATGTGAAAGC	TATTAAGGAC	CAAAATATACT	ACTGTTTCATA	AGAAGAAATT	12180
	ACTTTCTAAA	CAGTAACTGA	AAATACCTAG	AGTTAAACTT	GCTGTGGATT	TTGCTTGGC	12240
	AGTTGTCTAT	TTACATTATT	TGTCAAAGGA	AATGTGTTTG	GCAGTTAAAA	ATCTTCTCTT	12300
	AGATTTAGTG	GTGGACTTTA	ACCTCTTAAA	TAAATGTTAG	TATATCAGAT	TGTGTCCTTG	12360

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AAAAATATTT TACTGTATG AATCATGACA ACGTCTAAAT CTTTACTATT CTTCTGGCAA 12420
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TGCTGTAATAT ATTTAAAGTT AAACATTATG TGTGTATATT TGAAAGAAAA GTACTTTTGA 12840
TATTTTCATTT TTAATAAATA AAATTGCCAA TGAAAAAATA

```

**A210 Protein sequence:**

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1  
 Unigene number: Hs.23796  
 Probeset Accession #: NM\_014253  
 Protein Accession #: NP\_055068  
 Signal sequence: none found  
 Transmembrane domains: 318-340  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MEQTDCPKFYQ PLPKVKHEMD LAYTSSSDES EDGRKPRQSY NSRETLHEYN QELRMNYSQ 60  
 SRKRKEVEKS TQMEFCEETS HTLCSGYQTD MHSVSRHGVO LEMGSDVDTE TEGAASPDHA 120  
 LRMWIRGMKS EHSSCLSSRA NSALSITDIT HERKSDGENG FKFSFVCCDM EAQAGSTQDV 180  
 QSSPHNQTFP RPLPPPPPPP HACTCARKFP PAADSLQRRS MTRRSQPSA APAPPTSTQD 240  
 SVHLHNSWVL NSNIPLETRH SLFKHGSGSS AIFSAASQNY PLTSNTVYSF PPRPLPRSTF 300  
 SRPAETFNKP YRCCNWKCTA LSATAITVTL ALLLAYVIAV HLPGLTLWQL PVEGELYANG 360  
 VSKGNRGTES MDTTYSPIGG KVSDKSEKKV FQKGRADITG EVDIGAQVMQ TIPPGLFWRF 420  
 QITTHHPYIL KFNISLAKDS LLGIYGRNNI PPTHTQFDFV KLMDGKQLVK QDSKGSDDTQ 480  
 HSPRNLITLS LQETGFIEMD DQGPWYLAFF NDGKMEQVF VLTATAIEMD DCSTNCNGNG 540  
 ECISGHCHCF PGFLGPDCAE DSCFVLCCGN GEYKKGHCVC RHGKNGPECD VPEBQCIDPT 600  
 CFHGHTCIMG VCICVPGYKG EICEEDCLD PMCSNHGICV KGECHCSTGW GGVNCEPLP 660  
 VCQEQCSGHG TFLLDAGVCS CDPKWTGSDC STELCTMECG SHGVCSRGC QCESGWVGPT 720  
 CERSCHSHC TEHGQCKDGK CECSPGWEGD HCTIAHYLDA VRDGCPLGCF GNGRCTLQDN 780  
 GWHCVQVQGW SGTGQNVVME MLCGDNLND GDGLTDCVDF DCCQSQNCYI SPLCQGSFDP 840  
 LDLIQSQSTL FSQHTSRLEFY DRIKFLIGKD STHVIPPEVS FDSRRACVIR GQVVAIDGTP 900  
 LVGVNVSLAH HSDYGTISR QDGSFDLVAI GGISVILIPD RSPFLPEKRT LWLPMNQPIV 960  
 VEKVTMQRVV SDPPSCDISN FISPNIPLP SPLTSPGGSC PERGTIVPEL QVVQEEIPI 1020  
 SSFVRLSYLS SRTPGYKTLR RILLTHSTIP VGMKVKHLTV AVEGRLTQKW PPAAINLVYT 1080  
 FAWNKTIDYG QKWNGLAEL VSVGYEYETC PDFILMEQRT VVLQGFEMDA SNLGDWLNK 1140  
 HHILNPQSGI IHKNGENMFP ISQPPVIST IMGNGHQRSV ACTNCGPAH NNKLFAPVAL 1200  
 ASGPDGVSIVY GDFNFVRRIF PSNGSVSILE LSTSPARKYY LAMPVSESL YLSDTNTRKV 1260  
 YKLKSLVETK DLSKNFEVVA GTGDQCLPFD QSHOGDGGRA SEASLNSPRG ITVDRHGFIY 1320  
 FVDGTMIRKI DENAVITTVI GSNGLTSTQP LSCDSGMDIT QVRLEWPTDL AVNPMONSLY 1380  
 VLDNNIVLQI SENRRVRIIA GRPIHCQVPG IDHFLVSKVA IHSTLESARA ISVSHSGLLF 1440  
 IAETDERKVN RIQQVTINGE IYIIAGAPTD COCKIDFNCD CFSGDDGYAK DAKMKAPSSL 1500  
 AVSPDGTLYV ADLGNVRIIT ISRNQAHND MNIYELASPA DQELYQFTVN GTHLHTLNLI 1560  
 TRDYVYNFTY NSEGDLAGIT SSNGNSVHIR RDAGGMPLWL VVPGQVYWL TISSNGVLKR 1620  
 VSAQGYNPAL MYPGNTGLL ATKSNGWGT TVYEYDPEGH LTNATFTTGE VSSFHSDLEK 1680  
 LTKVELDTSN RENVLMSTNL TATSTIYILK QENTQSTYRV NPDGSLRVTF ASGMEIGLSS 1740  
 EPHILAGAVN PTLGKCNISL PGEENANLIE WRQRKEQNGK NVSAFERRLR AHNRMLLSID 1800  
 PDHITRTGKI YDHRKFTLR ILYDQTRPI LWSFVSRYNE VNITYSPSGL VTFIQRGTWN 1860  
 EKMEVDQSK IISRTWADGK INSYTYLEKS VMLLLHSQRR YIFEYDQSDC LLSVTMPSMV 1920  
 RHSLQTMLSV GYRYNIYTPP DSSTSFIDY SRDGRLLQTL HLGTRRVLY KYTKQARLSE 1980  
 VLYDTTQVTL TYESSGVK TIHLMDHGF CTIRYRQTGP LIGRQIPRPS EEBLVNARFD 2040  
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 RGNDIFEVNS NGLLQKAYNK ASGNTVQYVY DGLGRRVASK SSLGQHLQFF VDATANPIRV 2280  
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 VFGKGIKFAI KDGIIVTADII GVANEDSRRL AAILANAHYL ENLHFTIEGR DTHYPIKLS 2580  
 LEEDLVLIQV TGGRRILENG VNVTVSQMST LLNGRTRRFA DIQLQHGALC FNIRYGTIVE 2640  
 EERNHVLEIA RQRAVAQAWT KEQRRLQEGE EGIRAWTEGE KQQLLSTGRV QGYDGYFVLS 2700  
 VEQYLELSDS ANNHFMQRS EIGRR

**A211 DNA SEQUENCE:**

Gene name: Solute carrier family 26, member 4  
 Unigene number: Hs.159275  
 Probeset Accession #: AF030880  
 Nucleic Acid Accession #: NM\_000441  
 Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTCAGCCTTC CCGGTTCCGG AAAGGGGAAG AATGCAGGAG GGGTAGGATT TCTTCTCTGA 60  
 TAGGATCGGT TGGGAAAGAC CGCAGCCTGT GTGTGTCTTT CCCTTGACC AAGGTGTCTG 120  
 TTGCTCGGTA ATAAACGCT CCACCTGCCT TCTGAGAGCG CTATAAAGGC AGCGGAAGGG 180  
 TAGTCCGCGG GGCATTCCGG GCGGGGCGCG AGCAGAGACA GGTATGCGCA GCGCCAGGCG 240  
 GCAGGTCGGA CCGCCCGCAG CTCCCGAGT ACAGCTGCAG CTACATGTG TCGCGGCGCG 300  
 TCTACAGCGA GCTCGCTTTC CAGCAACAGC ACGAGCGCG CCGCAGGAG CGCAAGACGC 360

5 TGCGGGAGAG CCTGGCCAAAG TGCTGCAGTT GTTCAAGAAA GAGAGCCTTT GGTGTGCTAA 420  
 AGACTCTTGT GCCCATCTTG GAGTGGCTCC CCAAATACCG AGTCAAGGAA TGGCTGCTTA 480  
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**A212 Protein sequence:**

Gene name: Solute carrier family 26, member 4  
 Unigene number: Hs.159275  
 Probeset Accession #: AF030880  
 Protein Accession #: O43511  
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317,  
347-369, 386-408, 420-442, 448-470, 486-508  
Cellular Localization: plasma membrane

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1      11      21      31      41      51
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AFGVLRKTLVP ILEWLKPYRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPVGYGLYSA 120
10 PFPILTYFIP GTSRHSVGP FPVVSMLVGS VVLSMAPDEM FLVSSSNGTV LNTTMDTAA 180
RDTARVLIAS ALTLVLGIIQ LIFGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSQKLKIVL 240
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PIEVIVTIIA TAISYGANLE KYNAGIVKS IPRGFLPPEL PVSFLFSEML AASFISIAVVA 360
YAIASVVGK YATKYDYTID GNQEFIAFGI SNIPSGFPSC FVATTALSRT AVQESTGGKT 420
15 QVAGIISAAI VMIALALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV 480
IIVFTCIIVSI IIGLDLGLLA GLIFGLLTIV LRVPFSPWNG LGSIPSTDYI KSTKNYKNIE 540
EPQGVKILRF SSPIFYGNVD GPKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT 600
KNGIISDAVS TNNAFEPDED IEDLEELDIP TKEIEIQVDW NSELVPVKVNV PKVPIHSLVL 660
20 DCGAISFLDV VGVRSRLRVIV KEFQRIDVNV YFASLQDYVI EKLEQCGPFD DNIRKDTFFL 720
TVHDAILYLQ NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEEBLDV QDEAMRTLAS 780
QDEAMRTLAS

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#### 25 A213 DNA SEQUENCE:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]  
Unigene number: Hs.98280  
Probeset Accession #: AA418000  
Nucleic Acid Accession #: NM\_021614  
Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

30

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1      11      21      31      41      51
|      |      |      |      |      |
CGGCGGCAGC AGCCCATGCC TCCGGTGCAA CAGCTGCGCC TCCTCCGGTG CCCCGGCGGC 60
35 GGGGGCGGGA GATAACCTGT CCTGTGCTGT CCGCACTCC TCGCCCGGCG GCGCCTTCOG 120
GACCCGCACC TCCTGCGCGC TGTGGGCTC GTCTGTCTGC TGCTGTCTGC GCTGTGTCGG 180
CCGGGGCAGC CAGCTCAATG TGAGCGAGCT GAGCGCGTCC AGCCATGCCA GTGCGCTCCG 240
GCAGCAGTAC GCGCAGCAGT CCGCGCAGCA GTCGGGGTCC GCCTCCCACT ACCACCAAGT 300
CCACAGCCTG CAGCCCGCGC CCGCCGCCAC GGGCAGCCTC GGCAGTCTGG GCTCCGCGCC 360
40 CCGCTCTCG CACCCACACC ACCACCCGCA CCGGGGCGAC CACCAGCACC ACCAGCCCA 420
GGCGCGCGCG GAGAGCAACC CCTTCACCGA AATAGCCATG AGCAGCTGCA GGTACAACGG 480
GGGCGTCATG CGGCGCTCA GCAACTTGAG CGGTCCTCCG CGGAACCTCC ACGAGATGGA 540
CTCAGAGGCG CAGCCCTGCT AGCCCCCGCG GTCTGTCCGA GGAGGTGGCG GCGGTCCTCT 600
CCGCTCTGCA CAGCTGCGCG CCGCGCGCGC TGTGTGCTCC TCAGCCCCCG AGATCGTGGT 660
45 GTCTAAGCCC GAGCACAACA ACTCCAACAA CCTGGGCTCT TATGGAACCG GCGGCGGAGG 720
CAGCACTGGA GGAGGCGCGC GCGGTGGAGG GAGCGGGCAC GGCAGCAGCA GTGGCACCAC 780
GTCCAGCAAA AAGAAAAACC AGAACATCGG CTACAAGCTG GGCCACCGCG GCGCCCTGTT 840
CGAAAGAGCG GAGGAGCTCA GCGACTACGC GCTCATCTTC GGCACTGTTC GCATCGTGGT 900
CATGTCTATC GAGACCGAGC TGTGCTGGGG CGCTACGAC AAGCGCTCGC TGTATTCCTT 960
50 AGCTCTGAAA TGCTTATCA GTCTCTCCAC GATCATCTCG CTCGGTCTGA TCATCGTGTA 1020
CCACGCCAGG GAATATCAGT GTTTCATGGT GGACAATGGA GCAGATGACT GGAGAATAGC 1080
CATGACTTAT GAGCGTATTT TCTTCATCTG CTTGGAATA CTGGTGTGTG CTATTCATCC 1140
CATACCTGGG AATTATACAT TCACATGGAC GGCCCGGCTT GCCTTCTCCT ATGCCCATC 1200
55 CACAACACCC GCTGATGTGG ATATTATTT ATCTATACCA ATGTTCTTAA GACTCTATCT 1260
GATTGCCAGA GTCATGCTTT TACATAGCAA ACTTTTCACT GATGCCCTCT CTAGAAGCAT 1320
TGGAGCACTT AATAAGATAA ACTTCAATAC ACGTTTGTAT ATGAAGACTT TAATGACTAT 1380
ATGCCCAGGA ACTGTACTCT TGGTTTTTAG TATCTCATTA TGGATAATTG CCGCATGGAC 1440
TGTCGAGCTT TGTGAAAGGT ACCATGATCA ACAGGATGTT ACTAGCAACT TCCTTGAGGC 1500
GATGTGTTTG ATATCAATAA CTTTCTCTC CATTGTTTAT GGTGACATGG TACCTAACAC 1560
60 ATACTGTGGA AAGGAGTCT GCTTACTTAC TGGAAATTAT GGTGCTGGTT GCACAGCCCT 1620
GGTGGTAGCT GTAGTGCCAA GGAAGCTAGA ACTTACCATA GCAGAAAAAC ACGTGACAAA 1680
TTTCATGATG GATACTCAGC TGAATAAAG AGTAAAAAAT GCAGCTGCCA ATGTACTCAG 1740
GGAAACATGG CTAATTATCA AAAATACAAA GCTAGTGAAA AAGATAGATC ATGCAAAAGT 1800
65 AAGAAAACAT CAACGAAAT TCTGCAAGC TATTCATCAA TTAAGAAGTG TAAAAATGGA 1860
GCAGAGGAAA CTGAATGACC AAGCAACAC TTTGGTGGAC TTGGCAAGA CCCAGAACAT 1920
CATGTATGAT ATGATTCTG ACTTAAACGA AAGGAGTGAA GACTTCGAGA AGAGGATTGT 1980
TACCCGGAAC ACAAACTAG AGACTTTGAT TGGTAGCATC CACGCCCTCC CTGGGCTCAT 2040
AAGCCAGACC ATCAGGCAGC AGCAGAGAGA TTTCAITGAG GCTCAGATGG AGAGCTACGA 2100
70 CAAGCAGCTC ACTTACAATG CTGAGCGGTC CCGGTCCTCG TCCAGGAGGC GCGGTCCTC 2160
TTCCACAGCA CCACCAACTT CATCAGAGAG TAGCTAGAAG AGAATAAGTT AACCAAAAA 2220
TAAGACTTTT TGCTCAATAT TTTAGCTTTT ATTGTAAGC CCCTATGGTT 2280
CTAATCAGCG TATCCGGGT TCTGATGTCA GAATCCTGGG AACCTGAACA CTAAGTTTAA 2340
GGCCAAAATG AGTGAACACT CTTTTTTTTT CTTTCAGATG CACAGGGAAT GCACCTATTA 2400
75 TTGCTATATA GATTGTTCTT CCTGTAATTT CACTAACTTT TTAATCATGC ACTTCAACA 2460
AACTTTACTA CTACATTATA TGATATATAA TAAAAAAGT TAATTCGGA

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#### A214 Protein sequence:

80 Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]  
Unigene number: Hs.98280  
Probeset Accession #: AA418000  
Protein Accession #: NP\_067627  
Signal sequence: none found  
Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

Calmodulin binding domain: 412-488  
Cellular Localization: plasma membrane

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MSSCRYNGGV MRPLSNLSAS RRNLHEMDSE AQPLQPPASV GGGGGASSPS ADAAAAAASVS 60
SSAPEIVVSK PEHNNSNNLA LYGTGGGGST GGGGGGGGSG HGSSSSGTRSS KKKNNQNIYK 120
LGHRRALFEK RRRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180
10    LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIPFICLE ILVCAIHPIF GNYTFTWTAR 240
LAFSYAPSTT TADVDIILSI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300
VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQDD VTSNPLGAMW LISITPLSIG 360
YGDMPVNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVENFM MDTQLTKRVK 420
15    NAAANVLRET WLIYKNTKLK KKHDKHVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV 480
DLAKTQNMVY DMISDLNERS EDPEKRIVTL ETKLETIGS IHALPGLISQ TIRQQQRDFI 540
EAQMESYDKH VTYNAERSRS SSRRRSSST APPTSSESS

```

**A215 DNA SEQUENCE:**

Gene name: CGI-86 protein  
Unigene number: Hs.109201  
Probeset Accession #: AW161450  
Nucleic Acid Accession #: NM\_016029  
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

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25      1      11      21      31      41      51
      |      |      |      |      |      |
CTGCGATCCC GCAGGCGAGC GACGCGACTC TGGTGC GGCG CGTCTTCTTC CCCCCGAGCT 60
GGGCGTGCGC GCGCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGGCG 120
30    TGCTCTGCTC CTGTGGTGCA CTGCTGCGCT TCCTGAGGGC TGAAGGCGAC CTGACGCTAC 180
TATGGGCGGA GTGGCAGGGA CGACGCCAGC AATGGGAGCT GACTGATATG GTGGTGTGGG 240
TGACTGGAGC CTGAGGTGGA ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACCTAGGAG 300
TTTCTCTTGT GCTGTCAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAG AGAAGATGCC 360
TAGAGAAATG CAATTTAAAA GAAAAAGATA TACTTGTGTT GCCCTTGAC CTGACCGACA 420
35    CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
TGGTCAACAA TGGTGAATG TCCAGCGTCT CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAAG CAAGGAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660
TATCTGTACC TCTTTCATT GGATCTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTTTTA 720
40    ATGGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCGAG 780
GACCTGTGCA ATCAATATT GTGAGAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840
GCAATAATGG AGACCACTCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900
TCAGCATGGC CAATGATTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960
45    CATATTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020
AAAGGATTGA GAACCTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080
AGACAAACA TGAATGAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200
ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
50    AGATTGCCAT GAATCTTGCA AA

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**A216 Protein sequence:**

Gene name: CGI-86 protein  
Unigene number: Hs.109201  
Probeset Accession #: AW161450  
Protein Accession #: NP\_057113  
Signal sequence: 1-26  
Transmembrane domains: 183-206, 221-243  
Cellular Localization: plasma membrane

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65      1      11      21      31      41      51
      |      |      |      |      |      |
MNWELLWLWL VLCALLLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVMVVTGASS 60
GIGELAYQL SKLGVSLVLS ARRVHELERV KRRCLENGNL KEKDILVLPL DLTDTGSHEA 120
ATKAVLQEFQ RIDILVNNGG MSQRSLOMDT SLDVYRKLE LNYLGTVSLT KCVLPHEMER 180
KQGKIVTVNS ILGIISVPLS IGYCASKHAL RGFFNGLRTE LATYPGLIIV NICPGPVQSN 240
IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISBQP PLLVTYLLWQY 300
70    MPTWAWIWN KMGKKRIENF KSGVDADSSY FKIPKTKHD

```

**A217 DNA SEQUENCE:**

Gene name: Homo sapiens mRNA; cDNA DKFPz56401763 (from clone DKFPz56401763)  
Unigene number: Hs.27373  
Probeset Accession #: F13036  
Nucleic Acid Accession #: AC012478  
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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80      1      11      21      31      41      51
      |      |      |      |      |      |
ATGCGCGCGC TGCGCGTGCC CGCCCGGCTC CTGCGCGTGC TGCTGCTGCG GCTCCTGGCC 60
GCTCCGCGCG CCGCGCGCAG CAGAGCGGAG TCGCTCTCCG CGCGGTGCGC CGAACCCGAG 120
CGCGAGTGGC GCGCACCGCC CGCCCGGGGG CCGCGGAACA CCACCCGCTT TGGGCTCGGG 180
CGCGCGGGCG GCAGCGGCAG CTCAGCTCC AACAGCAGTG GCGACGCTCT GGTGACCCGC 240

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ATTTCATCC TCTCCGCGA CCTACCCACC CTCAAGGCAG CGGTGATCGT GGGTTCCGCC 300
TTTACCAACC TCTCATCGC CTGCCCTGCTG CTGCGCGTCT TCAGGTCCGG AAAGAGGTGA 360
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGGCCCA 420
CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
TCTTTCGCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCAGCAA GATGCAGTGG AAGGCCCTGAT 600
GGTGGAAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAAGTTGG 660
TCAGCTGCAA CTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTGCGT CGGAGGTGTT 720
GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGGGTGTC AGGCATCTGC 780
TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACACAA TGGAGTTGCT TCTGCCACCC 840
TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAAATGCGAG 900
CTGAATCTCA TGGAAAGCT GGATTCTCT GCTTACGCA GAAACACCCG GGCTCCATCT 960
GCCAGTGCT TGCCTGCTG CTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCTTTTACAC ACAAACCATG 1080
AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGCCGAGC GGGGCACCTT TTGTGAAGAC 1140
AGAGCAGTGA CTAAGGTTCT CCAGGCTAGC TCTTTCTCCA AACAGCTGGG CTGGAAGCCA 1200
GCCCTAGAGT GTGGGTTTCT CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
ACCCATCCTG TCAGTTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
AGGGGTGTTT GGGGTCGCGG GCAGTCTCTG CATGGCGGAG GGTGAGGGG TACCGCAACT 1380
TGCTTTTGGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440
ATCTGTCTCC CTTGCTGTGC CGTGGAAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
GTCTTGTGCT CATTTGAGCA GAGCCCAACAA AAGGCAGCTG CTGCCACGG GGAGCCTGTC 1560
AAACGAGGGC CCACTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCACTGTA GGATGTCACT 1680
CACCTGGAG GAGACTTGGG TGGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
GATGAGCAGT GCCAGAGAT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCTT 1860
TCCCCCGAC AGCCCTGTT TCTGTCCAGG CCTTGA
  
```

#### A218 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)  
 Unigene number: Hs.27373  
 Probeset Accession #: F13036  
 Protein Accession #: FGENESH predicted  
 Signal sequence: 1-27  
 Transmembrane domains: 94-115, 448-469  
 Cellular Localization: not determined

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1 11 21 31 41 51
| | | | |
MRAVPLPAPL LPLLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTTLLIACLL LRVFRSGKRL 120
KKTTRKYDIIT TPAERVEMAP LNEDEDEDED STVFDIKYRV SLPAALRRQL PQOQTLLTVP 180
VPPPFILID LPARCSGRPD GGIRPGKTCF PANWHFVBSW SAATWGVKDW TWKPSVGGV 240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHPFKVPT STPHGFRQLQ 300
LNLMELKSS ALRRNTRAPS ARCLPLVLAE MAABESDLPN PWHFSAATGS PIKTLTYQTM 360
STLGLDVFVG AGQRGTFCEB RAVTKVLQGS SFSKQLRWKP ALESFPHHL RLLRECPPLS 420
THFVRLARSD ARGQASLTGR RVFRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLPYK 480
ICLPCCAVERH LREAKRSSVT VLASFQSPQ KAAAHAHGEPT KRGPSSQLTR HTPCPGWGITH 540
ANLQTIPTDQ QGEGFPREDVT HPGGDLGVA NFYLEEBGFQ DGRQKQWLM SEEGPPSLTG 600
CERLTGSHHF SSHSKWSFL SFRQPLELSR P
  
```

#### A219 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTA AGAGAGTGGG 60
GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
CAGCAAGGT ACAACACCTT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
TCCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAGT CAACATGTG 240
TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAATCG GGCTCCAGGT 300
GAACCAACA ATAGGCAAAA AGATGAGSAC TGGTGGAGA TCTACATCA GAGAGAAAAA 360
GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
GCTGCTGTGA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAACGTG 540
ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGGTTTGA GTCAACCACT GGGAAACTTC 600
AGCTACAAAT TTCTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
ACCATGCAGT GTATGTCTCT TGGAGAAATG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGA 780
AGCTTCCCAT GGAACACAC CTTGATACAT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840
GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
GCTGTGACAT CGAGGGCOGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
CTGCTGGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
CTGCAGGAC CAGCCAGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCCA 1080
GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140
CTTCTAGTG CTTCTGGCAG TTTCGGTTAT GGGTCCAGCT GTGAGTCTCT CTGTGAGCAG 1200
GGTTTTGTGT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC 1260
  
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GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320  
GTGAGGTGTG CTATTCCTCC TATTGGAGAA TTCACCTACA AGTCTCTTTG TGCCTTCAGC 1380  
TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440  
TGGACAGAG AGGTTCCTTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCGGGA 1500  
AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCCA CTGTGTGCAA GTTCGCTGT 1560  
CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGACAT GTGGAGCCAC AGGACACTGG 1620  
TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680  
CTTTCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740  
TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800  
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A220 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)  
Unigene number: Hs.89546  
Probeset Accession #: M24736  
Protein Accession #: NP\_000441  
Signal sequence: 1-22  
Transmembrane domains: 555-573  
C-lectin domain: 23-139  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRTHLVAI QNKKEIEYLN 60  
SILSYSPSY WIGIRKVN NVVWVGTKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120  
DVGMMWDERC SKIKLLALCYT AACINTSCSG HGECVETINN YTCCKDPGFS GLKCEQIVNC 180  
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
ECDAVTNPAN GFVECFQNPNG SPPWNTTCTF DCEBGFELMG AQSILQCTSSG NWDNEKPTCK 300  
AVTCRAVRQP QNGSVRCSSHS PAGEFTFKSS CNPTCEEGFM LQGPQVECT TQGWTTQIIP 360  
VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420  
EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAPS CEBGFELYGS TQLECTSQGQ 480  
WTEEVFSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKPAC PEGWTLNGSA ARTCGATGHW 540  
SGLLPTEAPR TESNIPLVAG LSAAGLSLLT LAPFLMLLRK CLRKAKEFVP ASSQSLSESD 600  
GSYQRPYSYL

Taxol ProstateA221 DNA SEQUENCE

Gene name: ESTs; Liprin A2  
Unigene number: Hs.306480  
Probeset Accession #: NS1002  
Nucleic Acid Accession #: NS1002  
Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGTGCC 60  
CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120  
GAAAGGGATC GTCTTCTAGA CACCTTCGG GAGACCCAGS AAAGCCTCTC ACTTGCCGAG 180  
CAAAGACTTC AGGATGTCAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTGAGCC 240  
CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300  
COGGAATTGG CTGCACTGAC AAAAGAATTA AATGCCTGCA GGGAAACAACT TCTAGAAAAG 360  
GAAGAAGAAA TCTCTGAAC TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420  
TTGGAGTGCC TTGTGTACG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480  
GCCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCAC TGAATCTTTG 540  
TTTGAGCACC ACAAGGCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600  
AGAGTCTCTG CACTGGAAGA AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCTTGGCT 660  
GAACAAATG TTCTATACA AAGAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720  
CATCTTGAAG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTC CAATGGTTCT 780  
ATAGACTCAA CCGATGAAC TAGTCAAATA GTTGAAC TACAAATGCT TGAAGAAGCAA 840  
AACTATGAAA TGGCCAGAT GAAAGAACGT TTAGCAGCCC TTCTTCCCG AGTGGGAGAG 900  
GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATT AAACAGAGA AATGAACACC 960  
AAGTATCAA GGGACATTAG GGAGGCCATG GCACAAAGG AAGATATGGA AGAAAGAATT 1020  
ACAACCCCTG AAAAGCGTTA CCTCAGTGCT CAGAGAGAA CTACCTCCAT ACATGACATG 1080  
AATGATAAAC TAGAAAATGA GTTAGCAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140  
AAAAACAGAC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200  
AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAACTGG CTCAGAGAA TGCAGCCCTA 1260  
ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAACGTA TGAGACATTT AGAGGGTCAA 1320  
CTTGAAGAGA AGAATCAAGA ACTTCAAGA GCTAGGCAAA GAGAGAAAAT GAATGAGGAG 1380  
CATACACAGA GATTATGGA TACGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCTA 1440  
CAACTACTCT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATCAAGAA 1500  
TCAGAACTT TCAGAAAGAA TCTTTAAGAA TCTTTACATG ATAAGGAAAAG ATTAGCAGAA 1560  
GAAATTGAAA AGCTGAGATC TGAACCTGAC CAATTGAAAA TGAGAACTGG CTCTTTAATT 1620  
GAACCCACAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA 1680  
TCCTTAGTGG ACAGCCAGTC TGATTACAGA ACAAATAAAG TAATAAGAAAG ACCAAGGAGA 1740  
GGCCGATGG GTGTGGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACAGTGG 1800  
AATAGAACTC AACAGATTGG AGTACTAAGC AGCCACCCCT TTGAAAGTGA CACTGAAATG 1860  
TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTAGCT CAATGGATCT TCTCTCTCCA 1920  
AGTGGTCTAT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GGTAGCCATC 1980  
AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGCG TGCTGAAGAA 2040  
ATTGAAAATA GAGTGGCTAG TGTGAGCCTC GAAGGCCTGA ATTTGGCAAG GGTCCACCCA 2100

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GGTACCTCCA TTACTGCCTC TGTTACAGCT TCATCGCTGG CCAAGTTCATC TCCCCCAGT 2160
GGACACTCAA CTCCAAAGCT CACCCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220
GTCATGACAC TGCCAAAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCGAT TGTGGAAGAA 2280
GATGGTGGAG AGGACAAAGC AACAATTAAA TGTGAAACTT CTCTCTCTCC TACCCTTAGA 2340
GCCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400
TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTTGGTAGTG CCAACAGCAG CCAAGACTCT 2460
CTTCACAAAG CCCCCAAGAA GAAAGGAAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA 2520
AAAGAAAAAG CTCGACTTGG GCAGCTCCGA GGCTTTATGG AGACTGAAGC TGCAGCTCAG 2580
GAGTCCCTGG GGTTAGGCAA ACTCGGAAC CAAGCTGAGA AGGATGGAAG ACTAAAGAAA 2640
AAGCATGAAC TTCTTTGAAGA AGCTCGGAGA AAGGGAATTAC CTTTGGCCCA GTGGGATGGG 2700
CCAACTGTGG TGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760
TGCCGAGCCA ACGTGAAGAG TGGTGCCATC ATGTCTGCTT TATCTGACAC TGAGATCCAG 2820
AGAGAAATTG GAATCAGCAA TCCACTGCAT CGCTTAAAC TTCCATTAGC AATCCAGSAG 2880
ATGGTTTCCC TAACAAGTCC TTCAGCTCCT CCAACATCTC GAATCCTTC AGGCAAGGTT 2940
TGGGTGACTC TTCTTTGAAGA AGCTCGGAGA AAGGGAATTAC CTTTGGCCCA GTGGGATGGG 3000
GAAGGAAGCT GGGCCAGTGG TCGGTTTTTT CTACAGACCC TGGCTTATGG AGATATGAAT 3060
CATGAGTGGA TTGGAATGGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120
TTTATGGAAT GCTTGGTAGA TGCAAGAATG TTAGATCACC TAACAAAAAA AGATCTCCGT 3180
GTCCATTTAA AAATGGTGGG TAGTTTCCAT CGAACAGATT TACAATATGG AATTATGTGC 3240
TTAAAGAGGT TGAATTAATG CAGAAAAGAA CTAGAAAGAA GACGGGAAGC AAGCCACAT 3300
GAAATAAAG AGTGTGGT GTGGAGCAAT GACCGAATTA TTCGCTGGAT ACAAGCAATT 3360
GGACTTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420
CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480
ACCCAGGCAA GGCAGATTCT TGAAGAGAAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540
AGGCGACTGG ATGAAGTGA TGACAGAAC TTCAGACGTG GATCAACCTG GAGAAGGCAG 3600
TTTCCTCTCT GTGAAGTACA TGAATCAGC ATGATGCCTG GGTCTCAGA AACATTACCA 3660
GCTGGATTTA GGTAAACCA ACCTCTGGG CAATCAAGAA AAATGACAA AGATGTTGCT 3720
TCATCAAGAC TGCAGAGGTT AGACAACTCC ACTGTTGCGA CATACTCATG TCTCGAGTAA 3780
GCGGCCGCTT TAA
  
```

**A222 Protein sequence:**

Gene name: ESTs; Liprin A2  
 Unigene number: Hs.306480  
 Probeset Accession #: N51002  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: none found  
 AAA domain: 286-539  
 SAM domains: 895-964, 1017-1084, 1105-1177  
 Cellular Localization: not determined

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1 11 21 31 41 51
| | | | |
MMCEVMPTIN EDTFMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLLDTRL ETQESLSLAQ 60
QRLQDVIYDR DSLQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEL NACREQLLEK 120
EEEISELKAE RNNTRLLEH LECLVSRHER SLRMTVVKRG AQSPSGVSSE VEVLKALKSL 180
FEHKKALDEK VRERLRVSLR RVSALEELA AANQEIVALR EQNVHIQRKM ASSEGSTESE 240
HLEGMEFQK VHEKRLSNGS IDSTDTSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300
VEQEAETARK DLKTEEMNT KYQDIREAM AQKEDMEERI TLEKRYLSA QRESTSIHDM 360
NDKLENELAN KESTELRMEB KNRQLQERLE LAEQKLQQTH RKAETLPEVE AELAQRIAAL 420
TKAEERHGN EERMRHLEGQ LEEKNQELQR ARQREKNBEE HNKRLSDTVD RLLTESNERL 480
QLHLKERMAA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKLRSELD QLMKRTGSLI 540
EPTIPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRPRR GRMGVRRDEP KVKSLGDHEW 600
NRTQQIGVLV SHPFESDTEM SDIDDDRET IFSSMDLLSP SGHSDAQTLA MMLQQLDAI 660
NKEIRLIQEE KESTELRMEB IENRVASVSL EGLNLRVHP GTSITASVTA SSLASSSPFS 720
GHSTPKLTFR SPAREMDRMG VMTLPDLRK HRRKIIVVEE DGREDKATIK CETSPPPTFR 780
ALRMHTLPSL SYENDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKGI KSSIGRLFGK 840
KEKARLQQLR GFMEATAAAQ ESLGLGKIGT QAEKDRRLKK KHELLEEARR KGLPFAQWDG 900
PTVVANLELW LGMPANWVAA CRANVKSIAI MSALSDEIQ REIGISNPLH RLKRLRLAIQE 960
MVSILTSPSAP PSTRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCFVP LQTLAYGDMN 1020
HEWIGNEWLP SLGLPQYRSY FMECLVDARM LDHLTKKDLR VHLKMDVSPH RTSLQYIGIMC 1080
LKRINLYDRK LERRREASQ BIKDVLVWSN DRIIRWIAI GLREYANNIL ESGVHGSLIA 1140
LDENFDYSSL TLLQLIPTQN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ 1200
FPPREVHGIS MMPGSETLFE AGFRLTTTSG QSRKMTTIVA SSRLQRLDMS TVRTYSCLC
  
```

**A223 DNA SEQUENCE**

Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Nucleic Acid Accession #: NM\_016570  
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

75  
 80

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1 11 21 31 41 51
| | | | |
ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTTCG 60
AAGGTTCTCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
TTTACAACTA TGGCTTTATT AACCATAATG GAATCTCAG TATATCAAGA TACATGGATG 180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
ACTGTTGCCA TGAAGTGTCA ATATGTTTGA GCGGATGTAT TGGATTAGC AGAAACAATG 300
GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420
CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
  
```

5  
10  
GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAAATAAA 540  
GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600  
CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTGATAGAAT AGATCATTTG 660  
TCTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAACCTGA AAAAAATTGCT 720  
ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780  
TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840  
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT 900  
ATGGTGACAG TTAGTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960  
ATTGTTGGAG GAATCTTTTC AACCAACAGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020  
10 GAAATAATTT GCTGTCTGTT CAGACTYGA TCCTATAAAC CTGTCAATTC TGTTCTCTTT 1080  
GAGGATGGCC ACACAGACAA CCACCTTACCT CTTTATAGAAA ATAATACACA TGA

15 A224 Protein sequence:  
Gene name: CDA14  
Unigene number: Hs.26813  
Probeset Accession #: N32912  
Protein Accession #: NP\_057654  
Signal sequence: none found  
20 Transmembrane domains: none found  
Cellular Localization: nuclear

25  
30  
1 11 21 31 41 51  
| | | | | |  
MRLNRKKTSLVVKELDAPF KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60  
KYEYEVKDFP SSKLRINIDI TVAMKQCVVG ADVLDAETM VASADGLVYE PTVFDLSPQQ 120  
KEWQRMQLQLI QSRLEQEHSL QDVIFKSAPK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180  
VAGNFHITVG KAIHPHPRGHA HLAALVNHES YNFSHRIDHL SPGLVFAII NPLDGTEDIA 240  
IDHNQMPQYF ITVVPTKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300  
MVTVEEHMP FWQPFVRLCG IVGGIFSTTG MLHGIGKFIV EIIICRFRIG SYKFPVNSVPF 360  
EDGHTDNHLP LLENNTN

35 Uterine  
A225 DNA SEQUENCE:  
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
40 Nucleic Acid Accession #: AA487468  
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

45  
50  
55  
1 11 21 31 41 51  
| | | | | |  
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60  
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTACAG TTTCTTCCAA CCTTGCCATT 120  
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180  
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
ATGGTTATTC ATCACTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCCC 300  
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
GAAACCACTG ATAAGAATTT ATCACTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420  
GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
TATGAGCCTC GGGATTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540  
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCAT 600  
55 GAGAAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAAT 660  
TTACTATTTA GTTTTITTTAA TGTGTTTGCA ATAGTCTTAT TAAATATAAT GTTTTITTTAA 720  
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

60 A226 Protein sequence:  
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
65 Protein Accession #: none found  
Signal sequence: 1-23  
Transmembrane domains: none found  
Cellular Localization: secreted

70  
75  
1 11 21 31 41 51  
| | | | | |  
MLHSALGLCLLVTVSSNL ALAIKKEKRP PQTLRSGWGD DITWVQTYEE GLPYAQSKSK 60  
PLMVIHLED QYQSALKKV PAQNEEQEM AQNKFIIMNL MHETTCKNLS PDGQYVPRIM 120  
FVDPSPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

80 A227 DNA SEQUENCE  
Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
Unigene number: Hs.285529  
Probeset Accession #: AA460530  
Nucleic Acid Accession #: NM\_003667  
Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GTGGCGGC	CAACCTCT	AGTCCCGC	GCGCTTCT	TGCGCGCC	CGCCGTGG	60
5	TCAGGAAC	GGCGTCTG	GCTGCAGC	CCCGCTGAG	TGCAGAAC	CACGGAGG	120
	CGCCCGGCG	GCCACGGC	GTAGCAGT	GGTCTGCT	TCCGCGCG	TCCGGCTCG	180
	GGCCCGCTAC	TTCGGGCAC	ATGGACAC	CCCGCTCG	TGTGCTCT	TCCTTGCTG	240
	TGCTGCTGCA	GCTGGCGACC	GGGGGACG	CTCCAGGT	TGGTGTGT	CTGAGGGGT	300
	GCCCCACACA	CTGTCTTTC	GAGCCGAG	GCAGGATGT	GCTCAGGG	GACTGCTCG	360
	ACCTGGGGCT	CTCGGAGCT	CCTTCCAA	TCAGGCTCT	CACCTCTAC	CTAGACCTCA	420
10	GTATGAACAA	GATAGCTCAG	CTGCTCCCA	ATCCCTGCC	CAGTCTCGC	TTCTGGAGG	480
	AGTTAGCTCT	TGCGGGAAC	GCTCTGACAT	ACATTCCCA	GGGAGCATTC	ACTGGCCTTT	540
	ACAGTCTTAA	AGTTCTTATG	CTGCAGAATA	ATCAGCTAAG	ACACGTACCC	ACAGAAGCTC	600
	TGCAGAAATT	GCGAAGCCTT	CAATCCCTGC	GTCTGGATGC	TAACCAATC	AGCTATGTGC	660
	CCCCAAGCTG	TTTCAGTGGC	CTGCATTCCC	TGAGGCACCT	GTGGCTGGAT	GACAATGCGT	720
15	TAACAGAAAT	GCTAGGCAAC	GCTTTTAGAA	GTTTATCGGC	ATTGCAAGCC	ATGACCTTGG	780
	CCCTGAACAA	AATACACCAC	ATACCAGACT	ATGCCCTTGG	AAACCTCTCC	AGCTTGTGTAG	840
	TTCTACATCT	CCATAACAAT	AGAAATCCACT	CCCTGGGAAA	GAAATGCTTT	GATGGGCTCC	900
	ACAGCCTTGA	GACTTTAGAT	TTAAATTACA	ATAACCTTGA	TGAATTCGCC	ACTGCAATTA	960
20	GGACACTCTC	CAACCTTAAA	GAACTAGGAT	TTCATAGCAA	CAATATCAGG	TCGATACCTG	1020
	AGAAAGCATT	TGTAGGCAAC	CCTTCTCTTA	TTACAATACA	TTTCTATGAC	AATCCCATCC	1080
	AATTGTGTGG	GAGATCTGCT	TTTCAACATT	TACCTGAACT	AAGAACACTG	ACTCTGAATG	1140
	GTGCCTCACA	AATAACTGAA	TTTCTGATT	TAACTGGAAC	TGCAAACCTG	GAGAGTCTGA	1200
	CTTTAACTGG	AGCACAGATC	TCATCTCTTC	CTCAACCGT	CTGCATCAG	TTACCTAATC	1260
25	TCCAAGTGCT	AGATCTGTCT	TACAACCTAT	TAGAAGATT	ACCCAGTTT	TCACTCTGCC	1320
	AAAAGCTTCA	GAAATTTGAC	CTAAGACATA	ATGAAATCTA	CGAAATTAAG	GTTGACACTT	1380
	TCCAGCAGTT	GCTTAGCCTC	CGATGCTGTA	ATTTGGCTTG	GAACAAAATT	GCTATTATTTC	1440
	ACCCCAATGC	ATTTTCCACT	TTGCCATCCC	TAATAAAGCT	GGACCTATCG	TCCAACCTCC	1500
	TGTGCTCTTT	TCCATATACT	GGGTACATG	GTTTAACTCA	CTTAAATTA	ACAGGAAATC	1560
30	ATGCCTTCTA	GAGCTTGATA	TCATCTGAAA	ACTTCCAGA	ACTCAAGGTT	ATAGAAATGC	1620
	CTTATGCTTA	CCAGTGCTGT	GCATTTGGAG	TGTGTGAGAA	TGCCTATAAG	ATTCTAATC	1680
	AATGGAATAA	AGGTGACAAC	AGCAGTATGG	ACGACCTTCA	TAAGAAAGAT	GCTGGAATGT	1740
	TTCAGGCTCA	AGATGAACGT	GACCTTGAAG	ATTTCTGCT	TGACTTTGAG	GAAGACCTGA	1800
	AAGCCCTTCA	TCTAGTGCAT	TGTTCACTT	CCCCAGGCC	CTTCAAAACC	TGTGAACACC	1860
35	TGCTTGATGG	CTGGCTGATC	AGAATTGGAG	TGTGGAACAT	AGCAGTTCTG	GCACTTACTT	1920
	GTAATGCTTT	GGTGACTTCA	ACAGTTTTC	GATCCCTCT	GTACATTTC	CCCATTAAC	1980
	TGTTAATTGG	GGTGATCGCA	GCAGTGAACA	TGCTCACGG	AGTCTCCAGT	CCCGTGTCTG	2040
	CTGTTGTGGA	TGCGTTCACT	TTTGGCAGCT	TTGCAAGACA	TGGTGCCTGG	TGGGAGAAATG	2100
	GGGTGTGGTG	CCATGTACCT	GGTTTGTGT	CCATTTTGT	TTCAGAAATCA	TCTGTTTTC	2160
40	TGCTTACTCT	GGCAGCCCTG	GAGCGTGGGT	TCTCTGTGAA	ATATTCTGCA	AAATTGTGAA	2220
	CGAAAGCTCC	ATTTTCTAGC	CTGAAAGTAA	TCATTTTGCT	CTGTGCCCTG	CTGGCCTTGA	2280
	CCATGGCCGC	AGTTCCCTCG	CTGGGTGGCA	GCAAGTATGG	CGCCTCCCT	CTCTGCCCTG	2340
	CTTTGCCCTT	TGGGAGGCC	AGCAACCATG	GCTACATGGT	CGCTCTCATC	TTGCTCAATT	2400
	CCCTTGTCTT	CCTCATGATG	ACCATTGCCT	ACACCAAGCT	CTACTGCAAT	TGGACAAGG	2460
45	GAGACCTGGA	GAATATTGG	GACTGCTCTA	TGGTAAACA	CATTGCCCTG	TGTCTCTTCA	2520
	CCAACTGCAT	CCTAAACTGC	CCTGTGGCTT	TCTTGTCTT	CTCCTCTTAA	ATAAACCTTA	2580
	CATTATTACA	TCTTGAAGTA	ATTAAGTTTA	TCCTTCTGGT	GGTAGTCCCA	CTCTCTGCAT	2640
	GTCTCAATCC	CCTTCTCTAC	ATCTGTGTCA	ATCCTCACTT	TAAGGAGGAT	CTGGTGAGCC	2700
	TGAGAAGACA	AACCTACGTC	TGGACAAGAT	CMAAACACCC	AAGCTTGTAT	TCAATTAATC	2760
50	CTGATGATGT	CGAAAAACAG	TCCTGTGACT	CAACTCAAGC	CTTGGTAACC	TTTACCAGCT	2820
	CCAGCATCAT	TTATGACCTG	CCTCCAGTTC	CCGTGCCATC	ACCAGCTTAT	CCAGTGACTG	2880
	AGAGCTGCCA	TCTTTCTCT	GTGGCATTTG	TCCCATGTCT	CTAATTAATA	TGTGAAGGAA	2940
	AATGTTTTC	AAGGTTGAGA	ACCTGAAAT	GTGAGATTGA	GTATATCAGA	GCAATTAATTA	3000
	ATAAGAAGAG	CTGAGGTGAA	ACTCGGTTTA	AA			

**A228 Protein sequence**

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
65	MDTSRLGVLL	SLPVLQLAT	GGSSPRSGVL	LRGCPHCHC	EPDGRMLLRV	DCSDLGLSEL	60
	PSNLSVPTSY	LDLSMNNISQ	LLPNPLPSLR	FLBELRLAGN	ALTYIPKAP	TGLYSLKVLN	120
	LQNNQLRHVP	TEALQNLRLS	QSLRLDANHI	SYVPPSCPSG	LHSLRLWLWD	DNALTEIPVQ	180
70	AFRSLAQFA	MTLALNKH	IPDYAPGNLS	SLVVLHLENN	RIHSLGKKCF	DGLHSLTLD	240
	LNYYNLDDEF	TAIRTLNLSK	ELGFHSNNIR	SIPEKAFVGN	PSLITIHFDY	NPIQFVGRSA	300
	FQHLPELRTL	TLAGASQITE	FFDLTGTAHL	ESLTLTGAQI	SSLPTQVCNQ	LPNLQVLDSL	360
	YNLLEDLPFS	SVCQKLQKID	LRHNEIYEIK	VDTPQQLLSL	RSLNLAWNKI	AIHPNAPST	420
	LPSLIKLDSL	SNLSSFPIT	GLHGLTHLKL	TGNHALQSLI	SEENFPPELV	TEMPYAYQCC	480
75	AFGVCSNAYK	ISNQWNGKDN	SSMDLHKKD	AGMFOAQDER	DLEDPLDPE	EDLKALHSVK	540
	CSPSPGPFKP	CEHLLDGWLI	RIGVWTIAVL	ALTQNALVTS	TVFRSPLYIS	PIKLIGVIA	600
	AVNMLTGVSS	AVLAGVDAFT	FGSFARHQA	WENGVGCHVI	GFLSIFASES	SVPLLTALAL	660
	ERGFVSKYSA	KFETKAPFSS	LKVIILLCAL	LALTMARVPL	LGGSKYGASP	LCLPLPFGE	720
	STMGMVALI	LLNSLCFLM	TIAYTKLYCN	LDKGDLNLI	DCSMVKHIAL	LLPTNCLINC	780
80	PVAFLSFSSL	INLTPISEV	IKFILLVVVP	LPACLNPLLY	ILFNPHFKED	LVSLEKQTYV	840
	WTRSKHPSLM	SINSDVBEKQ	SCDSTQALVT	FTSSSITYDL	PPSSVSPSPAY	PVTESCHLSS	900
	VAFVPC						

Table 75: See Table 1

Table 76A depicts Seq ID No; UnigeneID; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

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Seq ID No:	Sequence ID No for sequences in table				
Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigeneID:	Unigene number				
Unigene Title:	Unigene gene title				
Pred Subcell Loc:	Predicted sub-cellular localization				
Seq ID No	Pkey	ExAccn	UnigeneID	Unigene Title	Pred Subcell Loc
Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid	plasma membrane
Seq ID 3 & 4	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	plasma membrane
Seq ID 5 & 6	429423	AI016712	Hs.287797	Integrin, beta 1 (fibronectin receptor,	plasma membrane
Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
Seq ID 17 & 18	414577	AK56548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	plasma membrane
Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
Seq ID 35 & 36	423961	D13666	Hs.136348	perlestin (OSF-2os)	secreted
Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
Seq ID 39 & 40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 41 & 42	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 43 & 44	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	secreted
Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	secreted
Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
Seq ID 57 & 58	411789	AF245505	Hs.72157	Adicran	secreted
Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
Seq ID 63 & 64	421552	AF026692	Hs.105700	secreted fritzled-related protein 4	secreted
Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 73 & 74	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	plasma membrane
Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 107 & 108	432201	AI538613	Hs.288241	Transmembrane protease, serine 3	plasma membrane
Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
Seq ID 115 & 116	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-II	intracell
Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
Seq ID 119 & 120	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 121 & 122	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 123 & 124	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
Seq ID 127 & 128	452679	Z42387	Hs.63883	transmembrane, prostate androgen induced	plasma membrane
Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
Seq ID 131 & 132	422048	NM_012445	Hs.288126	spodinin 2, extracellular matrix protein	secreted
Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
5	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
10	Seq ID 157 & 158	413324	V00571	Hs.75294	coricotropin releasing hormone	secreted
	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	secreted
	Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
15	Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uropod 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13645	Hs.97234	uropod 2	plasma membrane
	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 (Hsa	plasma membrane
20	Seq ID 176 & 177	402075			ENSP0000021056:Plasma membrane calcium	secreted
	Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
25	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159551	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
	Seq ID 194 & 195	404875			NM_022819: Homo sapiens phospholipase A2	intracell
30	Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	plasma membrane
	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
	Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
35	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
40	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			C15000305: g[3806122]gb AAC69198.1  (AF0	intracell
	Seq ID 221 & 222	405932			C15000305: g[3806122]gb AAC69198.1  (AF0	intracell
	Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
45	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
	Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
	Seq ID 233 & 234	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	secreted
50	Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
	Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
55	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	ESTs	
	Seq ID 252	429466	M85835	Hs.12827	ESTs	
60	Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
	Seq ID 255 & 256	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	plasma membrane
	Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
65	Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
	Seq ID 265 & 266	444471	AB020684	Hs.11217	KIAA0877 protein	plasma membrane
	Seq ID 267 & 268	409395	U46745	Hs.336678	dystrobrevin, alpha	secreted
	Seq ID 269 & 270	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
	Seq ID 271 & 272	433800	AI034361	Hs.135150	lung type-4 cell membrane-associated gly	plasma membrane
70	Seq ID 273	458435	AA18718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 274	458435	AA18718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 275 & 276	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	plasma membrane
	Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	secreted
	Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	plasma membrane
75	Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KCOT-lik	plasma membrane
	Seq ID 283 & 284	404049			NM_018937: Homo sapiens protocadherin be	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
	Seq ID 287 & 288	404029			NM_018936: Homo sapiens protocadherin be	plasma membrane
	Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
80	Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
	Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	plasma membrane
	Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gb3hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
	Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
10	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
20	Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	midline (neurite growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progesterone-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001596	Hs.85266	integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
40	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
45	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalinin	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
50	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
60	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188"gi 12738842 ref NP_073725.1  p	secreted
	Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter	plasma membrane
70	Seq ID 435 & 436	407242	M18728		gbHuman nonspecific crossreacting antig	plasma membrane
	Seq ID 437 & 438	407242	M18728		gbHuman nonspecific crossreacting antig	plasma membrane
	Seq ID 439 & 440	407242	M18728		gbHuman nonspecific crossreacting antig	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
80	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176558	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (Intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted



5	Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AJ694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 471 & 472	452194	AJ694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW359771	Hs.52620	integrin, beta 8	plasma membrane
10	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
	Seq ID 483 & 484	428187	AJ687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
15	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	secreted
	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neuropsin/ovasins) (KLKB)	secreted
20	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	secreted
25	Seq ID 511 & 512	453392	U23752	Hs.32984	SRF (sex determining region Y)-box 11	intracell
	Seq ID 513	431989	AW972870	Hs.291069	ESTs	
	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
	Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
30	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (	secreted
35	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
	Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
40	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	secreted
	Seq ID 541 & 542	407792	AJ077715	Hs.39384	putative secreted ligand homologous to f	secreted
	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheri	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95795	Hs.276695	Homo sapiens protein mRNA, complete cds	plasma membrane
45	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
50	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
	Seq ID 561 & 562	418386	AJ765805	Hs.26691	ESTs	plasma membrane
	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AJ420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
55	Seq ID 569 & 570	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 571 & 572	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	X51405	Hs.75360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
60	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	plasma membrane
	Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
65	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	plasma membrane
	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	intracell
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
70	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
	Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
75	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI186431	Hs.296638	prostate differentiation factor	secreted
80	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
	Seq ID 621 & 622	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.26538	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	clckkopf (Xenopus laevis) homolog 4	secreted



Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

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Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

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Table 76C:

20 Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

25 Strand: Indicates DNA strand from which exons were predicted.  
 NT\_position: Indicates nucleotide positions of predicted exons.

25

Pkey	Ref	Strand	NT_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59958
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

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Table 77 provides Pkey, Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

	Seq ID No:	Sequence ID No for sequences in table		
5	Pkey:	Unique Eos probeset Identifier number		
	Disease Indications:	Diseases designated for coverage as described in Table 1		
	Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
15	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
20	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
25	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
30	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
35	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
40	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab, sm, CTL, imaging
	Seq ID 69 & 70	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
45	Seq ID 71 & 72	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 73 & 74	409079	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 79 & 80	451398	breast, ovarian	CTL
50	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab, sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
55	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab, sm, CTL, imaging
	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
60	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
	Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
65	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
70	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab, CTL, imaging
	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
75	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
80	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 422330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	CTL, diagnostic
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	Ab, sm, CTL, imaging
25	Seq ID 194 & 195 404875	bladder	sm, CTL
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, CTL, imaging
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, diagnostic
	Seq ID 200 & 201 420876	pancreas, bladder	Ab, sm, CTL, imaging
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	sm, CTL
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
	Seq ID 206 & 207 446673	bladder	sm, CTL
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	Ab, CTL, imaging
	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	sm
40	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	sm
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, CTL, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, diagnostic
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 438380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic
	Seq ID 263 & 264 419704	glioblastoma	sm, CTL
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	Ab, sm, CTL, imaging
	Seq ID 267 & 268 409395	glioblastoma	Ab, CTL, diagnostic
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, imaging
	Seq ID 273 458435	glioblastoma	
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
75	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428295	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, sm, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging

	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
	Seq ID 323 & 324 423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
10	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 428610	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
15	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
	Seq ID 359 & 360 418462	lung, bladder	Ab, imaging
	Seq ID 361 & 362 410274	lung, renal	diagnostic
	Seq ID 363 & 364 439606	lung, bladder, head & neck, cervical	Ab,sm, imaging
30	Seq ID 365 & 366 404877	lung, bladder	CTL
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 369 & 370 109424	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	Ab,sm, CTL, imaging
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	Ab,sm, CTL, imaging
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	CTL, diagnostic
	Seq ID 391 & 392 332180	lung	Ab, sm, imaging
45	Seq ID 393 & 394 408790	lung	Ab,sm, CTL, imaging
	Seq ID 395 & 396 408790	lung	Ab,sm, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, imaging
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, sm, diagnostic
55	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, imaging
	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, CTL, diagnostic
	Seq ID 419 & 420 428486	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, diagnostic
	Seq ID 431 & 432 429547	pancreas, head & neck, lung, ovarian	Ab,sm, CTL, imaging
	Seq ID 433 & 434 425921	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	CTL
	Seq ID 441 & 442 432596	pancreas, breast	Ab, CTL, imaging
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	CTL
70	Seq ID 445 & 446 423685	pancreas, uterine, colon	Ab, CTL, diagnostic
	Seq ID 447 & 448 428392	pancreas	Ab,sm, CTL, imaging
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab, CTL, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
75	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab, CTL, diagnostic
	Seq ID 469 & 470 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	Ab, diagnostic

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
5	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, sm, imaging
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436982	ovarian, fibrosis	Ab, CTL, diagnostic
20	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	
	Seq ID 515 & 516 409178	ovarian, breast	Ab, CTL, diagnostic
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 527 & 528 452097	ovarian	Ab, sm, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	Ab, sm, CTL, imaging
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	CTL
35	Seq ID 539 & 540 411773	ovarian	Ab, sm, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, sm, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, sm, CTL, imaging
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, sm, CTL, imaging
	Seq ID 567 & 568 433466	prostate	Ab, CTL, diagnostic
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, CTL, imaging
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, sm, diagnostic
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, sm, CTL, imaging
	Seq ID 583 & 584 412628	prostate	Ab, CTL, diagnostic
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
70	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, CTL, diagnostic
75	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, imaging
	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 623 & 624 439018	uterine, stomach, prostate	Ab, sm, CTL, imaging
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	CTL
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	Ab, CTL, diagnostic
80	Seq ID 629 & 630 456662	uterine, ovarian	CTL
	Seq ID 631 & 632 418281	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 633 & 634 429903	lung	sm

Table 78

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM\_001400

Coding sequence: 251..1399

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	AAAGCTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	180
	CTCGCCTGAC	CCTCTAGCGT	TCGTCTGGAG	TAGCGCCACC	COGGCTTCCT	GGGGACACAG	240
	GGTTGGACAC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCACCGCA	GCTCGGTCTC	300
	TGACTACGTC	AACATGATA	TCATCGTCCG	GCATTACAAC	TACACGGGAA	AGCTGAATAT	360
15	CAGCGCGGAC	AAGGAGAAC	GCATTAAACT	GACCTCGGTG	GTGTTCAATC	TCATCTGCTG	420
	CTTTATCATC	CTGGAGAAC	TCCTTGCTTT	GCTGAOCATT	TGAAAACCA	AGAAATTCCA	480
	CCGACCCATG	TACTATTTTA	TTGGCAATCT	GGCCCTCTCA	GACCTGTTGG	CAGGAGTAGC	540
	CTACACAGCT	AACCTGCTCT	TGCTGGGGC	CACCACTTAC	AAGCTCACTC	CCGCCAGTGT	600
	GTTCCTGGCG	GAAGGGAGTA	TGTTTGTCGC	CCTGTGAGCC	TCGTTGTCA	GTCTCTCGC	660
20	CATCGCCATT	GAGCGCTATA	TCACAATGCT	GAAAAATGAAA	CTCCACACCG	GGAGCAATAA	720
	CTTCGCGCTC	TTCTGCTTAA	TCAGCGCCTG	CTGGGTCTATC	TCCTCATCC	TGGGTGGCCT	780
	GCCTATCATG	GGCTGGAAGT	GCATCAGTGC	GCTGTCCAGC	TGCTCCACCG	TGCTGCCGCT	840
	CTACACAGAG	CACATATATCC	TCCTCTGCAC	CACGGTCTTC	ACTCTGCTTC	TGCTCTCCAT	900
	GTCTATTCTG	TACTGAGAAA	TCTACTCCTT	GGTCAGGACT	CGGAGCCGCC	GCTGACGTTT	960
25	CCGCAAGAAC	ATTTCCAAGC	CCAGCCGACG	CTCTGAGAA	TGCTGGGCG	TGCTCAAGAC	1020
	CGTAATATATC	GTCTGAGGCG	TCCTCATCGC	CTGCTGGGCA	CGCTCTTCA	TCCTGCTCCT	1080
	GCTGGAGTGT	GGCTGCAAGG	TGAAGACCTG	TGACATCCTC	TTGAGAGCGG	AGTACTTCTT	1140
	GGTGTAGCTT	GTCTCAACT	CCGGCACCAA	CCCATCATTT	TACACTCTGA	CCAACAAGGA	1200
	GATGCGTGGG	GCCTCATATC	GGATCATGTC	CTGCTGCAAG	TGCCCGAGCG	GAGACTCTGC	1260
30	TGGCAAAATTC	AAGCGACCCA	TCATGCGCGG	CATGGAATTC	AGCCGACGCA	AATCGGACAA	1320
	TTCTCTCCAC	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAA	1380
	CGTCAACTCT	TCTTCTAGAA	ACTGGAAGCT	GTCCACCCAC	CGGAAGCGCT	CTTTACTTGG	1440
	TCGCTGGCCA	CCCGAGTGT	TGGAAAAAAA	TCTCTGGGCT	TCGACTGCTG	CCAGGGAGGA	1500
	GCTGCTGCAA	CCGAGAGGGA	GGAAAGGGGA	GAATACGAAC	AGCCTGGTGG	TGTGGGTTGT	1560
35	TGGTGGGTAG	AGTTAGTTCC	TGTGAACAAT	GCATGCGGAA	GGGTGGAGAT	CAGGTCCCGG	1620
	CTTGGAATAT	ATATTCTAAC	CCCTGGAGC	TTTGATTTTG	CACCTGAGCA	AAGGTCTAGC	1680
	ATTGTCAAGC	TCCTAAAGGG	TTCAATTTGGC	CCCTCCTCAA	AGACTAATGT	CCCATGTGTA	1740
	AAGCGTCTCT	TTGTCTGGAG	CTTTGAGGAG	ATGTTTTCTT	TCATTTAGT	TTCAAAACCA	1800
40	AGTGAGTGTG	TGCATCTCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCACCA	CCCCACCTTC	1860
	CCCTCCCTTC	ATACCCCTCC	TCAACGTTCT	TTTACTTTAT	ACTTTAACTA	CCTGAGAGTT	1920
	ATCAGAGCTG	GCGTGTGGGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTGAGTAGC	1980
	TAGGCTGTGG	GAGATGGAAG	ATGGTTTGGG	GGTGTAAGAC	AATGTCTCTC	GCTGAGGCCA	2040
	AAGTTTCCAT	GTAAAGCGGA	TCGGTTTTTT	GGAATTTGGT	TGAAGTCACT	TTGATTTCTT	2100
45	TAAAAAACAT	CTTTTCAATG	AAATGTGTTA	CCATTTTATA	TCCATTGAAG	CCGAAATCTG	2160
	CATAAGGAAG	CCCACTTTAT	CTAATGATA	TTAGCCAGGA	TCCTTGTTGT	CCTAGGAGAA	2220
	ACAGACAAGC	AAAAACAAAGT	GAAAAACGAA	TGGATTAATC	TTTGCAAAAC	AAGGGAGATT	2280
	TCCTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGCTCTTC	CCACTTTTGT	TGATGTTTAT	2340
	TTCAAGATCT	TGTGTGATTC	ATTTCAGCA	ACAACATGTT	GTATTTTGT	GTGTTAAAG	2400
50	TACTTTTCTT	GATTTTGTAA	TGTATTTGTT	TCAGGAAGAA	GTCATTTTAT	GGATTTTCTT	2460
	AACCGGTGTT	AACTTTCTTA	GAATCCACCC	TCTTGTGCCC	TTAAGCATTA	CTTTAACTGG	2520
	TAGGGAACGC	CAGAACTTTT	AAGTCCAGCT	ATTCAATAGA	TAGTAATTGA	AGATATGTAT	2580
	AAATATTACA	AAGAATAAAA	ATATATTACT	GTCTCTTTAG	TATGTTTTC	AGTGCAATTA	2640
	AACCGAGAGA	TGCTCTGTTT	TTTTAAAAAG	AATAGTATTT	AATAGTTTTC	TGACTTTTGT	2700
55	GGATCATTTT	GCATCATAGCT	TTATCAACTT	TTAAACATTA	ATAAACTGAT	TTTTTTAAAG	

Seq ID NO: 2 Protein sequence

Protein Accession #: NP\_001391

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60	MGPTSVPLVK	AHRSSVSDYV	NYDIIVRHYN	YTGKLNISAD	KENSIKLTST	VFILICCFII	60
	LENIFVLLTI	WMTKFKFHRPM	YFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
	BGSMFVALSA	SVFSLLAIAI	ERYITMLRKM	LHNGSNRNL	FLLLISACVI	SLILGGLPIM	180
65	GWNCISALSS	CSTVLPYHK	HYILFCTTVF	TLLLLSIVIL	YCRIYSLVRT	RSRLTFRKN	240
	ISKASRSSEK	SLALLKTVII	VLSVFIACWA	PLFILLLLDV	GCKVKTCDIL	FRAEYFLVLA	300
	VLSGNTNPII	YTLTNKEMRR	AFIRIMSCCK	CPSGDSAGKF	KRPILAGMEF	SRSKSDNSSH	360
	PQKDEGNPE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #: NM\_002205.1

Coding sequence: 1..3149

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	CGCCGACCCC	CGCTSSGTCC	GCTGCTGTTG	CTGCTSSGTG	CGCCGCCACC	CAGGGTGGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTAA	COGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
80	CCCAAGGCTA	ATACAGGCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTT	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAAG	CTCTGGGCTC	360
	CTGGAGTCTT	CACTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGTGAG	420
	TGGTTGCGGG	CAACAGTTCT	AGCCCATGGC	TCCTCCATCT	TGGCATGGGC	TCCACTGTAC	480
	AGCTGGGCGA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACTGTCTA	CCTCTCCACA	540
	GATAACTTCA	CCGGAATCTT	GGAGTATGCA	CCCTGCGGCT	CAGATTTTCA	CTGGGCGAGC	600

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ATTGCAGAA CTATTATCCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780  
CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGSC TGTGTGTGAA 840  
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Seq ID NO: 4 Protein sequence  
Protein Accession #: NP\_002196.1

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LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVGTCLST 180  
DNFTRILEYA PCRSDFSMAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFVQ GQILSATQEQ 240  
IAESYYPEYL INLVQQQLQT RQASSIYDDS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300  
GYVTILNGSD IRLSYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360  
EVRGVYVYLG HPAGIEPTPT LTLTGHDFFG RFGSSSLTPLG DLDQDGVNDV AIGAPFPGGT 420  
QQGVVVFVFG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGG YPDLIVGSFG 480  
VDKAVVYRGR FIVSASASLT IFFAMPNPEE RSCSLEGNFV ACINLSFCLN ASGKHVADSI 540  
GPTVELQLDW QKQKGGVRRR LPLASRQATL TQTLIIONGA REDCREMKIY LRNSESEFRDX 600  
LSPHIALNPF SLDPQAPVDS HGLRPLALHY SKSRIEDKQ ILLDCGENDI CVPDLQLEVP 660  
GEQNHVYLDG KNALNLTFHA QNVGEGGAYE AELRVTPAPE AEYSGLVRHP GNFSSLSCDY 720  
FAVNSRLLV CDLGNPMKAG ASLNGGLRFT VPHLRDTKKT IQDFQILSK NLNNSQSDV 780  
SFRLSVEAQA QVTINGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840  
SQGVLELSCF QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLSH QXKREAPSR 900  
SASSGPIILK CPEAECFRLR CELQPLHQOE QSLSQLHFRV WAKTFLQREH QPFSLQCEAV 960  
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Seq ID NO: 5 DNA sequence  
Nucleic Acid Accession #: NM\_002211.1  
Coding sequence: 1..2397

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GAATGCACCG CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
AGTTCAGAAA TCTGCAGTAA CAATGGAGAG TGGCTCTGCG GACAGTGTGT TTGTAGGAAG 1620
AGGGATAATA CAAATGAAAT TTATTCTGGC AAATCTCGCG AGTGTGATAA TTTCAACTGT 1680
GATAGATCCA ATGGCTTAAT TTGTGGAGGA AATGGTGTTC GCAAGTGTG TGTGTGTGAG 1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTT TGGATACTAG TACTTGTGAA 1800
GCCAGCAACG GACAGATGCG CAATGGCGCG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT 1860
ACAGATCCGA AGTTTCAAGG GCAAACTGTG GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
GCTGAGCATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAA GAAAGACAA 1980
TGCAACAGG AATGTTCCTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
CAGCCGTTCC AACCTGATCC TGTGTCCCAT TGTAAAGGAGA AGGATGTGGA CGACTGTGG 2100
TTCTATTTTA CGTATTCACT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT 2160
CCAGAGTGTG CCCTGTGTC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAAAT 2220
GTTCTTATTG GCCTTGCATT ACTGCTGATA TGAAGCTTT TAATGATAAT TCATGACAGA 2280
AGGGAGTTTG CTAAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAATAA 2340
CCTATTATTA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGG AAAATGA

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Seq ID NO: 6 Protein sequence  
Protein Accession #: NP\_002202.1

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1 11 21 31 41 51
| | | | |
MNLQPIPWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STPLQEGMPT 60
SARCDLLEAL KKKGCPDDI ENPRGSKDIK KNRNVTNRSK GTAELKLPED ITQIQPQQLV 120
LRLRSGEPQT FTLKFKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180
RIGFGSPVEK TMVPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKGE VFNELVGQR 240
ISGNLDSPEG GFDALMQVAV CGSLIGWRNV TRLLVFSFDA GFHFAGDGKL GGIIVLPNDGQ 300
CHLENNMYTM SHYDYPSIA HLQKLSENN IQTIFAVTEE PQPVYKELKN LIPKSAVGL 360
SANSNNVQL IIDAYNSLSS EVILENGKLS EGVITISYKSY CKNGVNGTGB NGRKCSNISI 420
GDEVQFEISI TSNKCPKIDS DSPKIRPLGF TEEVEVILQY ICECEQSGE IPSPFKCHGE 480
NGTFECGACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCQCVCRK 540
RDNTHIYSG KPCEDNPNFC DRNGLICGG MGVCCKRVE CNPNYTGSA DCSLDSTCE 600
ASNGIQNGR GICEGVCCK TDPKFQGTQ EMCQTCLGVC AEHKECVQCR AFNKGKUDT 660
CTQECSEYNI TKVESRDKLP QVQPDVPSH CKEKDVDDCW FYPTYSVNGN NEVMVHVVEN 720
PECPTGPDI PIVAGVVGIGI VLIGLALLLI WKLMIIDHR REFAPKFEKE MNAKWDGTEN 780
PIYKSAVTTV VNPKYEGK

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Seq ID NO: 7 DNA sequence  
Nucleic Acid Accession #: NM\_002425  
Coding sequence: 26..1453

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1 11 21 31 41 51
| | | | |
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AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCAGCAAA TACCTAGAAA AGTACTACRA CCTOGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATG TTAATAAAAT CCAAGGAATG CAGAAGTTC TTGGGTTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTCC TGGCATGCGG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGAAGAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
CGTTGCTGCT CATGAACCTG GGCCTCCTT GGGGCTCTTT CACTCAGCCA ACACGGAAGC 720
TTGATGTATC CACTCTACCA ACTCAITCAC AGAGCTCGCC CAGTTCGCCC TTTGCAAGA 780
TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCA CAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTGGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTTTGGCC 1020
CTCTCTTCCA TCAATTTTGG ATGCTGCATA TGAAGTTAAG AGCAGGGACA CCGTTTATTT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGTG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT 1560

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GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCCTC 1620  
 ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680  
 ATGTATTTCCT ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740  
 CTT

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Seq ID NO: 8 Protein sequence  
 Protein Accession #: NP\_002416

10 1 11 21 31 41 51  
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 MHLAFLVLLC LFVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVQKF RRKDSNLIVK 60  
 KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120  
 PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS FAVKEHGFY SFDGPGHSLA 180  
 HAYPPGPGLY GDHFPDDDEK WTEDASGTNL FLVAHELGH SLGLFHSANT EALMPLYLYN 240  
 15 FTELAGFRLS QDDVNGIQSL YGPPPPASTEE PLVPTKSVPS GSEMPAKCOP ALSFDAISTL 300  
 RGEYLPFKDR YFWRSSHWNP EPEPHLISAF WPSLPSYLD AYEVSNRDVT FIFKGNFEWA 360  
 IRGNEVQAGY PRGIHTLGFPT PTIRKIDAAV SDKEKKKTYF PAADKYWRFD ENSQSMEOQF 420  
 PRLIADDFPG VEPKVDVAVLQ AFGFFYFSPG SSQFEEDPNA RMVTHILKSN SWLHC

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Seq ID NO: 9 DNA sequence  
 Nucleic Acid Accession #: XM\_058189.2  
 Coding sequence: 169..774

25 1 11 21 31 41 51  
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 GAAGACCAGC TCAGCTCTTC AGTTGTGTGAT CATGTCTAT TGTTCTCCAA ACAGTAAACC 60  
 AGTATTTCAC ACTGAGATTG TCGGCTCGGG GTATATTCCA ATTCGCGTC TCCTCATGAA 120  
 TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTTCCTAAG AGGGCAAAAT GGGGTCTCGG 180  
 AAGTGTGGAG GCTGCTTAAG TTGTTTGTCT ATTCCGCTTG CACTTTGGAG TATAATCGTG 240  
 30 AACATATTAT TGTATTTCCT GAATGGGCAA ACTTCCTATG CATCCAGCAA TAAACTCACC 300  
 AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360  
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAACTGTC 420  
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTCTT 480  
 GGATACCTGC TGGTCACTTC TGCTTGGGT CTTGTCCAAG GGCCATATTG CCGCACCCCTT 540  
 35 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA 600  
 TGGATTCACT GCCTGGAACC TGCACTGTT GTGGAGTGA ACATCATTTT ATTTTCCATT 660  
 CTCATAACCC TCAGTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720  
 TCCAAGATAC TGTGTGGGAG CTATTCACTG ATCTTCCAGC CTGGAATCAT TTGAATAAGG 780  
 40 ACAAAATGTT TTCCATTATC AAGACATGGC CATCTATCTA AATATTATAT CAACTGTGTA 840  
 GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCATT TGGTGTATT TGTGAAAAA 900  
 TTTGCAGTCC TCACTGCACA TGCAAGTATA CCACCCCTCC ATTTAGTATG TTTTAAAGT 960  
 AATATGCATC AGAACTTCA GAAATACCTC TGCCCTTTGA TCAACAAAT CCATTTCCTA 1020  
 GAATCTGTAC TAGGGAAGTA AATAAGAATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080  
 45 TGCAACATTA TTTAATATTC TGGAAAATG GAAACACCCC AAAATCTTAA ACTCAGAGGA 1140  
 AGGATTAAAT AAAGAGTGGT ACATCTGTGA AATGTTTTCT GATATTAATA AAAAAATTAA 1200  
 AAAAAAATA AAGAGTACTA CATGGTTGTA AAA

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Seq ID NO: 10 Protein sequence  
 Protein Accession #: XP\_058189.1

55 1 11 21 31 41 51  
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 MGSRRCKGCL SCLLIPLALW SIIVNILLYP PNGQTSYASS NKLTNYVWYF EGICFSGIMM 60  
 LIVTTVLVLV ENNMNYKCCQ SENCSSKKYVT LLSIIFSSLG IAFSGYCLVI SALGLVQGPY 120  
 CRTLDGWEYA FEGTAGRPLT DSSIWIQCLE PAHVVEWNII LFSILITLSG LQVIICLIRV 180  
 VMQLSKILCG SYSVIFQPGI I

60

Seq ID NO: 11 DNA sequence  
 Nucleic Acid Accession #: NM\_002421.2  
 Coding sequence: 1..1409

65 1 11 21 31 41 51  
 | | | | | |  
 ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTG ACACAGCTTC 60  
 CCAGCGACTC TAGAAACACA AGAGCAGAGT GTGGACTTAG TCAGAAATA CCTGGAATAA 120  
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCAGTG 180  
 GTTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTACTGG GAAACCAAGT 240  
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCGTGATG GCTCAGTTT 300  
 70 GTCCCTCACTG AGGGGAACCC TCGCTGGGAG CAACACATC TGACCTACAG GATTGAAAAT 360  
 TACAGCCAGC ATTTGCCAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420  
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480  
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGAAC TGGAGGAAAT 540  
 CTGTCTCATG CTTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600  
 75 GAAAGTGGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTGCGGC TCATGAAGTC 660  
 GGCCATTCTC TTGGACTCTC CCAATTCTACT GATATCGGGG CTTTGATGTA CCTAGCTAC 720  
 ACCTTCAGTG GTGAGTTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780  
 GGACGTTCCT AAAATCTGT CCAGCCCATC GGCCCAAAA CCCCAGAGC ATGTGACAGT 840  
 AAGCTAACCT TTGATGCTAT AACTAAGATT CGGGGAGAGG TGATGTTCTT TAAAGACAGA 900  
 80 TTCTACATGC GCACAAATCC CTCTCAACCG GAAGTTGAGC TCAATTTTCA TTCTGTTTTT 960  
 TGSCCAACAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCGACAG AGATGAAGTC 1020  
 CGGTTTCTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080  
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140  
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200  
 GATGAATATA AAGGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCTT 1260

GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTCTTTTCAT 1320  
 GGAACAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380  
 AATAGCTGGT TCACTGCAG GAAAAATTAG

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Seq ID NO: 12 Protein sequence

Protein Accession #: NP\_002412.1

1	11	21	31	41	51	
MHSFPLLLL	LFWGVVSHSF	PATLETQEQD	VDLVQKYLEK	YYNLKNDGRQ	VEKRRNSGPV	60
VEKLKMQQEF	FGLKVTGKPD	AETLKVMKQP	RCGVDPVAQF	VLTEGNPRWE	QTHLTIRIEN	120
YTPDLPRADV	DHAIEKAPOL	WSNVTPLTFT	KVSEGGADIM	ISFVRGDHRD	NSPFDGPGGN	180
LAHAFQPGPG	ICGDAHFDED	ERWTNNFREY	NLHRVAAHEL	GHSGLSLHST	DIGALMYPGY	240
TFSGDVQLAQ	DDIDGIQAIY	GRSQNPVQPI	GPQTPKACDS	KLTFDAITTI	RGEVMPFKDR	300
FYMRNTNPFYP	EVELNPFISV	WPQLPNGLEA	AYEFADRDEV	RPFKGNKYWA	VQQQNVLHGY	360
PKDIYSSFGF	PRTVKHIDAA	LSEENTGKTY	FFVANKYWRY	DEYKRSMDPG	YPKMIAHDFP	420
GIGHKVDVAV	MKDGFFYPFH	GTRQYKFDPK	TKRILTLQKA	NSWFNCRKN		

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Seq ID NO: 13 DNA sequence

Nucleic Acid Accession #: NM\_002421.2

Coding sequence: 1..1409

1	11	21	31	41	51	
ATGCACAGCT	TTCTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
TACTACAACC	TGAAGAATGA	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCCAAGT	180
GTTGAAAAAT	TGAGGCAAA	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACAGAT	240
GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCTGATGT	GGCTCAGTTT	300
GTCTCTACTG	AGGGGAAACC	TGCTGGGAG	CAACACATC	TGACCTACAG	GATTGAAAA	360
TACACGCCAG	ATTTGCCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACCT	420
TGGAGTAATG	TCACACCTCT	GACATTCAAC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AACCTCTCCT	TTGATGGACC	TGGAGGAAAT	540
CTTGCTCATG	CTTTTCAACC	AGGCCCAAGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
GAAAGGTGGA	CCAACAATTT	CAGAGAGTAC	AACCTACATC	GTGTGCGGCG	TCATGCCCTC	660
GGCCATTCTC	TTGCACTCTC	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
ACCTTCAGTG	GATGATGTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
GAACGTTCCC	AAAATCCTGT	CCAGCCCATC	GGCCCAAAA	CCCCAAAAGC	ATGTGACAGT	840
AAGCTAACCT	TGATGCTAT	AACCTACGAT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900
TTCTACATGC	GCACAAATCC	CTTCTACCGG	GAAGTTGAGC	TCAATTTTAT	TTCTGTTTTC	960
TGGCCACAAC	TGCCAAATGG	GCTTGAAGCT	GCTTACGAAT	TTGCCGACAG	AGATGAAGTC	1020
CGGTTTTTCA	AAGGGGAATA	GTAAGTGGCT	GTTTACGGAC	AGAATGTGCT	ACACGGATAC	1080
CCCAAGGACA	TCTACAGCTC	CTTTGGCTTC	CCTAGAACTG	TGAAGCATAT	CGATGCTGCT	1140
CTTTCTGAGG	AAAACACTGG	AAAAAOCCTAC	TTCTTTGTTG	CTAACAAATA	CTGAGGATAT	1200
GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCAAAA	TGATAGCACA	TGACTTTTCT	1260
GGAATTGGCC	ACAAAGTTGA	TGCAGTTTTC	ATGAAAGATG	GATTTTCTTA	TTTCTTTTCT	1320
GGAACAGAC	AATACAAATT	TGATCCTAAA	ACGAAGAGAA	TTTGACTCT	CCAGAAAGCT	1380
AATAGCTGGT	TCACTGCAG	GAAAAATTAG				

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Seq ID NO: 14 Protein sequence

Protein Accession #: NP\_002412.1

1	11	21	31	41	51	
MHSFPLLLL	LFWGVVSHSF	PATLETQEQD	VDLVQKYLEK	YYNLKNDGRQ	VEKRRNSGPV	60
VEKLKMQQEF	FGLKVTGKPD	AETLKVMKQP	RCGVDPVAQF	VLTEGNPRWE	QTHLTIRIEN	120
YTPDLPRADV	DHAIEKAPOL	WSNVTPLTFT	KVSEGGADIM	ISFVRGDHRD	NSPFDGPGGN	180
LAHAFQPGPG	ICGDAHFDED	ERWTNNFREY	NLHRVAAHAL	GHSGLSLHST	DIGALMYPGY	240
TFSGDVQLAQ	DDIDGIQAIY	GRSQNPVQPI	GPQTPKACDS	KLTFDAITTI	RGEVMPFKDR	300
FYMRNTNPFYP	EVELNPFISV	WPQLPNGLEA	AYEFADRDEV	RPFKGNKYWA	VQQQNVLHGY	360
PKDIYSSFGF	PRTVKHIDAA	LSEENTGKTY	FFVANKYWRY	DEYKRSMDPG	YPKMIAHDFP	420
GIGHKVDVAV	MKDGFFYPFH	GTRQYKFDPK	TKRILTLQKA	NSWFNCRKN		

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Seq ID NO: 15 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 141..1580

1	11	21	31	41	51	
TCTGCGTGTG	CCGGGGCTAG	GGGCTGGAAG	TCCTGGCTCT	AGTTGCACCT	CGGAAGGAAA	60
AGGCAACAG	AGGAGGGAAG	GCGTCTTAGG	ACTGCCTGGA	TCCAGAGCAC	TTTCTCTGGC	120
CTCTACAGGC	CTGTGTGCT	ATGGGTTCCC	CCGCGCGCCC	GGAGGGAGCG	CTGGGCTACG	180
TCGCGAGTT	CACCTGCCAC	TCCTCCGACG	TGCTGGGCAA	CCTCAACGAG	CTGCGCCTGC	240
GCGGGATCCT	CACCTGAGTC	ACGCTGCTGG	TTGGGGGACA	ACCCCTCAGA	GCACACAAGG	300
CAGTTCTCAT	CGCCTGCAGT	GGCTTCTTCT	ATTCAATTTT	CCGGGGCGGT	GCGGGAGTGG	360
GGGTGGAGCT	GCTCTCTCTG	CCGGGGGGTC	CCGAAGGAGG	AGGCTTCGCC	CCTCTATTGG	420
ACTTCATGTA	CACCTCGGCG	CTGCGCCTCT	CTCCAGCCAC	TGCACCGACA	GCTCTAGCGG	480
CCGCCACCTA	TTTGCAGATG	GAGCACGTGG	TCCAGGCGATG	CCACCGCTTC	ATCCAGGCCA	540
GCTATGAACC	TCTGGGATC	TCCCTGCGCC	CCCTGGAAGC	AGAACCOCOA	ACACCCOCAA	600
CGGCCCTTCC	ACCAGGTAGT	CCCAGGCGCT	CCGAAGGACA	CCCAGACCCA	CCTACTGAAT	660
CTCGAAGCTG	CAGTCAAGGC	CCCCCAGTC	CAGCCAGCCC	TGACCCCAAG	GCCTGCAACT	720
GGAAAAAGTA	CAAGTACATC	GTGCTAAACT	CTCAGGCGCT	CCAAGCAGGG	AGCCTGGTCG	780

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GGGAGAGAAG TTCTGGTCAA CCTTGCCCCC AAGCCAGGCT CCCAGTGGGA GACGAGGCCT 840
CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTCCT GGTCCCCAGA 900
GCAGGCTCTC TCCAACTGCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960
CCTACCTCCT CATCTCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC 1020
CACTACCCGG AAGTGAATTT TTCACTGTCC AGAACTGTGA GGCTGTGGCA GGGTGCTCAT 1080
CGGGCTGGGA CTCCTTGGTT CCTGGGGAGC AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140
GGTCTTGGTT CGCTACAAG GGCAACCTTG CCAGTCATCG TACAGTGCAC ACAGGGGAAA 1200
AGCCTTACCA CTGCTCAATC TGGGAGCCCC GTTTTAAACG GCCAGCAAC CTGAAAACGC 1260
ACAGCCGCAT CCATTCCGGA GAGAAGCCGT ATAAGTGTGA GACGTGCGGC TOGCGCTTTG 1320
TACAGGTGGC ACATCTGGCG GCGCACGTGC TGATCCACAC CGGGGAGAAG CCTACCCCTT 1380
GCCCTACCTG CGGAACCCGC TTCCGCCACC TGACAGCCCT CAAGAGCCAC GTTCGCATCC 1440
ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGCCCT GCATTTCCGG CACAAGATC 1500
AACTGCGGCT GCATCTGCGC CAGAAACACG GAGCTGCTAC CAACACCAA GTGCACTACC 1560
ACATTCTCGG GGGGCCCTAG CTGAGCGCAG GCCCAGGCC CACTTGCTTC CTGCGGTGG 1620
GAAAGCTGCA GCGCCAGGCG TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGG 1680
CACTTTGGTA TCAGAAATTT CCACCTCTCT AATTCTCAC TGGGGAGAGC AGGGGTGGCA 1740
GATCCTGGCT AGATCTGCTT CTGTTTGTCT GGTCAAACCT TCITCCCAAC AAGCCAGATT 1800
GTTTCTGAGG AGAGAGCTAG CTAGGGGCTG GAAAGGGGGA GAGATTGGAG TCCTGGTCTC 1860
CCTAAGGGAA TAGCCCTCCA CCTGTGGGCC CCATTGCATT CAGTTTATCT GTAAATATAA 1920
TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTTATTGCA TTGCATTTC CACTCCCTC 1980
TTCCACAAGT GTGATTAAAA GTGACCAGAA ACACAGAAGG TGAGATCACA GCTCTGCTGG 2040
CAGAGATTAC TAGCCCTTGG CTCTCTCGTT TGGCTTGGGT ATTTTATATT ATTTCTGTCA 2100
TAACTTTAT CTTTAGAATT GTTCTTCTC CTGTTTGTTC GCTGTATTAGT TTGTTTAAAA 2160
TGGAAAAAGG GGTCTCTGTG GTTCTGCCCC TGTAAATCTA GGTCTGGAAC CTTTATTGT 2220
TCTAGGGCAG CTCCTGGGAC ATGCGGGATT GTGGAATTGG GTCAGGAACC CTCTCTGGTA 2280
TTCTGGATGT TGTAGGTTCT CTAGCAGTCT AGAAATGGAT ACAGACATTT CTCTGTCTCT 2340
CAAGGGTGAT AGGAACCAT ATGTTGAGCC CAAAATGGAA GTAATAATAA ATGCCTCCTG 2400
GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCCGTA TCACTCCAAC TGGAGGCTGT 2460
GGGTGTGGGG GATTCTGTAT CTGGATTCCG TATCACTCCA AGTGGAGGCT GGCAGGTTTT 2520
CTGCAAGAT GTTCCAGAA CTAAATGTCT CCATTAATCT GGTCACTTGG GTTGGCTCT 2580
GCTGTATCCA TCTATAGTGG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCCTCC 2640
CACGGGGGCC TGTCTTAGC ACTGAGTTGA TCGCTCCATG GGGGAGAGAT CAGACATTCC 2700
TTATCAGAGA TGTATGACCC TTTCTGACT CTGCCAGTC TCTATGAATG TTATGGCCTA 2760
GGGAAGAATC ATGAAACTCT TTAGCTTGAT TAGATGGTAA ACAGTGTAA CCATCCTTT 2820
ACTACAGAGG CATATGGGTT TGAATGTTAC CTGGGGTTCT CTCTATTGAG TTGAGCCCTC 2880
TCTTCTTTA GTGGGTTTGG GACATCTTCT GGCAAGTGT CAGATGCCAG AACCTTCTTT 2940
TCCTCTAGAA GGGATGGTGC TTGTAACCT TACCTTTTAA AAGCTGGGTC TGTGACCTGG 3000
TCTTCCATC CCTGCAATCC TGTCTGGAAC CAGTGAATGC ATTAGAACCT TCCATAGGAA 3060
AAGAAAGGG GCTGAGTTCC ATTCTGGGT TGTGTAGTT TGGTTGGGAT TATTGTTGGC 3120
ATTACAGATG TAAAGATTG ACTAGCCCAT AGGCCAAAGG CCTGTTCTAG TTGACCAAGT 3180
TTCAAGTAGG ATTAAGAGGT TGGTTGAGG GTGCAGTTTC TGGTGATGGC CAGGTAGGTA 3240
GAAAGTGAGG AACAGGGTTG CCTCTGGCT GGGTGGAGTC TCTGAAATGT TAGAAGAAGC 3300
GCTGAAGCCT TGATTGATAG TTCTGCCCT TGTGCGCTG GGGCTTATCT GATTATGGGA 3360
CGAGGGTAGA AAGTAAGAAG CACTTTTGA TTTGTGGGT AGAACTTCAA CAATAAGTCA 3420
GTTCTAGTGG CTGTGCGCTG GGGACTAGT AGAAAGCTAC TCTTCTCCCT CTCCCTCTT 3480
TCTCCCATG GCCCCTCTG AGAATTAAAG AAGGAAGAAG GGAAGGCGGA GGAGTCTATA 3540
AGAAGGAATC ATGATTCTA TTTAGCAGAT TGGATGGGCA GGTGAGGAAT GCCTGGGGGT 3600
AGAAATGTTA GATCTTGCAA CATCAGATCC TTGGAATAAA GAAGCCTCTC TGYGCWRAAA 3660
AAAAA      AAAAA

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Seq ID NO: 16 Protein sequence  
Protein Accession #: FGENESH predicted

55  
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1 11 21 31 41 51
| | | | |
MGSPAAPEGA LGYVREPTRH SSDVLGNLNE LRLRGILTDV TLLVGGQPLR AHKAVLIACS 60
GFPYSLFRGR AGVGVDLVSL PGGPEARFPA PLLDFMYTSR LRLSPATAPA VLAAATYLM 120
EHVVQAEHRF IQASYEPLGI SLRPLEAEPF TPPTAPPFGS PRRSEGHDP PTERSCSQG 180
PPSPASPDPK ACNWKYKYI VLNSQASQAG SLVGERSSGQ PCPQARLPSP DEASSSSSSS 240
SSSSESGPIP GPQSRLSPTA ATVPFKCGAP ASTPYLLTSQ AQDTSGSPSE RARPLPGSEF 300
FSQNCBAVA GCSGLDSLVS PGDEDKPYKC QLCRSSFRYK GNLSHRTVH TGEKPYHCSI 360
CGARFNRPAN LKTHSRHSG EKPYKCTCG SRFVQVAHLR AHVLIHTGEK PYPCTPGTR 420
FRHLQTLKSH VRIHTGEKPY HCDPQSLHFR HKSQRLRLHLR QKHGAATNTK VHYHILGGP

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Seq ID NO: 17 DNA sequence  
Nucleic Acid Accession #: XM\_039209  
Coding sequence: 1..2049

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1 11 21 31 41 51
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AATGGGAACC CCCGGAAGCG CCTGAAAAGG AGAGACAGGA GGATGATGTC CCAGCTGGAG 180
CTGCTGAGTG GGGGAGAGAT GCTGTGGGT GGCCTTACC CTCGGCTGTC CTGCTGCTG 240
CGGAGTGACA GCGCGGGGCT AGGGGCGCTG GAGAATAAGA TATTTTCTGT TACCAACAA 300
ACAGAAATGT GGAAGTTACT GGAGGAAATC AAATGTGCAC TTTGCTCTCC ACATTCTCA 360
AGCCTGTGCC ACTCACCTGA GAGAGAAGTC TTGAAAGAG ACCTAGTACT TCCTCTGCTC 420
TGCAAGACT ATTGCAAGA ATTCTTTTAC ACTTGGCGAG GCCATATTCC AGGTTTCTCT 480
CAAAACAGTG CGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGGTGG GTTGTGCTTT 540
CCAGATTTTC CAAGAAAACA AGTCAGAGGA CCAGCATCTA ACTACTTGA CCAGATGGAA 600
GAATATGACA AAGTGGAGA GATCAGCAGA AAGCACAAAC ACAACTGCTT CTGATTCTAG 660
GAGGTTGTGA GTGGGCTGCG GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTGCGAA 720
CGTCTCTTCA TCTGGAAGAA AGAAGGTTAT GTGAAGATAC TTACCCCTGA AGGAGAAATT 780
TTCAAGGAGC TTATTTTGGA CATTACAAA CTTGTTTCAA GTGGAATAAA GGGAGGAGAT 840

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GAAAGAGGAC TGCTAAGCCT CGCATTCCAT CCCAATTACA AGAAAAATGG AAAGTTGTAT 900
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GTCTTTCTTG AAGTTGACAGA ACTCCACAGA AAGCATCTGG GAGGACAAC TCTCTTTGGC 1080
CCTGAOCCGT TTTGTACAT CATTCTTGGT GATGGGATGA TTACACTGGA TGATATGGAA 1140
GAAATGGATG GGTAAAGTGA TTTCACAGGC TCAGTGCTAC GGCTGGATGT GGACACAGAC 1200
ATGTGTAAAG TGCTTTATTC CATACCAAGG AGCAACCCAC ACTTCAACAG CACCAACCAAG 1260
CCCCCAGAG TGTTTGCTCA TGGGCTCCAC GATCCAGGCA GATGTGCTGT GGATAGACAT 1320
CCCACTGATA TAAACATCAA TTAAACGATA CTGTGTTTCA ACTCCAATGG AAAAAACAGA 1380
TCATCAGCCA GAATTCTACA GATAATAAAG GGGAAAGATT ATGAAAGTGA GCCATCACTT 1440
TTAGAAATCA AGCCATTAG TAATGGTCTT TTGGTTGGTG GATTGTGATA CCGGGGCTGC 1500
CAGTCAGAAA GATTGTATGG AAGCTACGTG TTTGGAGATC GTAATGGGAA TTTCCTAACT 1560
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GGGTCTGTA GAGGCTACTT TTCCGGTCAC ATCTTGGGAT TTGGAGAAGA TGAAC TAGT 1680
GAAGTTTACA TTTTATCAAG CAGTAAAAAG ATGACCCAGA CTCACATGG AAAACTCTAC 1740
AAAAATTGAG ATCCCAAAAG ACCTTTAATG CCTGAGGAAT GCAGAGCCAC GGTACAACCT 1800
GCACAGACAA TGACTTCAGA GTGCTCCAGG CTCTGTGCAA ACGGCTACTG CACCCCAACG 1860
GGAAAGTGCT GCTGCAGTCC AGGCTGGGAG GGGGACTTCT GCAGAACTGC AAAATGTGAG 1920
CCAGCATGTC GTCATGAGAG TGTCTGTGTT AGACOGAACA AGTGCTCTG TAAAAAGGA 1980
TATCTTGTGC CTCAATGTGA ACAAGTGAC AGAAACATCC GCAGAGTGAC CAGGGCAGAC 2040
ATCACTAG

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25 Seq ID NO: 18 Protein sequence  
Protein Accession #: XP\_039209

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1 11 21 31 41 51
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LLSGGEMLCG GFYPRLSCLL RSDSPGLGRL ENKIFSVTN TECKILLLEE KCALCSPHSQ 120
SLFHSFEREV LERDLVPLLL CKDYCKEFPY TCRGHIIPGL QTTADEFCFY YARKDGGLCF 180
PDPFRKQVRG PASNYLDQME EYDKVEEISR KHKHNCFCIQ EVVSQLRQPV GALHSGDGSQ 240
RLFILEKDEY VKILTPEGEI FKEPYLDINH LVQSGIKGGD ERGLLSLAFH PNYKQNGKLY 300
VSYTTHQERW AIGPHDHLIR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG 360
PDGFLLYILG DGMITLDDME EMDGLSDFTG SVLRDLVDTD MCNPVYSIPR SNPHFNTNQ 420
PPEVFAHLGH DPGRCVDRH PTDININLTI LCSDSNGKNR SSARILQIIK GKDYSEPSL 480
LEFKFESNRP LVGGFVYRGC QSERLYGSVY FCDRNGNFLT LQSPVTKQW QERPLCLGTS 540
GSCRGVPSGH ILGFGDEDELG EYILSSSKS MTQTHNGKLY KIVDPKRPLM PEECRATVQP 600
AQTLTSECSR LCRNGYCTPT GKCCSPGWE GDFCRTAKCE PACRHGGVCV RPNKCLCKKG 660
YLGFPQCEQVD RNIRRVTRAD IT

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45 Seq ID NO: 19 DNA sequence  
Nucleic Acid Accession #: NM\_014331.2  
Coding sequence: 1..1506

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AAGAGGAAGT TCACTTACTT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA 180
GGAATCTTCA TCTCTCTCTA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGCTCTG 240
ACCATCTGGA CGGTGTGTGG GGTCTGTGCA CTATTGGGAG CTTTGTCTTA TGCTGAATTG 300
GGAACACACTA TAAAGAAATC TGGAGGTCAT TACACATATA TTTTGGAAAT CTTTGGTCCA 360
TTACCACTCT TTGTACAGAT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT 420
GTGATATCCC TGGCAATTGG ACGCTACATT CTGGAACCAT TTTTATTACA ATGTGAAATC 480
CCTGAACCTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCTTAAAT 540
AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACTTTTGT CAAGCTCACA 600
GCAATCTGTA TAATTCTAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTCAT AACGCAGAAC 660
TTTAAAGACG CGTTTTCAGG AAGAGATTCA AGTATTAGGC GGTGGCCACT GGCTTTTAT 720
TATGGAATGT ATGCATATGC TGGCTGTTT TACCTCAACT TTGTACTGTA AGAAGTAGAA 780
AACCTGAAA AAACCATTC CTTGCAATA TGTATATCCA TGGCCATGCT CACCATTTGC 840
TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAAAT CTGAGGAGCT GCTGCTTTCA 900
AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG 960
ATCTTTGTG CCCTCTCCTG CTTTGGCTCC ATGAACGGTG GTGTGTTGCG TGTCTCCAGG 1020
TTATTTCTATG TTGGTCTCG AGAGGGTCAC CTTCAGAAA TOCTCTCCAT GATTCAATGTC 1080
CGCAAGCACA CTCCTTACC AGCTGTATT GTTTTGCAOC CTTTGACAAAT GATAATGCTC 1140
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GGGCTGGCAG TTGCTGGGCT GATTATCTT CGATACAAAT GCCAGATAT GCATGCTCCT 1260
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GTCCCTGCGT ATTATCTCT TATTATATGG GACAAGAAAC CCAGTGGGTT TAGAATAATG 1440
TCAGAGAAAA TAAACAGAA ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG 1500
TTATGAATTA ATGGACTTGA GATCTTGGCA ATCTGCCCAA GGGGAGACAC AAAATAGGGA 1560
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CAGTTATTTT TATTCAATATA TTTTAGCATA TTGCAACTAA TTTCTAAGAA ATTTAGTTAT 1680
AACTCTATGT AGTTATAGAA AGTGAATATG CAGTTATCT ATGAGTCGCA CAATTCTTGA 1740
GTCTCTGATA CCTACCTATT GGGGTTAGGA GAAAAGACTA GACAATTACT ATGTGGTCAT 1800
TCTCTACAC ATATGTAGC ACGCAAGA ACCTTCAAA TGAAGACTGA GATTTTCTG 1860
TATATATGGG TTTGTAAAG ATGGTTTAC ACACACTAGA TGCTATACT GTGAAAAGTG 1920
TTTTCAATTG TGAAAAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT 1980
ATTTTCAATT TGCAATGCAT TGCTTCCOCT TAGATACCAA TTTAGATAAC AAACACTCAT 2040
GCTTTAATGG ATTATACCA GAGCACTTGG AACAAAGGTC AGTGGGGATT GTTGAATACA 2100
TTAAAGAAAG GTTCTTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAACT 2160
AAAAATCCTT GAGAAATTAT TATGTCAGAT GTTTTTTCAT TCATTATCAG GAAGTTTTAG 2220

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5 TTATCTGTCA TTTTTTTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG 2280  
 AGCAAGAGTT AGTTTGGTAT TAAATCCTCA TTAGAACAAC CACCTGTTTC ACTAATAACT 2340  
 TACCCCTGAT GAGTCTATCT AAACATATGC ATTTTAAGCC TTCAAATTAC ATTATCAACA 2400  
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 CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT 3000  
 GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGAGGGCG 3060  
 15 GAGGTTGAG TGAGCCAAAG TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120  
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Seq ID NO: 20 Protein sequence  
 Protein Accession #: NP\_055146.1

20 1 11 21 31 41 51  
 MVRKPVVSTI SKGGYLQGNV NGRLPISLGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA 60  
 25 GIFISPKGVL QNTGVSVMGL TIWTVCGVLS LFGALSYAEL GTTIKRSGGH YTYILEVFGP 120  
 LPAPVVRWVE LLIIIRPATA VISLAFGRYI LEPPFIQCEI PELAIKLITA VGITVVMVLN 180  
 SMSVSWASRI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240  
 YGMAYAGWFF YLNFVTEVEE NPEKTIPLAI CISMATIGV YVLTNVAYPT TINAEELLS 300  
 NAVAVTFSEF LIGNVTSFSLV IFVALSCFSG MNGGVFAVR LFPYVASREGH LPEILSMIHV 360  
 30 RKHTLPAVI VLHPLTMIIML FSGDLDSLNL FLSPARWLF I GLAVAGLIYL RYKCPDMHRP 420  
 FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKPRWFRIM 480  
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Seq ID NO: 21 DNA sequence  
 Nucleic Acid Accession #: NM\_002422.2  
 Coding sequence: 64..1497

40 1 11 21 31 41 51  
 ACAAGGAGGC AGGCAAGACA GCAAGGCATA GAGACAACAT AGAGCTAAGT AAAGCCAGTG 60  
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 TTGGATGAGG CTGCAAGGGG TGAGGACACC AGCATGAACC TTGTTCAGAA ATATCTAGAA 180  
 AACTACTACG ACCTCAAAAA AGATGTGAAA CAGTTTGTTA GGAGAAAGGA CAGTGGTCTT 240  
 45 GTGTGTAAAA AAATCCGAGA AATGCAGAAG TTCCTTGGAT TGGAGGTGAC GGGGAAGCTG 300  
 GACTCCGACA CTCTGGAGGT GATGCGCAAG CCCAGGTGTG GAGTTCCTGA TGTGTGTCAC 360  
 TTCAGAACTT TTCTGGCAAT CCGAAGTGG AGGAAAACCC ACCTTACATA CAGGATTGTG 420  
 AATTATACAC CAGATTGGCC AAAAGATGCT GTTGATTCTG CTGTGAGAA AGCTCTGAAA 480  
 GTCTGGGAGG AGGTGACTCC ACTCACATTC TCCAGGCTGT ATGAAGGAGA GGCTGATATA 540  
 50 ATGATCTCTT TTGCACTTAG AGAACATGGA GACTTTTACC CTTTGTATGG ACCTGGAAAT 600  
 GTTTTGGGCC ATGCTTATGC CCTTGGGCCA GGGATTAATG GAGATGCCCA CTTTGATGAT 660  
 GATGAACAAAT GGACAAAGGA TACAACAGGG ACCAATTATT TTCTCGTTGC TGCTCATGAA 720  
 ATTGGCCACT CCCTGGGTCT CTTTCACTCA GCGAACACTG AAGCTTTGAT GTACCCACTC 780  
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 55 CAGTCCCTCT ATGACCTCC CCTGACTCC CCTGAGACCC CCTTGGTACC CACGGAACCT 900  
 GTCCCTCCAG AACCTGGGAC GCCAGCCAAC TGTGATCCTG CTTTGTCTTT TGATGCTGTC 960  
 AGCACTCTGA GAGGAGGAAAT CCTGATCTTT AAAGACAGGG ACTTTTGGCG CAAATCCCTC 1020  
 AGGAAGCTTG CAATGAAAT GCATTGTATC TCTTCATTTT GGCCATCTCT TCCTTCAGGC 1080  
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 60 TTCTGGGCCA TCAGAGGAAA TGAGGTACGA GCTGGATACC CAAGAGGCAT CCACCCCTA 1200  
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 65 GTTTTGAAG AATTGGGTT CTTTATTTT TTTACTGGAT CTTACAGTT GGAGTTTGAC 1440  
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 70 GGAACITGAG CGTGAATCTG TATCTTGCAG GTCAATTTTA TGTATTACA GGCATTCAA 1680  
 ATGGGCTGCT GCTTAGCTTG CACCTTGTCA CATAGAGTGA TCTTTCCCAA GAGAAGGGGA 1740  
 AGCACTCGTG TGCAACAGAC AAGTGACTGT ATCTGTGTAG ACTATTGTCT TATTTAATAA 1800  
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Seq ID NO: 22 Protein sequence  
 Protein Accession #: NP\_002413

75 1 11 21 31 41 51  
 MKSLPILLLL CVAVCSAYPL DGAARGEDTS MNLVQKYLEN YYDLEKOVKQ FVRRKDSGPV 60  
 VKIIREMQKF LGLEVTGRKL SDTLEVMRKP ROGVDPVGHF RTPPGIPKWR KTHLTYYRIVN 120  
 80 YTPDLPIKAV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYPFDGPGNV 180  
 LAHAYAPGPG INGDAHFDDE EQWTKDTTGT NLPLVAHEHI GHSLGLFHSA NTEALMYPLY 240  
 HSLDITRFR LSQDDINGIQ SLYGPPFDSP ETPLVPEFV PPEPGTPANC DPALSFDVAV 300  
 TLRGEILIFK DRHPWRKSLR KLEPELHLIS SFWPSLPSPV DAAYEVTSKD LVPIFKGNQF 360  
 WAIRGNEVRA GYPRGIHTLG FPPTVRKIDA AISDKENKNT YPFVEDKYWR FDEKRNSEMP 420  
 GPPKQIAEDF PGIDSKIDAV FFEFGFFYFF TGSSQLEFDP NAKKVTHTLK SNWNLNC

Seq ID NO: 23 DNA sequence  
Nucleic Acid Accession #: NM\_006528  
Coding sequence: 57..764

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GCGATGCTCG	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCCTG	CCCTAGACT	180
ACCGACCCCTG	CCGGGCCCTA	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
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GCGACGATGC	TGTCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCCGGCTG	CAAGTGAGTG	360
TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTCTCT	TAATCTAAGT	TCATGACAT	420
GTGAAAAATT	CTTTCCCGGT	GGGTGTCAAC	GGAAACCGAT	TGAGAACAGG	TTTCCAGATG	480
AAGCTACTTG	TATGGGCTTC	TGCGCACCAG	AGAAAAATCC	ATCATTTTGC	TACAGTCCAA	540
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CCTGTGATGC	TTTCACCTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660
AGGATTGCAA	ACGTGCATGT	GCAAAAGCTT	TGAAAAAGAA	AAAGAAGATG	CCAAAGCTTC	720
GCCTTGCCAG	TAGAATCCGG	AAAAATCGGA	AGAAGCAATT	TTAAACATTC	TTAATATGTC	780
ATCTTGTGTT	TCTTTATGGC	TTATTGCTCT	TTATGGTTGT	ATCTGAAGAA	TAATATGACA	840
GCATGAGGAA	ACAAATCATT	GGTGATTAT	TCACCAAGTT	TTATTAATAC	AAGTCACTTT	900
TTCAAAAAAT	TGGATTTTTT	TATATATAAC	TAGCTGCTAT	TCAAATGTGA	GTCTACCAT	960
TTTAATTTAT	TTTCAACTG	TTTGTGAGAC	GAATTCTTGC	AATGCATAAG	ATATAAAGC	1020
AAATATGACT	CACCTCATTC	TTGGGGTGGT	ATTCCTGATT	TCAGAAGAGG	ATCATAACTG	1080
AAACAACATA	AGACAATATA	ATCATGTGCT	TTTAACATAT	TTGAGAATAA	AAAGGACTAG	1140
CC						

Seq ID NO: 24 Protein sequence  
Protein Accession #: NP\_006519

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MDPARPLGLS	ILLFLTEAA	LGDAAEPTG	NNAEICLLPL	DYGPCRALLL	RYYYDRYTQS	60
CRQFLYGGGE	GNANNFYWE	ACDDACWRIE	KVPKVCRLQV	SVDDQCEGST	EKYFFNLSM	120
TCEKFFSGGC	HRNRIENRFP	DEATCMGFCA	PKKIPSPFCS	PKDEGLCSAN	VTRYFENPRY	180
RTCDAFYTG	CGGNDNNFVS	REDCKRACAK	ALKKKKKMPK	LRFASRIKI	RKKQF	

Seq ID NO: 25 DNA sequence  
Nucleic Acid Accession #: NM\_005458.1  
Coding sequence: 1..2825

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GGCTGGGCGC	GGGGCGCCCC	CGGGCGCGCG	CCCAGCAGCC	CGCCGCTCTC	CATCATGGGC	180
CTCATGCCGC	TCACCAAGGA	GGTGGCCAAG	GGCAGCATCG	GGGCGSGTGT	GCTCCCCGCC	240
GTGGAACCTG	CCATCGAGCA	GATCGGCAAC	GAGTCACTCC	TGCGCCCTTA	CTTCTCTGAC	300
CTGCGGCTCT	ATGACACGGA	GTGCGACAAC	GCAAAAGGCT	TGAAAGCCTT	CTACGATGCA	360
ATAAAATAAG	GGCCGAACCA	CTTGATGGTG	TTTGGAGGGG	TCGTCTCCATC	CGTCACATCC	420
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ATTCGCGGCT	GGTACGAGCC	TTCTTGTGTG	GAGCAGGTGC	ACAAGGAAGC	CAACTCATCC	900
CGCTGCGCTC	GGAAGAACTC	GCTTGTCTGC	ATGGAGGGCT	ACATTGGGCT	GGATTTCTGAT	960
CCCTGAGCTC	CCAAGCAGAT	CAAGACCATC	TCAGGAAAGA	CTCCACAGCA	GTATGAGAGA	1020
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GGCATCTGGG	TCTCGCCCAA	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
CGGCACCAGC	GGATCCAGGA	CTTCAACTAC	ACGGACCACA	CGCTGGGCAG	GATCATCCTC	1200
AATGCCATGA	ACGAGACCAA	CTTCTTCGGG	GTCAAGGGTC	AAGTTGTATT	COGGAATGGG	1260
GAGAGAATGG	GGACCATTA	ATTTACTCAA	TTTCAAGACA	GCAGGGAGGT	GAAGGTGGGA	1320
GAGTACAACG	CTGTGGCCGA	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCCAAGGA	1380
TCCGAACACC	CAAAAGACAA	GACCATCATC	CTGGAGCAGC	TGCGGAAGAT	CTCCCTACCT	1440
CTCTACAGCA	TCTCTCTGCG	CCTCACTATC	CTCGGATGAT	TCTGGGCGAG	TGCTTTTCTC	1500
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AACCTTATCA	TCTTGGAGGG	GATGCTCTCC	TATGCTTCCA	TATTTCTCTT	TGGCCTTGAT	1620
GGATCCTTTG	TCTCTGAAAA	GAOCTTTGAA	ACACTTTGCA	COGTGAGGAC	CTGGATTTCT	1680
ACCGTGGGCT	ACACGACCGC	TTTGGGGGCC	ATGTTTGCAA	AGACCTGGAG	AGTCCAGGCC	1740
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GTGGGGGGCA	TGCTGCTGAT	CGACCTGTGT	ATCCTGATCT	GCTGGCAGGC	TGTGGACCCC	1860
CTGCGAAGGA	CAGTGGAGAA	GTACAGCATG	GAGCCGGACC	CAGCAGGACG	GGATATCTCC	1920
ATCCGCGCTC	TCTTGGAGCA	CTGTGAGAAC	ACCAATATGA	CCATCTGGCT	TGGCATOGTC	1980
TATGCTTACA	AGGGAATCTT	CATGTTGTTT	GGTTGTTTCT	TAGCTTGGGA	GACCCGCAAC	2040
GTACGCTACC	CGCACTCAA	CGACAGCAAG	TACATCGGGA	TGAGTGTCTA	CAAGTGGGGG	2100
ATCATGTGCA	TGATCGGGGC	CGCTGTCTCC	TTCTGTACCC	GGGACCGACC	CAATGTGACG	2160
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10 Seq ID NO: 26 Protein sequence  
 Protein Accession #: NP\_005449.1

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 LYSILSALTI LGMIMASAFI PFNIKRNQK LIKMSPPYMN NLIIILGMLS YASIFLFGLD 540  
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 VGMILLIDL ILICWQAVDP LRRTEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLIV 660  
 YAYKGLMLLF GCFLANETRN VSIPALNSDK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ 720  
 FCIVALVIIF CSTITLCLVF VPKLITLRTN PDAATQNRFP QFTQNKKED SKTSTSVTSV 780  
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Seq ID NO: 27 DNA sequence  
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Protein Accession #: NP\_000441.1

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DVGWMDNERC SKKKLALCYT AACTNTSCSG HGECEVETINN YTCKCDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240
ECDAVTNPAN GEVECFQNPQ SPFWNTTCTF DCEEGFELMG AQLSLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPQAVECT TQGWQWQIIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWON 420
EKPTCEAVRC DAVHOPPGLR VRCAHSPIGE FTYKSCAFS CEEGFELYS TQLECTSQGQ 480
WTEEVPSQCV VKCSLAVPG KINMSCSGEP VFGTVCKPAC PEGWTLNGSA ARTCGATGHW 540
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Seq ID NO: 30 Protein sequence  
Protein Accession #: NP\_008967.1

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1 11 21 31 41 51
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LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM\_000963

Coding sequence: 135..1949

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Seq ID NO: 32 Protein sequence  
Protein Accession #: NP\_000954

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  GYKSWFAFSN LSYVTRALPP VPDDCPTPLG VKGKKQLPDS NEIVEKLLLR RKFPIDPQGS 180
  NMMAFAFAQH FTHQFFKTDH KRGPAFTNGL GHGVDLNIHY GETLARQRLK RLFKDGKMKY 240
10  QIIDGEMYPY TVKDTQAEML YPPQVPEHLR FAVGQEVFGL VPGLMMYATI WLRHNVRVCD 300
  VLKQEHPEWG DEQLFQTSRL ILIGETIKIV IEDYVQHLGS YHFKLKFDPE LLFNKQFQYQ 360
  NRIAAEFNTL YHWHBLLPDT FQIHDQKYNV QPFIYNNISL LEHGITQFVE SPTRQIAGRV 420
  AGGRNVPPAV QKVSQASIDQ SRQMKYQSFN EYRKRFMLKP YBSFEELTGE KEMSAEAL 480
15  YGDIDAVELY PALLVEKPRP DAIPGETMVE VGAPPSLKGL MGNVICSPAY WKPSTFGGEV 540
  GFQIINTASI QSLICNNVKG CPFTSFSVPD PELIKTVTIN ASSRSGLDD INPTVLLKER 600
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Seq ID NO: 33 DNA sequence  
Nucleic Acid Accession #: NM\_001508.1  
Coding sequence: 1..1361

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  CCGAGATTG AGGTGGCCAC CTGGATCAAA ATCACCCCTTA TTCTGGTGTG CTTGATCATC 120
  TCGTGATGG GCCTTCTGGG GAACAGCGTC ACCATTGGGG TCACCCAGGT GCTGCAGAAG 180
  AAAGGACTACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
  TTGGTGTTC TCATGGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC 300
  AGTCCAGCT ACACCTGTC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
30  GCTACGCTGC TCACTGTGCT GACGCTCAGC TTTGAGOGCT ACATCGCCAT CTGTACCCCC 420
  TTCAGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTGCTCTGG 480
  GTCACCTCCG CCTGTGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTTG 540
  GTGAAGTGA CAGGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCGG CCACCAAGAG 600
  CAGCCCCAGA CTCCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
35  CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTGCTGG TCCTGCTCTC CGTAGCCTTC 720
  ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGCTGCTG GGCCTGGGGC 780
  AOGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
  ACCATCATCT TCCTGAGGCT GATTGTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG 900
  ATTGCGAGGA TCATGGCTGC GGCCAAACCC AAGCAGCACT GGACGAGGTC CTACTTCCGG 960
40  GGTACATGTA TCCTCTCTCC CTTCCTGGAG ACGTTTTTCT ACCTCAGCTC GGTATCAAC 1020
  CGCTCTCTGT ACACGGTGTG CTCGAGCAG TTTCCGCGGG TGTGCTGTGA GGTGCTGTGC 1080
  TGCCGCTGT CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGCGGTGACA TGCGCACTCC 1140
  ACCACCGACA GCGCCCGCTT TGTGAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
  TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGACGAGGC CGAGCCCCAG 1260
45  TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAACC 1320
  AATTCTGCTG CAGAGAAATG TTTTCAGGAG CATGAAGTTT GA

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Seq ID NO: 34 Protein sequence  
Protein Accession #: NP\_001499.1

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  KGYLQKEVTD HMYSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
55  ATLLHLVTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVH VTSALVALPL LFAMGTETPL 180
  VNVPSSHRLT NCRSSRHHB QPETSNNMSIC TNLSSRWTFV QSSIFGAFVH YLVVLLSVAF 240
  MCWNMQVLM KSQKSLAGG TRFPQLRKSE SEESRTARRQ TIIPLRLIVV TLAVCMFNPQ 300
  IRRINAAKPK KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFQVLK 360
60  CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLPASRRQS SARRTEKIFL STFQSEAEPO 420
  SKSQSLSLSS LEPNSGAKPA NSAAENGFBQ HEV

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Seq ID NO: 35 DNA sequence  
Nucleic Acid Accession #: NM\_006475.1  
Coding sequence: 28..2538

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70  AGTCGTATCA GGGGTGCGGA CCAAGGCCCA AATGTCTGTG CCTTCAACA GATTTTGGGC 180
  ACCAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
  AAAACGACTG TTTTATATGA ATGTGCCCTT GGTATATGA GAATGGAAGG AATGAAAGGC 300
  TGCCAGCAGT TTTTGCCCAT TGACCATGTT TATGGCACTC TGGCATGCTT GGGAGCCACC 360
75  ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATGAGGG AAAGGGATCC 420
  TTCATCTACT TTGACCGAG TAATGAGGCT TGGGACAAC TGGATTCTGA TATCGTAGA 480
  GGTTTGGAGA GCAACGTGAA TGTGGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
  AAGAGATGTT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT 600
  TTGGGGCTTT TCATTAAACA TTATCCTAAT GGGGTGTGCA CTGTTAATTG TGCTCGAATC 660
80  ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGCCATG TCATTGACOG TGTGCTTACA 720
  CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
  GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACTC 840
  TTTGCTCCCA CCAATGAGGC TTTTGAAGAA CTTCCACGAG GTGTCTTACA AAGGTTTCATG 900
  GGAGACAAGT TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
  TCTGAGTCTA TTAATGGGAG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

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5  
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 CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA OGGATCTTGT GGCCCAATTA 1200  
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 TGCATSGAGA AAGGAGTAA GCAAGGAGA AACGGTGCBA TTCACATATT CCGCGAGATC 1500  
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 AGACTGATTA AGAAGGGTGA AACAATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA 2220  
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 GAAAGATCA TTACAGGTCC TGAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA 2340  
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 GAAGGTGGTG ATGGTCATT ATTGAAGAT GAAGAAATTA AAGACTGCTC TCAGGGAGAC 2460  
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 ACAGAAAGAA AATCTCAAAA TAATTTCTGAA CACAAATTTA ATATTTTTTT TTCTGAATGA 2700  
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 CACCTTACAG CCTTTTTCAT CTGACATTA AAGTTCTGG CTAACCTTGG AATCCATTAG 2820  
 AGAAAAATCC TTGTCAACAG ATTCAATACA ATTCAAATCG AAGAGTTGTG AACTGTTATC 2880  
 CCATTGAAAA GACGAGCCTC TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940  
 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000  
 TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA 3060  
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 TCTCAACGTT TTCAATAAAA CCATTTTTC GATATAAAGA GAATTACTTC AAATTGAGTA 3180  
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Seq ID NO: 36 Protein sequence  
Protein Accession #: NP\_006466.1

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1 11 21 31 41 51  
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 KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLSNVNV E LNALHSHMI NKRLTKDLK 180  
 NGMIIPSMYN NLGLFINHYE NGVVTVNCAR I IHGNQIATN GVHVVIDRVL TQIGTSIQDF 240  
 IEAEDLSSF RAAAITSDIL EALGRDGHPT LFAPTNEAPE KLPRGVLERF MGDKVASEAL 300  
 MKVHILNTLQ CSESIMGGAV FETLEGNTIE IGCDDSIIV NGIKMWNKID IVTNNGVIHL 360  
 IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLAPVFN NAFSDTLMS 420  
 VQRLKLILQ NHLLKRVGL NELYNGQILE TIGGKQLEVF VYRTAVCIEN SCMEKGSKQG 480  
 RNGAIIHIFR I IKLPAEKLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA 540  
 FKGMTSEERE ILIRDKNALQ NIILYHLTPG VPIGRGPEPG VTINILKTTQG SKIFLKEVND 600  
 TLLVNELKSK ESDIMTNGV IHVVDKLLYP ADTPVGNQDL LEILNKLKLY IQIKFVRGST 660  
 FKEIPVTVTY TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGPEP FRLIKEGETI 720  
 TEVIHGEPII KKYTKIIDGV PVEITEKETR BERIITGPEI KYTRISTGGG ETEBTLKRL 780  
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Seq ID NO: 37 DNA sequence  
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Coding sequence: 40..417

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1 11 21 31 41 51  
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 GACCTTAAC AATTGCCCC AAGCCCTTCC TGGAGAAAA TTGAAATCAT TGCTACACTG 240  
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 AAGAAAGTTC TGAAGTTTCG AAAATCTCAA CGTTCTGCTC AAAAGAAAGAC TACATAAGAG 420  
 ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA 480  
 TTCCAAGGA GGATGGCATA TAATACAAAG GCTTATTAAAT TTGACTAGAA AATTTAAGAA 540  
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 TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCAACCAA CACATCCCA 720  
 CTCACAACAG CTGCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCAGAGAG 780  
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 TGAATCTTG CTGAAGCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900  
 CTACAGGCCT CACACACAA GTGTCTGAGA GATTCTGCT GATTGTTATT GGGTATCACC 960  
 ACTGGAGATC ACCAGTGTGT GGCTTTTCAA GCCTCTTTC TGGCTTTGGA AGCCATGTGA 1020  
 TTCCATCTTG CCGCTCAGG CTGACCACCT TATTCTTTT TGTTCCTCTT TGCTTCAATC 1080  
 AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCTTCT CTCTCTCCA GTGCACCTGT 1140  
 CATATGCTCT GATTATCTG AGTCAACTCC TTTCTCATCT TGTCCCCAAC ACCCCACAGA 1200

5 AGTGCTTCTT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT 1260  
 AAAATAAACCT TTTTGGACAC ACAAAATTATC TTAAAACTOC TGTTCACCTT GGTTCAGTAC 1320  
 CACATGGGTG AACACTCAAT GGTTAACTAA TTCTTGGGTG TTTATCCTAT CTCTCCAACC 1380  
 AGATTGTGAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCTGTTTCT TCACACGTG 1440  
 CTAATAATAC TGTGGAACCT GGTTTTAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500  
 TGGCAACCAAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCTATGTTG 1560  
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620  
 GATGCAACAT CCTGTCTTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680  
 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740  
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800  
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 TCTAAGATCT AACAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATATG 1920  
 AGTTTATTG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980  
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040  
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 CTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220  
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 AAAAATCTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340  
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 TCAATTATCA TATATATACA TACATGCATA CACTCTCAAA GCAAAATATT TTTCACTTCA 2460  
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 TATCAATAAA TAGACCATTA ATCAG

25 Seq ID NO: 38 Protein sequence  
 Protein Accession #: NP\_002407

30 1 11 21 31 41 51  
 MKKSGVLFLL GIILLVLIGV QGTFVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60  
 IEIIATLKNQ VQTCLNPDSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR 120  
 QKKTT

35 Seq ID NO: 39 DNA sequence  
 Nucleic Acid Accession #: NM\_006670  
 Coding sequence: 85..1347

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 GAGCGGGGCT TGGGGCTGGC GCGACTAGCG CTGGTACTCC TGGGGTGGGT CTCTCGTCT 180  
 TCTCCCACTT CCTGGGACCT CTCTCTCTCC TCCTCGGCGC GGTTCCTGGC TTCGCGCGTG 240  
 TCGCGCCAGC CCGCGCTGCC GGAACAGTGC CCGCGCTGT GCGAGTGCTC CGAGGCAGCG 300  
 45 CGCAGATCA AGTGCGTTAA CGCAATCTG ACGAGGTGCG CCAAGGACCT GCGCGCTAC 360  
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 50 AGTCCCTCTG TGAACCTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660  
 CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720  
 CGCGCTTCGG AGCTGGCCAG CAACCACTTC CTTTAACCTG CCGGGGATGT GCTGGCCCCA 780  
 TCGCGCTGGC TCAGGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTG 840  
 55 TCCTTCGCGA ACCTGACACA TCTAGAAAGC CTCCAACCTG AGGACATGCT CCTCAAGGTC 900  
 CTTCAAAAG GCACCTCTGC TGAATTGCAA GGTCTACCCC ACATTAGGTT TTTCTGGAC 960  
 AACAAATCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAACA 1020  
 GAGGTAGTGC AGGGCAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080  
 GTCTCTCTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCACTCCCTG 1140  
 60 CAAACCTCTT ATGCTCTCCT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200  
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 AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380  
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440  
 65 TAGATAACAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCTCTG TTATGTAAAG 1500  
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 TTCTTTTCT TGGAACTCCT CAACAAGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620  
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 CTGCAGACGT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860  
 AGAGCATGCT TACATTTTAC TGTCTGCAAT ATTACAAAAA ATAACCTTGA ACTTCATAAC 1920  
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 75 TTTTAATAAA CTCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040  
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80 Seq ID NO: 40 Protein sequence  
 Protein Accession #: NP\_006661

1 11 21 31 41 51  
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 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL 120  
 AALNLSGSR LDEVRAAGFEH LPSLRQLDLS HNLADLSPP APGSGNASVS APSPLVELIL 180  
 NHIVPPEDER QNRSPGQNVV AALLAGRALQ GLRRLLEASN HFLYLPDRVL AQLPSLRHLD 240

LSNNSLVSLT YVSPRNLTSL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWCDC 300  
 HMADMVTLWK ETEVVQKDR LTCAYPERMR NRVLLELNSA DLDGDPILPP SLQTSYVFLG 360  
 IVLALIGATF LLVLYLNRKG IKWMENIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

5

Seq ID NO: 41 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..927

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 TTCTCCTCCT CGGCGCCGTT CTGGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCCGGAC 180  
 CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240  
 15 AATCTGACCG AGGTGCCCCA GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300  
 AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCCGGG ATGTGCTGGC CCAACTGCCC 360  
 AGCCTCAGGC ACCTGGACTA AAGTAATAAT TGGCTGGTGA GCCTGACCTA GGTGCTCTTC 420  
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 AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACATTA GGGTTTTCTT GGACAACAAT 540  
 20 CCCTGGGTCT CGGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600  
 GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGAGAA AAATGAGGAA TCGGGTCTCT 660  
 TTGGAATCA ACAGTGACTG CCTGGAATGT GACCCGATTC TTCCCCATC CCGTCAAAAC 720  
 TCTTATGCTT TCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCTT CCGGTTTTTG 780  
 TATTTGAACC GCAAGGGGAT AAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840  
 25 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900  
 AGTTCTAACT CGGATGTCCT CGAGTGA

30

Seq ID NO: 42 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
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 35 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLASNHFLY LPRDVLALPL 120  
 SLRHLDSLNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELOGL PHIRVPLDNN 180  
 PMVDCDHMAD MVTWLKETE VQKDRILTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240  
 SYVFLGIVLA LIGAIPLVLV YLNRKGIKKW MENIRDACRD HMEGYHYRYE INADPRLTNL 300  
 SSNSDVLBE

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Seq ID NO: 43 DNA sequence  
 Nucleic Acid Accession #: NM\_058173  
 Coding sequence: 68..340

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 TGCCCGAGAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTGTA 180  
 50 TGATGAAGCC CCGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240  
 TACCACCTGA ACCACCGCTG CTCTTACCAC TGCTCGTAAA GACATTCCAG TTTTACCCAA 300  
 ATGGGTTGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT 360  
 TCTGCAATTG GGTCACAACT ATTCATGCTT CCGTGATT CATCCAATA CTTACCTTGC 420  
 CTACGATATC CCCTTATCT CTAATCAGTT TATTTTCTT CAAATAAAAA ATAACATGA 480  
 55 GCGAGCTAAC AT

55

Seq ID NO: 44 Protein sequence  
 Protein Accession #: NP\_477521

60 1 11 21 31 41 51  
 | | | | | |  
 MKFLAVLVLL GVSIFLVSAQ NPPTAAPADT YPATGPADDE APDAETTAAA TTATTAAPT 60  
 ATTAASTTAR KDIPVLPKWV GDLPNRGRVCP

65

Seq ID NO: 45 DNA sequence  
 Nucleic Acid Accession #: NM\_000095.1  
 Coding sequence: 26..2299

70 1 11 21 31 41 51  
 | | | | | |  
 CAGCACCCAG CTCCCGGCCA CGGCATGGT CCCGACACC GCCTGCGTTC TTCTGCTCAC 60  
 CTGCGCTGCC CTGGGGCGGT CGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGGCC 120  
 GCAGATGCTT CGGGAATGAC AGGAAACCAA CGCGCGCGTG CAGGACGTGC GGGACTGGCT 180  
 GGGGCGAGAG GTGAGGAGAG TCAGCTTCCT GAAAAACAG GTGATGGAGT GTGACGCGTG 240  
 75 CGGATGAGAG CAGTCAATAC GCACCGGCTT ACCGAGGTG CGGCGCTGTC TCCACTGGCG 300  
 GCGCGGCTTC TGCTTCCCGG GCGTGGCGTG CATCCAGAG GAGAGCGGCG GCGCTGCGG 360  
 CCCTGCCCC CGGGGCTTCA CGGGCAACGG CTGCACTGTC ACGACGTCA ACGAGTGCAA 420  
 CGCCACCCC TGCTTCCCGG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCGCTGCGA 480  
 GGCTTGCCCC CGGGGTGACA GCGGCCCCAC CCACAGGGC GTGGGGCTGG CTTTGGCCAA 540  
 80 GGCCACACAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACGTGCT 600  
 CCCCACTCC GTGTGATCA ACACCGGGG CTCTTCCAG TGGGCGCGT GCCAGCCGG 660  
 CTTGCTGGGC GACGAGCGT CGGGTGCCA GCGGGGCGCA CAGGCTTCT GCCCGACGG 720  
 CTGCCCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCTTA GAGCGGATG GCTGCGGCTC 780  
 GTGCGTGTGT CGGTTGGCT GGGCGGCAA CGGATCCTC TGTGGTGGG ACACGTGACT 840  
 AGACGCGTTC CGGACGAGA AGCTGCGCTG CCGGAGCGG CAGTGCGCTA AGGACAACTG 900

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CGTGACTGTG CCCAATCTAG GGCAGGAGGA TGTGGACGGC GATGGCATCG GAGACGCTG 960
CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGG 1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGGGTGGG ACAACTGGCG 1080
GTCCCAAGAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGGCA 1140
CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCGGAC AACTGCCCTA GGGTACCCAA 1200
CTCAGACCAAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCGTGTGACA ACTGTCCCCA 1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGAATCTCGG GACAACTGTC CACGGTGGC 1380
TAACAGTGGC CAGGAGGACT CAGACCAAGA TGGCCAGGGT GATGCCTGGG ACGACGAAGA 1440
CGACAATGAC GAGTCCCTG ACAGTCCGGA CAATGCGCGC CTGGTGCTTA ACCCGGCCA 1500
GGAGGACGGG GACAGGGAAG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
GGTGGTAGAC AAGATCGAGG TGTGTCCGGA GAAOGCTGAA GTCACGCTCA CCGACTTCAG 1620
GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGAOCGG CAGATTGACC CCAACTGGGT 1680
GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAAATGAAC AGCGACCCAG GCCTGGCTGT 1740
GGGTACACTT GCGTCCCTG GCGTGGACTT CGAGGGCAAG TTCCATGTGA ACACGGTCAC 1800
GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCCAGGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGAAG CAGATGAGG AAAAGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
GCCTGGCATC CAATCTCAAG CTGTGAAGTC TTCCACAGGC CCGGGGGAAC AGCTGGCGAA 1980
CGCTCTGTGG CATAACAGG ACACAGAGTC CCAGGTGGGG CTGCTGTGGA AGGACCCGGG 2040
AAACGTGGGT TGAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGACCC GGCCCAAGT 2100
GGGCTACATC AGGCTGCGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
CTTGGACACA ACCATGCGGG GTGGCCGCGT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
TCAGCTGGGG CAAGCCTTAG GACCAAGGGT AGGACCCGCC GGATGACAGC CACCTCCACC 2340
GCGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGGAAGTGAG 2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGACGGG
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Seq ID NO: 46 Protein sequence  
Protein Accession #: NP\_000086.1

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1 11 21 31 41 51
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MVPDTCALL LTLAALGASG QGQSPILGSDL GPQMLRELQE TNAALQDVVD WLRQGVREIT 60
PLKNTVMEDC ACGMQQSVRT GLPSVRPLH CAPGFCPPGV ACIQTESGGR CGPCPAGFTG 120
NGSHCTDVNE CNAHPCPPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
INECTVQHVN CVPNSVCINT RGSFQCGPQ PGFVGDAQSG CQRGAQRFCP DGSFSSCHEH 240
ADCVLERDGS RSCVCRVWGA GNGILCGRDT DLDGPPDEKL RCPEPQCRKD NCVTVPNSGQ 300
EDVDRDGIID ACDPDDADGG VPNEKDNCPV VRNPDQRNTD EDKWDACDN CRSQKNDQK 360
DTDQDGRGDA CDDIDIGDRI RNQADNCPRV PMSDQKSDSG DGIQDADCN FQKSNPDQAD 420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDMDGVFDS 480
RDNCRLVFNP GQEDADRDVG GDVCQDDFDA DKVVDKIDVC PENAEVLTLD FRAFTVVLID 540
PEGDAQIDPN WVVLNQGREI VQTMNSDPLG AVGYTAFNGV DFEGTFHVNT VTDDYAGFI 600
FGYQDSSSFY VVMWQMEQT YWQANPPRAV AEPGIQLKAV KSSTGPEQL RNALWHTGDT 660
ESQVRLWKD PRNVGWKDKK SYRWPLQHRP QVGYIRVRPY EGPELVADSN VVLDTMNRGG 720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA
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Seq ID NO: 47 DNA sequence  
Nucleic Acid Accession #: NM\_001565.1  
Coding sequence: 67..363

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1 11 21 31 41 51
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AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTCTGAC TCTAAGTGGC 120
ATCAAGAGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CTGTGTAATC CAAGGTCTTT AGAAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
CGTGTGTAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
TCGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCRAAG AAATGTCTAA AAGATCTCCT 360
TAAACCAGGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA 480
GTCACTATAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
GGTTAATGTT CATCATCTTA AGCTATTCAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
GCTCTACTGA GGTGCTATGT TCTTAGTGGG TGTCTGACC CTGCTTCAAA TATTTCCTC 660
ACCTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTCTGCG TTTGGGGTTT ATCAGAATTC 720
TCAGAATCTC AATAACTAA AAGGTATGCA ATCAAACTCG CTTTAAAG AATGCTCTT 780
ACTTCATGGA CTTCCACTGC CATCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
CATACAATTC CAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
CTTATTATAT GAAAGACTGT ACAGAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
TTTTCAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG
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Seq ID NO: 48 Protein sequence  
Protein Accession #: NP\_001556.1

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80

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1 11 21 31 41 51
| | | | |
MNQTAILICC LIPLTSLGIQ GVPLSRTVRC TCISISNPV NPRSLEKLEI IPASQFCPRV 60
EIIATMKKKG EKRLNPFESK AIKNNLLKAVS KEMSKRSP
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Seq ID NO: 49 DNA sequence  
Nucleic Acid Accession #: XM\_057014  
Coding sequence: 143..874

1 11 21 31 41 51  
 5 GGGAGGGAGA GAGGCGGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCTCGGAG 60  
 CGGGCGGGAG CCACACGCTG ACCACGTTCC TCTCTCGGT CTCTCGGC TCCAGCTCG 120  
 CGCTGCCCG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCGCCTCCC CCGAGCGCT 180  
 CCGCGGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CGTCCGAGCG CCTCTGAGAT 240  
 CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300  
 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360  
 10 CATTCCGGGT ACACCTGGGA TCCCAGGTCG GGATGGATTG AAAGGAGAAA AGGGGAATG 420  
 TCTGAGGGAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480  
 ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540  
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAAAATGCA GAAATGCATG 600  
 CTGTACGCGT TGGTATTTC AATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTGA 660  
 15 AGCTATRAAT TATTTGGACC AAGGAAGCCC TGAATGAAT TCAACAATTA ATATTTCATG 720  
 CACTTCTTCT TTGGAAGGAC TTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780  
 CTGGGTGGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840  
 TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900  
 TTTTATTATT ATGCCTTGG AATGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960  
 20 CATCTGAATG AAAAGCAAAG CTAATATATG TTACAGACCA AAGTGTGATT TCACACTGTT 1020  
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTATTAGT 1080  
 TGGTTAGAAT ACTTCTTCCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140  
 GGTCTTTTGT ATTCTCTCT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200  
 TGTACAATTT GTAATGTGA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260  
 25 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 50 Protein sequence  
 Protein Accession #: XP\_057014

30 1 11 21 31 41 51  
 MRPGQPAASP QRLRGLLLLL LLQLPAPSSA SEIPKKGKQA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSFG ANGIPGTGPI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSINYGIDL 120  
 GKIAECTFTK MRSNSALRLV FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIYLDQ 180  
 35 GSPEMNSTIN IHRTSSVBL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIIIE 240  
 LFK

Seq ID NO: 51 DNA sequence  
 Nucleic Acid Accession #: NM\_020974  
 Coding sequence: 81..3080

40 1 11 21 31 41 51  
 45 GGCCTCCGCG CACACCTCCC CGCGCGCGCG CCGCCACCGC CCGCACTCCG CGGCTCTGTC 60  
 CGCACAACGC TGAGCCATCC ATGGGGGTGG CCGGCCCGCA CCGTCCCGGG CGGCCTGGG 120  
 CGGTGCTGCT GCTGCTGCTG CTGCTGCCCG CACTGCTGCT GCTGGCGGGG GCGTCCCGC 180  
 CGGGTCCGGG CCGTGCOCG GGGCGCAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240  
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA 300  
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAATGARGC 360  
 TCAATGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGT 420  
 50 TTGATGGCTT CATGTGGCT CATGACGTC ATAATTGTCT TGATGTGAC GAGTGCTGG 480  
 AGAACAAATG CGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGTGCT 540  
 GCAAGAGGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTACCCG TCGGAAGAGG 600  
 GCCTGAGCTG CTAAGATAAG GATCAAGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660  
 GCAGCGTGGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
 55 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780  
 GCCCAGATG CAGCTGCCAT CCACAGTACA AGATGGGAGG AGCTGCCTTG 840  
 AGGAGAGGGA CACTGTCTCG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900  
 ATAAAGCTGG GAACCGCGCG CTGCTCATGG AAAAGTGTGC TGTCAACAAT GAGGCTGTG 960  
 ACOGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCTGTTT GGATTCATCT 1020  
 60 TCCAGTTGGA TGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080  
 GTGATCATTT CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CCGCTGCCAG AAAGGATTTA 1140  
 AATTATTAA AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200  
 GTGACCAAG CTGCATCAAC CACCCTGGCA CATTGCTTG TGCTTGCAAC CGAGGGTACA 1260  
 65 CCCTGTATGG CTTACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320  
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA 1380  
 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCTGCCC ACAAGTGTGT 1440  
 CACCCCGTGT GTCCCTGCAC TGCGGTAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500  
 GTCACCTCGG CATTACCTC TCTTCAGATG TCACCAACAT CAGGACAAGT GTAACTTTTA 1560  
 70 AGCTAAATGA AGGCAAGTGT AGTTTGAATA ATGCTGAGCT GTTTCCCGAG GGTCTGCGAC 1620  
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680  
 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCAACCTT AAGGAAATGT 1740  
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 TGAGCTGCAT CGTAAGAGCA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACCTCAGAA 1860  
 75 AGGCCGTCCA CAGGAGCAG TTTACCTCC AGCTCTCAGG CATGAACCTC GAGTGGCTTA 1920  
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCCT TGAGTGGGC CAGGGTCAAT 1980  
 CAGAAAACCA ATGTGTGAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040  
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100  
 GCCCAAGACC AGGAATTTCT GGGGCCCTGA AGACCCAGCA AGCTTGAAT ATGTCTGAAT 2160  
 80 GTGGAGTGT GTGTCAACTT GGTGAATATT CTGCAGATGG CTTTGCACTT TGCCAGCTCT 2220  
 GTGCCCTGGG CAGGTTCAGG CCTGAAGCTG GTGCAACTTC CTGCTTCCCC TGTGGAGGAG 2280  
 GCCTTGGCCAC CAACATCAG GGAGCTACTT CCTTCAGGA CTGTGAAACC AGAGTTCAAT 2340  
 GTTCACTGG ACATTTCTAC AACACCACCA CTCACGATG TATTCGTTCG CAGTGGGAA 2400  
 CATACAGCC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAT ACTACGACTG 2460  
 ACTTTGATGG TCCCAACAAC ATAAACCACT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520

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GAGATTTCAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580
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TCTTCTGTGC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT 2700
CCAAATCTGT GACAAACATAT GAAACCTGCC AGAAGCTAGG AGGCCCATC GCCTTCACCT 2760
CCAGGTCAAA GAAGCTGTGG ATTCAGTTC AATCCAAATGA AGGGAACAGC GCTAGAGGGT 2820
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GAGATGGCAG GCTCTATGCA TCTGAGAAAC ATCAGGAAAT ACTTAAGGAT AAGAAACTTA 2940
TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAGATAC ACAGCCACAG 3000
AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060
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CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGGTAAATT 3240
GAACITGGTT TTTCTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGCTGGCTT GAGCTGGACT 3360
TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCTCC TCAAGGAGTC 3420
TGATGTGAAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCTCTAGC 3480
CCGGCCTCTT CTAAGGGAGC CCTCTGCACT CGTGTGACAG CTCTGACCAG GCAGAACAGC 3540
CAAGAGGGGA GGGAGGAGGA CCCCTGCAGG CTCCCTCCAC CCACTCTGAG ACCTGGGAGG 3600
ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
AGTTCTAAGC AGTGCTCGTG AAAAAAAAAA GCAGAAAGAA TTAGAAATAA ATAAAAACTA 3720
AGCATTCTG GAGACAT

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Seq ID NO: 52 Protein sequence  
Protein Accession #: NP\_066025

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1 11 21 31 41 51
MGVAGRNRPG AANAVLLLLL LLPLLILLAG AVPPGRGRRA GPQEDVDECA QGLDDCHADA 60
LQNTPTSTYK CSCKPGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNRY CTCFDGFMIA 120
HDGHNCLDLD ECLENNNGGQ HTCVNVMGSY ECCKEGFFL SDNQHTCIHR SEEGLSMNNK 180
DHGCSHIGKE APRGSVACEC RPFELAKNQ RDCILTCNHG NGGQHSQDOD TADGPECSCS 240
PQYMHGTDGR SCLEREDIVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GCDRTCKDT 300
STGVHCSCPVP GTLQLDQKTR CKDIDECQTR NGGCDHFCNK IVGSFDCGCK KGFLLTDEK 360
SCQDVDECSL DRTCDHSCIN HPGTAFACAN RGYTLYGFTH CGDTNECSIN NGGQCVQCVN 420
TVGSYEQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGSDGC FLRCHSGIHL 480
SSDVTITRTS VTFFKLNEGKC SLKNAELFPE GLRPALEPKH SSVKESFRYV NLTKSSGKQV 540
PGAPGRPNST KEMFITVEFE LETNQKEVTA SCDLSVICVR TEKRLRKAIR TLRKAVERDQ 600
FHLQLSGMML DVAKKPPRTS ERQAESCQGV QGHAENQCVS CRAGTYDGA RERCILCPNG 660
TFQNEEQQMT CEPFCRPPNS GALKTPBAWN MSECGLCQFP GEYSADGFAP CQLCALGTFO 720
PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYPBFG 780
KNNCVSCPGN TTTFDQGSTN ITQCKNRRCG GELGDPFTYI ESPNYRPNYP ANTECTWTIN 840
PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSSNSVTYI ETCQTYRPI AFTSRSKLW 900
IQFKNBEGNS ARGFPVYVT YDEDYQELIE DIVRDGRLYA SENHQBIKD KKLKALFDV 960
LAHPQNYFKY TAQESREMFY RSFIRLLRSK VSRFLRPYK

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Seq ID NO: 53 DNA sequence  
Nucleic Acid Accession #: NM\_014211  
Coding sequence: 157..1479

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1 11 21 31 41 51
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GTCCGCTCTG TAGGCCTGAA GGACTTGCCC TAACAGAGCC TCAACAATA CCTGGTGATT 120
CCTACTCTAG CCCCTTGGTG TGAGCAGCTT CTCAACATGA ACTACAGCCT CCACCTGGCC 180
TTCTGTGTCT TGAGTCTCTT CACTGAGAGG ATGTGCTATC AGGGGAGTCA GTTCAACGTC 240
GAGGTGGGCA GAAGTGACAA GCTTTCCCTG CCTGGCTTTG AGAACCTCAC AGCAGGATAT 300
AACAATATTC TCAGGCCCAA TTTTGGTGGA GAAACCGTAC AGATAGCGCT GACTCTGGAC 360
ATTGCAAGTA TCTCTAGCAT TTCAGAGAGT AACATGGACT ACACAGCCAC CATATACCTC 420
CGACAGCGCT GGAATGAACA GCGGCTGGTG TTTGAAGGCA ACAAGAGCTT CACTCTGGAT 480
GCCCGCTCCG TGGAGTTCCCT CTGGGTGCCA GATACTTACA TTGTGGAGTC CAAGAAGTCC 540
TTCTTCCATG AAGTCACTGT GGGAAACAGG CTCATCCGCC TCTTCTCCAA TGGCACGGTC 600
CTGTATGCCC TCAGATCAC GACAACGTGT GCATGTAACA TGGATCTGTC TAAATACCCC 660
ATGGACACAC AGACATGCA GTTGCAGCTG GAAAGCTGGG GCTATGATGG AAATGATGTG 720
GAGTTCACTT GGCTGAGAGG GAACGACTCT GTGCGTGGAC TGGAACACCT GCGGCTTGCT 780
CAGTACACCA TAGAGCGGTA TTTCACTTCA GTCCACAGAT CGCAGCAGGA GACAGGAAAT 840
TACACTAGAT TGGTCTTACA GTTGTAGCTT CGGAGGAATG TTCTGTATTT CATTTTGAA 900
ACCTACGTTT CTTCACCTT CCTGGTGGTG TTGTCTGGG TTTCATTTTG GATCTCTCTC 960
GATTCAGTCC CTGCAAGAAC CTGCATTTGA GTGACGACCG GTTATCAAT GACCACACTG 1020
ATGATCGGGT CCGGCACTTC TCTTCCCAAC ACCAACTGCT TCATCAAGGC CATCGATGTG 1080
TACCTGGGGA TCTGCTTTAG CTTTGTGTTT GGGGCCCTGC TAGAATATGC AGTTGCTCAC 1140
TACAGTGTAT TACAGCAGAT GGCAGCCAAA GATAGGGGGA CAACAAAGGA AGTAGAAGAA 1200
GTCAGTATTA CTAATATCAT CAACAGCTCC ATCTCCAGCT TTAACCGGAA GATCAGCTTT 1260
GCCAGCATTG AAATTTCCAG CGACACGCTT GACTACAGTG ACTTGACAAT GAAACACAGC 1320
GACAGATTCA AGTTGTCTCT CGAGAAAAAG ATGGGCGAGG TTGTGATTA TTTCAAAAT 1380
CAAAACCCCA GTAATGTTGA TCACTATTCC AAACACTGCT TTCTTTGAT TTTTATGCTA 1440
GCCAATGTAT TTTACTGGGC ATACTACATG TATTTTGGAG TCAATGTTAA ATTTCTTGCA 1500
TGCCATAGGT CTCAACAGG ACAAGATAAT GATGTAAATG GTATTTTAGG CCAAGTGTGC 1560
ACCCACATCC AATGGTGCTA CAAGTGACTG AAATAATATT TGAGTCTTTC TGCTCAAAGA 1620
ATGAAGCTCC AACCATTTGT CTAAGCTGTG TAGAAGTCTT AGCATTATAG GATCTTGTA 1680
TAGAAACATC AGTCCATTCC TCTTTCATCT TAATCAAGGA CATTCCCATG GAGCCCAAGA 1740
TTACAAATGT ACTCAGGGCT GTTTATTCGG TGGCTCCCTG GTTTGCATT ACCTCATATA 1800
AAGAATGGGA AGGAGACCAT TGGGTAACCC TCAAGTGTC GAAGTTGTTT CTAAGTAAC 1860
TATACATGTT TTTTACTAAA TCTCTGCAGT GCTTATAAAA TACATTGTTG CCTATTTAGG 1920
GAGTAACATT TTCTAGTTTT TGTTTCTGGT TAAAAAGAAA TATGGGCTTA TGTCAATTCA 1980

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5 TTGGAAGTCA ATGCACTAAC TCAATACCAA GATGAGTTTT TAAATAATGA ATATTATTTA 2040  
 ATACCACAAC AGAATTATCC CCAATTTCCA ATAAGTCTTA TCATTGAAAA TTCAAATATA 2100  
 AGTGAAGAAA AAATTAGTAG ATCAACAATC TAAACAAATC CCTCGGTCTT AAGATACAAT 2160  
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25 Seq ID NO: 54 Protein sequence  
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TGGGCCCCAC CTCTTACTGC GAGCAGTCCG AGACATCGAG GTGGGAGAGG AGCTCACCAT 660
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CTGCTTTGAA TGTGACTGTT TCCGTGCGCA AACCCAGGAC AAGGATGCTG ATATGCTAAC 780
  
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5 TGGTGATGAG CAAGTATGGA AGGAAGTTCA AGAATCCCCTG AAAAAAATTG AAGAACTGAA 840  
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 CAAACTGCAG CTACATCAAG GCATGTTTCC CCAAGCAATG AAGAATCTGA GACTGGCTTT 1140  
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 10 CGGCGTGTGT CTTTGTTGAA TGCCTTATTG AGGTCACACA CTCTATGCTT TGTAGCTGT 1320  
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15 Seq ID NO: 62 Protein sequence  
 Protein Accession #: NP\_073580

1 11 21 31 41 51  
 20 MRCSQCRVAK YCSAKCQKKA WPDHIRECKK LKSCKPRYPF DSVRLLRGVV FKLMGAPSE 60  
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 CNSPTICNAE MQEVGVGLYP SISLLNHSDD PNCISIVPNGP HLLLRVRDI EVGEELTICY 180  
 LDMLMTSEER RKQLRDQYCF ECDPCRCQQT DKDADMLTGD EQVWKEVES LKKIEELKAH 240  
 WKWEQVLAMC QAIISNSER LPDINIYQLK VLDCAWDACI NLGLLEALF YGTRTMEPYR 300  
 25 IFFPGSHFVR GVQVMKVGKL QLHQGMFPQA MKNLRIFAADI MRVTHGREHS LIEDLILILLE 360  
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30 Seq ID NO: 63 DNA sequence  
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 Coding sequence: 238..648

1 11 21 31 41 51  
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 GGCAGGAAGA GAAGCGGCTT TCTGTCTGCC GGGGTGCGAG CGCAGAGGGG CAGTGCCATG 240  
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 40 ATGCCCAACC ACCTGCACCA CAGCACGCGG GAGAAGCCCA TCCTGGCCAT CGAGCAGTAC 420  
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 70 AATAATTGTA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT 2220  
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 80 TATTGGATAC TTAGTGGTT TCTTCACTGA CAATACTGAA TAAACATCTC ACGGAATTC

Seq ID NO: 64 Protein sequence  
 Protein Accession #: NP\_003005.1

1 11 21 31 41 51



5  
MFLSILVALC LNLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60  
YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPIKPCKSV QQRARDCEP LMKMYNHSWP 120  
ESLACDELVP YDRGVCISPE AIVTDLPEDV KWIDITPDM VQERPLDVC KRLSPDRCK 180  
KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTVVDV KBIFKSSSPI PRITQVPLITN 240  
SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDL SKRSIQWEER LQEQRRITVD 300  
KKKTAGRTSR SNPPPKPKGP PAPKPASPKK NIKTRSAQKR TNPKRV

10  
Seq ID NO: 65 DNA sequence  
Nucleic Acid Accession #: BC010423  
Coding sequence: 248..1780

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CAAGTGCAGG AGGCAAGAAC TCTGCAGCTT CCTGCCTTCT GGGTCAGTTC CTTATTCAAG 180  
TCTGCAGCCG GCTCCCAGGG AGATCTCGGT GGAACCTTCAG AAAOCTGGG CAGTCTGCCT 240  
TTCAACCATG CCCTGTGCC TGGGAGCCGA GATGTGGGGC CTGAGGCCCT GGCTGTGTCT 300  
20 GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCGCG GGTGAGCTGG AGAOCCTCAGA 360  
CGTGTAACT GTGGTGTGG GCCAGGACGC AAAACTGCC TGTCTTACC GAGGGGACTC 420  
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ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC CCGCTTACG AGGGCCGCGT 540  
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25 GCAGGCGGAT GAGGGCGAGT ACGAGTCCG GGTCAAGCAC TTCGCCCGCG GCAGCTTCCA 660  
GGCGCGGCTG CGGCTCCGAG TGCTGGTGCC TCCCTGCCCT TCACTGAATC CTGGTCCAGC 720  
ACTAGAAGAG GCCCAGGGCC TGACCTTGGC AGCCTCTGCG ACAGCTGAGG GCAGCCAGC 780  
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30 GCAGGCGGAT GAGGTGTGG TGTCCCATCC TGGCTGCTC CAGGACCAAA GATCACCACA 960  
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45 CTAGGCTGCG TCCTTCTGT TGACATGGGA GATTTTAGCT CATCTTGGG GCCTCCTTAA 1860  
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50 TGACTGTCCG TGGAGGGGTG ACTGTGTCCG TGGTGTGTAT TATGCTGTCA TATCAGAGTC 2100  
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55 TCTCCTACCA CTTCGAGGCC ATGGGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA 2400  
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ACTTTTAATT TTTTCTTTT TTTTCTTTG CCTTTTCCAT TAGTGTATT TTTTATTAT 2580  
60 TTTTATTATT ATTTTCTTT AGAGTTTGG TCCAGCTGG ACGATATAGC CAGACCTGCT 2640  
CTGTAAAAAA ACCAAAAACC AAAAAAAA AAAAAAAA

Seq ID NO: 66 Protein sequence  
Protein Accession #: AAH10423

65  
1 11 21 31 41 51  
MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE 60  
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70 DEGEYECRVV YDRGVCISPE AIVTDLPEDV KWIDITPDM VQERPLDVC KRLSPDRCK 180  
VTWDETVKGT TSSRSFKHSR SAAVTSEPHL VPSRSMNGQP LTCVVSHPGL LQDQRIITHL 240  
HVSFLAEASV RGLDQNLWE IGREGAMLC LSEGGPPPSY NWTRLDGPLP SGVRVDGDTL 300  
GFPLPTEHS GIYVCHVSN FSSRDSQVTV DVLDPOEDSG KQVDLVASV VVVGVIAALL 360  
FCLLVVVVVL MSRYHRRKAQ QMTQRYEEL TLTRENSIRR LSHHTDPRS QPESVGLRA 420  
EGHPDSLKDN SSCSVMSEEP EGRSYSTLT VREIETQTEL LSPGSGRAE EEDQDEGIKQ 480  
75 AMNHFPQENG TLRAPKPTNG IYINGRHLV

Seq ID NO: 67 DNA sequence  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274..1782

80  
1 11 21 31 41 51  
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GTGAAAGGAA AGGAAGATCA TTTTCATGCCT TGTGTATAAA GGTTCAGATT TCTGCTGATT 180



5 CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
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 15 ACAGTGTGTA AAGAGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080  
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 25 CGCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAAACCT 1680  
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 30 TTTTCAGGA GCGACCTGGG CAAAGACAGA GAAGCTCCA GAAGGAGAGA TTGATCOGTG 1980  
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Seq ID NO: 68 Protein sequence

Protein Accession #: NP\_001194

35 1 11 21 31 41 51  
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 40 DSGLEPVVTS CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECKNDLHPTL PFLKNRDFVD 120  
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 EQSQSSGSGS GLPLLVQRTI AKQIQMVQKI GKGRYGEVVM KWRGKEKVAV KVFFTEBAS 240  
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 45 TNEVDIPNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420  
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Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 166..1737

50 1 11 21 31 41 51  
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 55 AGTGCACTAG TGTGATCACT TCTTACTGCC GCCTCAGCT TCCAGCTCA ACTCAAGCAA 120  
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 60 GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360  
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 65 AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGGT 660  
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 80 CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCTGCGCAG CTGGCATGGC CCGGCTGCTG 1560  
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5 AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTGT TGTTTTGTGT TGTTTTAAGC 1920  
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Seq ID NO: 70 Protein sequence  
 Protein Accession #: Eos sequence

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 15 SRISWIIISIC VFVLTFSAPL ATVLNRFHGH RLVMVLGGLL VSTGMVAASF SQEVSHMYVA 120  
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 YSLLFVGLLQ LNVIFGALL RPIFIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240  
 GVELTTSFKN VPTHNLLELE PKADMQQVLV KTSFRPSEKK APLLDPSILK EKSFCYALF 300  
 GLFATLGFPA PSLYIIPLGI SLGIDQDRAA PLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360  
 20 IELICVILLT VSLFAPTFAT EPWGLMSCSI FPGFMVGTIG GTHIPLLAED DVVGIEKMS 420  
 AAGVYIFQIS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480  
 HHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 71 DNA sequence  
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 Coding sequence: 166..1737

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 TTAAGCTTTT GTTCCAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240  
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 35 GGTGCTCTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360  
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Seq ID NO: 72 Protein sequence  
 Protein Accession #: NP\_004685

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 YSLLFVGLLQ LNVIFGALL RPIIIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240  
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 GLFATLGFPA PSLYIIPLGI SLGIDQDRAA PLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360  
 IELICVILLT VSLFAPTFAT EPWGLMSCSI FPGFMVGTIG GLTFRCLLLM MSWALQKMS 420  
 80 AAGVYIFQIS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480  
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 Nucleic Acid Accession #: NM\_002184.1  
 Coding sequence: 256..3012

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Seq ID NO: 74 Protein sequence  
Protein Accession #: NP\_002175.1

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GKILDYEVL TRWKSHLQNY TVNATKLTVN LTNDRYLATL TVRNLVGKSD AAVLTIPACD 420
70 FQATHPMDL KAPFKDMLW VEWTTPRESV KKYILEWCVL SDKAPCITDW QQEDGTVHRT 480
YLRGNLAESK CYLITVTPVY ADGPGSPESI KAYLKQAPPK KGPTVRTKKV GKNEAVLEWD 540
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SHIAQSPPT PPRHNFNSKD QMYSNGFTD VSVVEIAND KKPFPEDLKS LDLFKKEKIN 720
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80 ESTQPLDSE ERPEDQLVD HVDGGDGLP RQQYFKQNC QHESPDIHS FERSKQVSSV 840
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Seq ID NO: 75 DNA sequence  
Nucleic Acid Accession #: NM\_022131  
Coding sequence: 11..2878

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Seq ID NO: 76 Protein sequence  
 Protein Accession #: NP\_071414

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Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 482...3007

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 TAACCACTCG ACCAAATTAA GTAAAGGCAT GTTCTTGGT CTCCATAATC TTGAATACTT 1800  
 50 ATATCTTGAA TACAATGCCA TTAAGGAAAT ACTGCCAGGA ACCTTTAATC CAATGCCTAA 1860  
 ACTTAAAGTC CTGTATTTAA ATAACAACCT CCTCCAAGTT TTACCACCA ATATTTTTTC 1920  
 AGGGGTTCTT CTAACCTAAG TAAATCTTAA AACAAACCAG TTTACCCTAT TACCTGTAA 1980  
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 CTGCTCCTGT GACCTGGTTG GACTGCAGCA ATGGATACAA AAGTTAAGCA AGAACACAGT 2100  
 55 GACAGATGAC ATCTCTGCA CTTCCTCCGG GCATCTCGAC AAAAAGGAAT TGAAGCCCT 2160  
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 TTACCTTATG GTACCACTTC CTGCAACAAC AACAAATACG GCTGATACTA TTTTACGATC 2280  
 TCTTACGAGC GCTGTGCCAC TGCTGTCTCT AATATTGGGA CTTCTGATTA TGTTCATCAC 2340  
 60 TATTTGTTTC TGTGCTGCA GGAATAGTGT TCTTGTCTCT CACCGCAGGA GAAGATACAA 2400  
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 65 TCTTTTGAA CAGGAAATC ATTCACCACT CACAGGGTCA AATATGAAAT ACAAACCCAC 2700  
 GAACCAATCA ACAGAAATTT TATCCTTCCA AGATGCCAGC TCATTGTACA GAAACATTTT 2760  
 AGAAAAAGAA AGGGAACCTT AGCAACTGGG AATCACAGAA TACCTAAGGA AAAACATTGC 2820  
 TCAGCTCCAG CCTGATATGG AGGCACATTA TCCTGGAGCC CACGAAGAGC TGAAGTTAAT 2880  
 GGAACACATTA ATGTACTCAC GTCCAAGGAA GGTATTAGTG GAACAGACAA AAAATGAGTA 2940  
 70 TTTTGAACCT AAGCTAAT TACATGCTGA ACCTGACTAT TTAGAAGTCT TGGAGCAGCA 3000  
 AACATAGATG GAGAGTTTGA GGGCTTTGCG AGAAATGCTG TGATTCTGTT TTAAGTCCAT 3060  
 ACCTTGTAAG TAAGTGCCCT ACGTAGTGT GTCATCAATC AGAACCTAAG CACAGCAGTA 3120  
 AACATGGGG AAAAAGAAAG AAGAAGAAAA GAAACTCAGG GATCACTGGG AGAAGCCATG 3180  
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Seq ID NO: 78 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 80 MRLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCNEEK DGTMLINCEA KGIRMVSEIS 60  
 VPPSRPFQLS LLNGLTMLH TNDPFGSLTNA ISIHGLFNFI ADIEIGAFNG LGLLKLHIN 120  
 ENSLEILKBD TFGHLENLEF LQADNNTFIV IEPSAPSKLN RLKVLILNDN AIESLPPNIF 180  
 RFVPLTHRLD RGNQLQLTLY VGFLEHIGRI LDQLLEDNKW ACNCDLLQLK TWLENMPPQS 240  
 IIGDVVCNSP PFFKGSILSR LKESICPTP PVYEHEDPS GSLHLAATSS INDSRMSTKT 300  
 TSILKLPTRA PGLIPYITKP STQLPGPYCF IPCNCKVLSF SGLLIHQGER NIBSLSDLRP 360

5 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNRRIE VLEEGSFNNL TRLQKLYLNG 420  
 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFFNPMFK LKVLYLNNL LQVLPPIHFS 480  
 GVPLTKVNLK TNQFTHLFVS NILDDLDTL QIDLEDNPMW CSDLVGLQQ WIQKLSKNTV 540  
 TDDILCTSPG HLDKKEKAL NSBILCPGLV NNPSMPTQTS YLMVTTPTAT TNTADTILRS 600  
 L TDAVPLSVL ILGLLHPIT IVPCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM 660  
 YGHKTTHTHT ERPSASLYEQ HMVSPMVHVY RSPSFGPKHL EEEEEERNEKE GSDAKHLQRS 720  
 LLEQENHESPL TGSNNKYKTT NQSTEFLSFQ DASSLYRNIL EKERELQLQG ITEYLKRNIA 780  
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10

Seq ID NO: 79 DNA sequence  
 Nucleic Acid Accession #: NM\_016640.2  
 Coding sequence: 39..1358

15 1 11 21 31 41 51  
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 20 TGGCTCCAT GACAGCGGAC AGCAAAGCTG CACGGCTGCG GCGGATCGAG CGCTGGCAGG 240  
 CGACGGTGCA CGCTCGCGAG TCGGTAGACG AGAAGCTGCG AATCCTCACC AAGATGCAGT 300  
 TTATGAAGTA CATGGTTTAC CGCAGACCT TCGCGCTGAA TGCCGACGCG TGGTACCAGT 360  
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 AGCCCGAACC CGAAGCTGAA CCTGCGCTGG ACCTCGCGGC GCTGCGTGCG GTGCGCTGCG 480  
 25 ACTGCTGCT GCAGGAGCAC TTCTACCTGC GCGCGAGGCG GCGCGTGCAC CGTTACGAGG 540  
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 TCAGCCACA CAACCCGCGC CTGGCCGCTG CCGCCCTCGA TTATAGATGC CCAGTTTCATT 660  
 TTTACTGGGT GCGTGGTGAA GAAATTATTC CTCGTGGTCA TCGAAGAGGT CGAATTGATG 720  
 ACTTGGGATA CCAGATAGAT GATAAACCAA ACAACAGAT TCGAATATCC AAGCAACTCG 780  
 30 CAGAGTTGT GCGATTTGAT TATTCTGTTC CTATAGAAAT CCCCACTATA AAATGTAAAC 840  
 CAGACAAAT TCCATTATTC AAACGGCAGT ATGAAACCA CATATTGTGT GGCTCAAAAA 900  
 CTGCAGATCC TTGCTGTAC GGTACACCC AGTTTCATCT GTTACCTGAC AAATTAAGAA 960  
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 CTATTGCAAG CCTTTTGTCT TGGACTGGAG CACAAGCTAT GTATCAAGGA TTCTGGAGTG 1080  
 35 AAGCAGATGT TACTCGACCT TTTGTCTCCC AGGCTGTGAT CACAGATGGA AAATACTTTT 1140  
 CCTTTTTCTG CTACCACTTA AATACTTTGG CACTGACTAC ACAAGCTGAT CAAATAAACC 1200  
 CTCGTAAAAA TATATGTTGG GGTACACAAA GTAAGCCTCT TTAAGAAACA ATTGAGGATA 1260  
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 40 GACCAAAAGA AGAAAAATCA CAGCTGTTGG AAAAAGTAAA AAGCATATT GATTGAGAAC 1380  
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 ATTAATAACA TTGATTTTGG AGACAAAAA AAAAAAAAAA AA

Seq ID NO: 80 Protein sequence  
 Protein Accession #: NP\_057724.1

45 1 11 21 31 41 51  
 | | | | | |  
 MAARCRWRPL LRGRPLSLHT AANAAATATE TTSQDVAAAT VARYPPIVAS MTADSKAARL 60  
 RRIRERQATV HAAESVDEKL RILTKMQFMK YMVYPQTFAL NADRWYQYFT KTVFLSGLPP 120  
 50 PPAEPEPEPE HAPEPLDLA ALRAVACDCL LQEHFYLRRR RRVHRYESB VISLPFLDQL 180  
 VSTLVGLLSP HNPALAAAL DYRCPVHFYW VRGEEIIPRG HRRGRIDDLR YQIDDKPMNQ 240  
 IRISKQLAEF VPLDYSVPPI IPTIKCKPDK LPLFKRQYEN HIFVGSKTAD PCCYGHTQFH 300  
 LLPDKLRER LRLQNCADQI EVVFRANAIA SLPAWTGAQA MYQGFWSAD VTRPFVSQAV 360  
 55 ITDGKYFSFF CYQLNTLALT TQADQNNPRK NICWGTQSKP LYETIEDMDV KGFNDVDVLLQ 420  
 IVHFLNLRPK EESQLEEN

Seq ID NO: 81 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..2070

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 65 CTACGGCAGA GCGACCGCGA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATOGAGCA TCTGAAGCGG 240  
 GAAAAACAAG GTGAGCGCGC GCGGGGCCCT AGGCGGGCCC TGCCCTCCCA GGCACACTCA 300  
 ACACCTGCCG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CTTGGGCTCA 360  
 70 GGGGGAACAC AGGACGGGGA GCGCCCTCCG ACTGTCTCTG CCCACCTGGC TGCACTGGCC 420  
 CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480  
 AGCCGTGGCT GGAAGATGTT ATGCAGCCAA GCACAGCAAG TGCTGCTCTC GGGGAAGCCCA 540  
 GGGCCTGAGG TCATTGCAAG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT 600  
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCGCCCTGCT TAGATCTTTG 660  
 75 CCTCAGATTG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCAC 720  
 ATGCTGGGGG CCCAGGGGAT ATGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACCA TGGGGAACAA GGGAGGAAGC AGAGTCCTGT TTCCCTTGCA CTGTGCCAAG 840  
 GCACCTCCCC ATCTGACAG CCGCCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATTTATCTT GGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960  
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 80 GACATGAGAA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCAGTGGAG 1080  
 CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCGCAGTGG TGGGAGCGCT 1140  
 GACAGGACAC GGGAAAGAGC CATGCTTTCC CTGGGACCT GCTGTTCAT GTGTCCCAAG 1200  
 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG 1260  
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5 AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGGC 1380  
 GCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440  
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500  
 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCAGA AGGCCGACCT GGAAGAGGAG 1560  
 CCGCTACTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGGCA GGCCAGAAAG 1620  
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680  
 AGGCAGATGG GGGCGGGGG ACACCCCCCA ATGATCCTGC CCCTTCCCT GCGAAAGCCC 1740  
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 10 ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860  
 CCGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCAAGC ATTTCCCAA GGTCTCCACC 1920  
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980  
 CTGAAGCAGA CCGGAAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040  
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15 Seq ID NO: 82 Protein sequence  
 Protein Accession #: PGENESH predicted

20 1 11 21 31 41 51  
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 QQHSEMLAK LHBEIEHLKR ENKGEFARGP RPALEPQAHS TLPLFQHRNT AINSSTRLGS 120  
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180  
 GPEVIAGRQV ATGCSFDLPP PSRAEMGRNP WDSPCPARSL PQIAAARPR ISSPMALSPH 240  
 25 MLGAQGIWTH SIQGSPLAIW AATMTGKGS RVLPFCHLSK ALPHPDGSGPH PAQDPGLWSQ 300  
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGGP FPSRCGNSSE 360  
 LFWAKQGPSR QPOPSCAGDA DRTREBAMLS LGTCCSMCPK PSCFPDGPFG NHLSRASAPL 420  
 GARWVICNGV WVEPGGSPFA RLKEGSSRTH RFGGKRGRLA GGSADTVRSP ADSLSMSSFPQ 480  
 SVKSIANSAN SQKARPPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGGARK 540  
 30 EKAEMASNAGA ACMGNSQHQG RQMAGAHFP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600  
 TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHPPKVST KSLSKKCLSP FVAERAILPA 660  
 LKQTPKNFPA ERQKRLQAMQ KRRLHRSVL

35 Seq ID NO: 83 DNA sequence  
 Nucleic Acid Accession #: NM\_005264.1  
 Coding sequence: 557..1954

40 1 11 21 31 41 51  
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 CAACTCGGCC CTTGAGGCTC TCGAAGATTA CGCATCTAT TTTTITTTTC TTTTITTTCT 180  
 TTTCTAGCGC CAGATAAAGT GAGCCCGGAA AGGGAAGGAG GGGGCGGGGA CACCATTGCC 240  
 CTGAAAGAA ATAAAGTAA ATAAACAAAC TGGCTCCTCG CCGCAGCTGG ACGCGGTGG 300  
 45 TTGAGTCCAG GTTGGGTGG ACCTGAACCC CTAAAGCGG AACCGCTCC CGCCTCGCC 360  
 ATCCCGGAGC TGAGTCCGG GCGGCGGTGG CTGCTGCCAG ACCCGAGATT TCCTCTTTCA 420  
 CTGGATGGAG CTGAACCTTG GCGGCCGAGA GCAGCACAGC TGTCCGGGGA TCGTGCACG 480  
 CTGAGCTCCC TCGGCAGAC CCAGCGCGCG CTGCGGATTT TTTTGGGGGG GCGGGGACCA 540  
 GCGCGCGGCC GGCACCATGT TCCTGGCGAC CCTGTACTTC GCGCTGCGC TCTTGGACTT 600  
 50 GCTCCTGTGC GCGAAGTGA GCGCGGAGA CCGCTGGAT TCGTGAAG CCAATGATCA 660  
 GTGCTTGAAG GAGCAGAGCT GCAGCACCAA GTACCGCACG CTAAGGCAGT GCGTGGCGGG 720  
 CAAGGAGACC AACTTACGCC TGGCATCCGG CCGTGGAGCC AAGGATGAGT GCGCAGCGCC 780  
 CATGGAGGCC CTGAGCAGA AGTGGCTCTA CAATCGCGC TGCAAGCGGG GTATGAAGAA 840  
 GGAGAAGAAC TGCCTGCGCA TTTACTGGAG CATGTACCAG AGCCTGCGG GAAATGATCT 900  
 55 GCTGGAGGAT TCCCATATG AACCACTTAA CAGCAGATT TCAGATATAT TCCGGGTGGT 960  
 CCCATTCTA TCAGATGTTT TTCAGCAAGT GGAGCACATT CCCAAGGGA ACAACTGCCT 1020  
 GGATGACAGC AAGGCTGCA ACCTCGACGA CATTGCAAG AAGTACAGT CCGGTACAT 1080  
 CACCCGTCG ACCACGAG TGTCCAAGA TGTCTGCAAC CGCCGCAAGT GCCACAAGGC 1140  
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 60 CTGCGCGGAC ATCGCTGCA CAGAGCGGAG GGCACAGACC ATCGTGCCTG TGTCTCTCTA 1260  
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 AGTCATGACC CCCAACTACA TAGACTCCAG TAGCCTCAGT GTGGCCCAT GGTGTGACTG 1500  
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 70 TTCCAATGGT AATTATGAAA AAGAAGGTCT CGTGTCTTCC AGCCACATAA CCACAAAATC 1860  
 AATGGCTGCT CCTCAAGCT GTGGTCTGAG CCCACTGCTG GTCTGTGTGG TAACCGCTCT 1920  
 GTCCACCTTA TTATCTTTAA CAGAAACATC ATAGCTGCAT TAAAAAATA CAATATGGAC 1980  
 ATGTAAAAAG AAAAAACCA AGTTATCTGT TTCCTGTTCT CTGTATAGC TGAATTTCCA 2040  
 GTTTAGAGC TCAGTTGAGA AACAGTTCCA TTCAACTGGA ACATTTTTTT TTTTCTTTT 2100  
 75 AAGAAAGCTT CTGTGATCC TTGGGGCTTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC 2160  
 AAACTCAGAA GGCCTTGGGA TATGCTGTAT TTTAAAGGGA CAGTTTGTAA CTGGGCTGT 2220  
 AAAGCAAACT GGGCTGTGT TTTOGATGAT GATGATCATC ATGATCATGA TGATTTAAC 2280  
 AGTTTACTT CTGGCCTTTC CTAGCTAGAG AAGGAGTTAA TATTTCTAAG GTAACCTCCA 2340  
 TATCTCTCTT AATGACATT ATTTCTAATG ATATAAATT CAGCTACAT TGATGCCAAG 2400  
 80 CTTTTTTGCC ACAGAAGA TTCTTACCAA GAGTGGGCTT TGTGGAACA GCTGGTACTG 2460  
 ATGTTCACTT TTATATATGT ACTAGCATTT TCCACGCTGA TGTTTATGTA CTGTAAACAG 2520  
 TTCTGCACTC TTGTACAAAA GAAAAACCA CCGGAATTCT

Seq ID NO: 84 Protein sequence  
 Protein Accession #: NM\_005264.1



1 11 21 31 41 51  
 5 MFLATLYFAL PLLDLLLSAE VSGGDRLDV KASDQCLKEQ SCSTKYRTL R QCVAGKETNF 60  
 SLASGLEAKD ECRSAMEALK QKSLYNCRCK RGMKKEKNCL RIYWSMYQSL QGNLLEDLESP 120  
 YEPVNSRLSD IPRVVPFISD VFQVVEHIPK GNMCLDAKA CNLDDICKKY RSAYITPCTT 180  
 SVSNDVGNRR KCHKALRQFF DRVPAKHSYG MLFPCSRDIA CTERRRQTIV PVCSEEREK 240  
 PNCLNLQDSC KTNVICRSL ADFFTNCQPE SRSVSSCLKE NYADCLLAYS GLIGTVMTPN 300  
 YIDSSSLVA PWDCSCNSGN DLEELCKPLN FFKDNTCLKN AIQAFNGSD VTMQPAFPV 360  
 10 QTTTATTTTA LRVKNKPLGP AGSENIPTL VLPCCANLQA QKLKSNVSGN THLCISNGNY 420  
 EKEGLGASSH ITTKSMAAPP SOGLSPLLVL VVTALSTLLS LTETS

Seq ID NO: 85 DNA sequence

Nucleic Acid Accession #: XM\_027172.1

Coding sequence: 143..1405

1 11 21 31 41 51  
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 GTTGGCTTGG GATTGAGGAG GGATGGATTC CAGTCTTAGC TTGCCACTTA TTAGGACTCC 180  
 TGAGAGCAGC CTCCATGAGG CCTGGACCA GTGCATGACC GCCCTGGACC TCTTCTCAC 240  
 CAACCACTTC TCAGAAGCAC TCAGCTACCT CAAGCCAGCA ACCAAGGAAA GCATGTACCA 300  
 25 CTCACCTGACA TATGCCACCA TCCTGGAGAT GCAGGCCATG ATGACCTTTG ACCCTCAGGA 360  
 CATCTGCTTT GCCGCAACA TGATGAAGGA GGCACAGATG CTGTGTGAGA GGCACCGGAG 420  
 GAAGTCTTCT GTAACAGATT CCTTCAGCAG CCTGGTGAAC GCGCCACGCG TGGGCCAATT 480  
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 30 TCCCTCTCAC GCCCTCAGCT GCCCAGCTGG GCCAGGCCGT CAGCATCTTT TCCTCCTGCA 660  
 GGACGAGAAC ATGGTGAAGT TCATCAAGG CGGCATCAAA GTTGGAAACA GCTACCAAGC 720  
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 40 ATGTGACATA CTCAGGGACA GGATAGACTG GGGGCGGGGG GGGGGCCAG AGAGAACCAA 1260  
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 45 CATTTTGTGA CTAAGAACCA GAGTCTTAGG CGGGGGCTGT ATTTGAGCCC AACGTCATGT 1560  
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 55 GTCACAAAGA GATTCTTAGT CACAAAGGAC AGAAACATGG CTCCCTCTGT CCAAGTAGAAC 2160  
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 70 TGTGACCTTA GATACCTTCC CTGCAAGCT CCAGGCAGCC GTTAGAAGT ACCCAATTG 3060  
 GCACCTGTTA GGAGACCTGT CATCTGCATC TGGTCCCTCC CCTCTCTCT CATGGAGGTC 3120  
 TCTCTGCTAG CCTCTGCTGG GAGCCAGCT GAAGGGGAAT TCTCTGGGTC TGGGGCAGGT 3180  
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5	TGGGAGGTTT	GGAGGATGCA	GAGGGGTGG	GGCTGGGTGG	GCACCGTCA	GGCTGACCAG	1740
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Seq ID NO: 90 Protein sequence

Protein Accession #: AAC39582.1

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75 LCYHTFLTIV LGTGNVNIEE AEKLLKPYLN RYPKGAIFLP FAGRIEVIK NIDAAIRFE 300  
ECCEAQHMK QFHEMCYWB L MWCFTYKQW KMSYFYADLL SKENCWSKAT YIYMKAAYLS 360  
MFGKEBHKPF QFHEMCYWB L MWCFTYKQW KSLPTEKFAL RKSRRYFSSN PISLPVPALE 420  
MMYTWNGYAV IKGQPKLTDG ILEIITKAE MLEKGFENBY SVDDECLVKL LKGLCLKYLK 480  
RVQEAENFR SISANEKKIK YDHYLIPNAL LELALLMEQ DRNEAIIKL SAKQNYKRY 540  
80 SMESRTHFR QAATLQAKSS LENSRSNVS SVSL

Seq ID NO: 91 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 31..906

1 11 21 31 41 51  
CGGGTGGACC CACGCGTCCG GGGAGAAAGG ATGGCCGGCC TGGCGGGCGG GTTGGTCCTG 60  
CTAGCTGGGG CAGCGGCGCT GGGAGGCGGC TCCAGGGGCG ACGGTAGACC GGTGTACCGC 120  
5 GACTGGGTAC TGCAGTGGGA AGAGCAGAAC TGCTCTGGGG GCGCTCTGAA TCACTTCGCG 180  
TCCCGCCAGC CAATCTACAT GAGTCTAGCA GGCTGGACCT GTGCGGACGA CTGTAAGTAT 240  
GAGTGTATGT GGGTCACCGT TGGGCTCTAC CTCCAGGAAG GTCACAAAGT GCCTCAGTTC 300  
CATGGCAAGT GGCCTTCTC CCGGTTCTGT TTCTTTCAAG AGCCGGCATC GGCCGTGGCC 360  
TCGTTTCTCA ATGGCCTGGC CAGCCTGGTG ATGCTCTGCC GCTACCGCAC CTTCGTGCCA 420  
10 GCCTCCTCCC CCATGTACCA CACCTGTGTG GCCTTCGCCT GGGTGTCCCT CAATGCATGG 480  
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GACTATGGCT ACAACCTGGT GGCCAAACGT GCTATTGGCC TGGTCAACGT GGTGTGGTGG 660  
CTGGCCTGGT GCCTGTGGAA CCAAGGCGCG CTGCCTCAAG TCGCAAGTGT CGTGGTGGTG 720  
15 GTCTTGCTGC TGCAGGGGCT GTCCTGTCTC GAGCTGTCTG ACTTCCACC GCTCTTCTGG 780  
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GACTGAAGAC CTTGGAGCGA GTCTGCCCA GTGGGGATCC TGGCCCGCCG CTGCTGGCCT 960  
CCCTTCTCCC CTCACCCCTT GAGATGATTT TCTCTTTTCA ACTTCTTGA CTGTGACATG 1020  
20 AAGGATGTGG GCCCAGAATC ATGTGGCCAG CCCACCCCTT GTTGGCCCTC ACCAGCCTTG 1080  
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CTCCTGGAGC TGAATCTGGG TGGAACTGAG TGTGCTCTTA GCTCTACCGG GAGGACAGCT 1200  
GCCTGTPTCC TCCCATCAG CCTCTCCCC ACATCCCCAG CTGCTGGCTT GGTCTCTGAA 1260  
25 GCCTCTGTCT TACCTGGGAG ACCAGGGACC ACAGGCCCTTA GGGATACAGG GGTCCCCCTT 1320  
CTGTATCCAC CCCACCCCTT CCTCCAGGAC ACCACTAGGT GGTGCTGGAT GCTGTCTCTT 1380  
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30 GTTGAGAGCC TGCCACCCTG TGTGCGGAGT GTGGGCCAGG CTGAGTGCAAT AGGTGACAGC 1620  
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GGTGTGTGCG GGGGAAGAGT GTGGCTTCAA AGTGTGTGT GTGCGAGGGG TGGGTGTGTT 1740  
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CGGTGAATGT GTCCACAGTT GAGAGGTTGG AGCAGGATGA GGAATCTCTG TCACCATCAA 1860  
35 TAATCACTTG TGGAGCGCCA CTGGGCCCAA GAGGCCACCT GGGCGGACAG CAGGAGCTCT 1920  
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40 TTTGGGAGG AGGAAGGGGC GATTTGAGGG AGAAGGGGAG AAGCTTTATG GCTGGGTCTG 2220  
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TCTGCCCCA CAGGAATAGA ATGGAGGGAG CTCCAGAAAC TTTCCATCCC AAGGCGATC 2400  
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Seq ID NO: 92 Protein sequence  
Protein Accession #: Eos sequence

50 1 11 21 31 41 51  
MAGLAARLVL LAGAAALASG SQGDREPVYR DCVLQCEQN CSGGALNHFR SRQPIYMSLA 60  
55 GNTCRDDCKY ECMVTVGLY LQEGHKVPQF HGKWPFSRFL PFQEPASAVA SPLNGLASLV 120  
MLCRVTFVP ASSPMYHTCV AFAMVSLNAW FWSVTFHTRD TDLTEKMDYF CASTVILHSI 180  
YLCCVRTVGL QHPAVVSAPR ALLLLMLTVH VSYLSLIRPD YGYMLVANVA IGLVNVVWML 240  
AWLWNRRL PHVRKCVVWV LLLQGLSLLE LLDFFPLFWV LDAHAHWIS TIPVHVLFFS 300  
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60 Seq ID NO: 93 DNA sequence  
Nucleic Acid Accession #: NM\_033419.1  
Coding sequence: 18..980

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AGTGCGAAGA GCAGAACTGC TCTGGGGGCG CTCGTAATCA CTTCGCTCC CGCCAGCCAA 180  
70 TCTACATGAG TCTAGCAGCG TGGACCTGTC GGGACGACTG TAAGTATGAG TGTATGTGGG 240  
TCACGCTTGG GCTCTACCTC CAGGAAGTGC ACAAGTGCC TCAGTTCCAT GGCAAGTGGC 300  
CCTTCTCCCG GTTCTCTGTT TTTCAAGAGC CGCATGGCC GGTGGCGCTG TTTCTCAATG 360  
GCCCTGGCCAG CCTGGTGTAT CTCTGCGGCT ACCGCACCTT CGTGGCCAGC TCTCCCCCA 420  
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75 TTTTCCACAC CAGGACACT GACCTCACAG AGAAATGGA CTACTTCTGT GCCTCCACTG 540  
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TGGTCACTGC CTCCCGGGCT CTCTGCTGTC TCATGCTGAC CGTGCAGTTC TCCTACCTGA 660  
GCCTCATCGC CTTCGACTAT GGCTACAAAC TGGTGGCCAA CGTGGCTATT GGCCTGGTCA 720  
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80 AGTGCGTGGT GGTGGTCTTG CTGCTGCAGG GCGTGTCCCT GCTCGAGCTG CTGACTTCC 840  
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ACGTCTCTTT TTTCAAGCTT CTGGAAGATG ACAGCTGTA CCTGCTGAAG GAATCAGAGG 960  
ACAAGTTCAA GCTGGACTGA AGACCTTGA GCGAGTCTGC CCCAGTGGGG ATCCTGCCCC 1020  
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5 CCTCACCAGC CTGGAGTCT GTTCTAGGGA AGGCCTCCCA GCATCTGGGA CTGAGAGTG 1200  
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 CAGGGGGTCC CCTTCTGTTA CCACCCCCA CCCTCCTCCA GGACACCACT AGGTGGTGCT 1440  
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 ACCAAGCTGC TGGGATTGGG AAGSAGTTT ACCCTGACCA TTGCCCTAGC CAGGTTCCCA 1560  
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 10 TGTGCTGCTG TCTGGTTGAG AGCCTGCCAC CGTGTGTCG GAGTGTGGG CAGGCTGAGT 1680  
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 CAGTGTGGAG ACGGGTGTG TCGGGGAAGA GGTGTGGCTT CAAAGTGTGT GTGTGCAGGG 1800  
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 15 GTCAACATCA ATAATCACTT GTGGAGGCC AGCTCTGCC AAGGCGCAC CTGGGCGGAC 1980  
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 GCCCGCTCC TGCACACCTC ACAGGGTCCC CACACAACAG TGCCCTCCAG AAGCAGCCCC 2100  
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 20 GCCATAGCCT GATTTTGGGG AGGAGGAAGG GCGATTGA GGGAGAAGGG GAGAAAGCTT 2280  
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 25 TCCTCTTTG AGGGAGGGA GCTATGCTAG GACTCCAACC TCAGGAGTCC GGTGGCCTG 2580  
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Seq ID NO: 94 Protein sequence  
 Protein Accession #: NP\_219487.1

30 1 11 21 31 41 51  
 MKDVGPESCG QPTPCWPSA LESVLGKASQ HLGLESGQPL YLLELNWGGT ECALSSTGRT 60  
 35 AACFLPISLL PTSPAALGP EALCLPGRPG TTGLRDTGGP LLLPPPTLLQ DTRHCWMLV 120  
 LWPAKVHGDG PHGLLRDQAA GIGKEPHFDH CPSQVPRPH HTPFQGGSS KPRARILCCC 180  
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Seq ID NO: 95 DNA sequence  
 Nucleic Acid Accession #: XM\_090469  
 Coding sequence:

40 1 11 21 31 41 51  
 45 ATGGGGTTTG GAGACCAGGG AACGGTGGA GGGAGCCTAG GAACGTGCAA AGATAGCTCC 60  
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 AGCCCAACAC CCTTGCATGG ACATCGGTC AACAGCCACC CATCAGGTGC TCATCAGAAA 180  
 CCACCTGAAG TGAATATGTT TGGAGCCAGT CAAGGTTTGC TGACATGGA AACAAACCAG 240  
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 50 ATGTCTCTTC CTGAGTGTCT CAGTGTCTGAT GCTGGCCAGG TGGAGCAGAG AAGACAAATG 360  
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 GCTGCCACC AGAAGACAC TTTCTTTTGG AAAGACATCA AGCACAAG TAAGTTCCAG 480  
 CAATCAGTTC AGCAGCAGAA TTGCATTAC AGCCCAAGAG AAAAAACCTG TGGGAATGTC 540  
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 55 CTCAGCCGCA GCCCGGCCCT GTCCCAAGT ACACCCATGG CGCCCTTCCC GAACCTCTGAC 660  
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 TGCCTCGCCG CGGCTCCAGA AGCCAGAAA CTCTTCTTCC TGCTGCCCTT TTATCCAGAT 780  
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 CTGCATCAAG AATCACCAGG TTCAATTCCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA 900  
 60 TGTATCAAG GGGCTCTGGG TGTGGCTGCT GAAGCAGCAT TTCATTACA GTTTTCCAGT 960  
 GAATGA

Seq ID NO: 96 Protein sequence  
 Protein Accession #: XP\_090469

65 1 11 21 31 41 51  
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 70 NSADTDWGTZ EGPGLDFAV AAHQEDTFPL KDIKHTSTFR QSVQQNCIY SPREKPGNV 180  
 RAPCAPPRRE APLALSRPWR LSRSPAPSPR TFMAPPFTSD RELDAPGPPP GLRSSAAAPH 240  
 CLPAPEPAQK LPFLFLYPD GSPPPKDILQ TLQHKAPGR LHQESPSGFP IGLCNRTAEF 300  
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75 Seq ID NO: 97 DNA sequence  
 Nucleic Acid Accession #: NM\_003474.2  
 Coding sequence: 37..3036

80 1 11 21 31 41 51  
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 CTTTAAAAA AATGAAGGCT TAGAAGAGCT CAGCGCGCGC GCGGGCCGTG CGCGAGGGCT 180  
 CCGAGCTGAG CTCGCGAGG CAGGAATACC CTCGCTCGC GACGCGCGC CCGCTCGGC 240  
 GCCCGGTGG GATGGTGCAG CGCTCGCGC CCGGCCGAG AGCTGCTGCA CTGAAGGCCG 300

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	GCCGGTGTCT	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
	CCTGATGAAG	TGTTCAGTGC	CTCTGTTCGG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
5	TTGCACTCCA	AGAATCATCC	AGAAGTGTCT	AATATTGAC	TACAAACGGG	AAGCAAAGAA	540
	CTGATCATAA	ATCTGGAAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
	TATCTGCAAG	ACGGTACTGA	TGTCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTGAC	660
	TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTGAG	CAGTCAGTCT	CAGCACTGCT	720
	TCTGGTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGCTTTAGA	ACCAATGAAA	780
10	AGTGCACCA	ACAGATACAA	ACTCTTCCCA	GCGAAGAAGC	TGAAAAGCGT	CCGGGGATCA	840
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	CAGACATGGG	CAAGAAGGCA	TAAAGAGAG	ACCCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960
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	CAGCGATTAA	TAGAGATTGC	TAATCACGTT	GACAAGTTTT	ACAGACCCTC	GAACATTGCG	1080
	ATCGTGTGG	TAGGCGTGGA	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
15	CCATTACCA	GCCTCCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAAA	1200
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	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCT	GGACCAATTCA	1320
	GACAATCCCC	TTGGTGCAGC	CGTGACCTCG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
	AATCATGACA	CACCTGGACG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
20	ATCATGAAAG	CTTCCACCGG	GTACCCATT	CCCATGGTGT	TCAGCAGTTG	CAGCAGGAAG	1500
	GACTTGGAGA	CCAGCCTGGA	GAAGAAGAA	GGGGTGTGCC	TGTTTAACT	GCGCGAAGTC	1560
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25	AAGCCGGAAG	CTGTGTGGCG	ACATGGGGCT	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
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	AGCCCTCACT	GCCACGCCAA	CGTGTACCTG	CAOGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
	GGCTACTGCT	ACAATGGCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTCT	ACTCTGGGGA	1920
	CCAGGTGCTA	AACCTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCCT	1980
30	TATGGCAACT	GTGGCAAAAT	CTCGAAGAGT	TCCCTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
	AAATGTGGAA	TCAAGGAGGT	GCCAGCGGCG	CAGTCATTGG	TACCAATGCC	2100	
	GTTCCTCACT	AAAACAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
	CACTGTACT	TGGGCGATGA	CATGCCGAGC	CCAGGGCTTG	TGCTTGCAAG	CACAAAGTGT	2220
	GCAGATGGAA	AAATCTGCCT	GAATCGTCAA	TGTCAAATA	TTAGTGTCTT	TGGGGTTCAC	2280
35	GAGTGTGCAA	TGCAGTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
	GAGGCCCACT	CTTCTGTGAC	AAGTTTGGCT	TTGGAGGAAG	CACAGACAGC	2400	
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	TGCTCTCTTG	CTGCCGGATT	TGTGGTTTAT	CTCAAAGGA	AGACCTTGAT	ACGACTGCTG	2520
40	TTTACAATA	AGAAGACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
	CGTGGCTTCC	AACCTGTGCA	GGCTCACCTC	GGCCACCTTG	GAAGAAGCCT	GATGAGGAAG	2640
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	GACATCAGCA	GACCCCTCAA	CGCCCTGAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
	CTTCTCTCCC	TCCACGGGGC	CCCACTGTCA	CCTAGCTGCC	CTGCCAGACC	CCTGCCAGCC	2820
45	AAGCCCTGAC	TTAGGCAAGC	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCCTCTG	2880
	CTCTGAGATC	CTCTGGGCGC	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCCAAGG	2940
	CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
	GTGCCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTTCAACAG	3060
	TGAAGACAGA	AGTTTGCATC	ATCTTTTCAGC	TCCAGTTGGA	GTTTTTTGTA	CCAACTTTTA	3120
50	GGATTTT	TAAATGTTAA	AACATCAATTA	CTATAAGAAC	TTTGAGCTAC	TGCCGTGAGT	3180
	GCTGTGCTGT	GCTATGGTGC	TCTGTCTACT	TGCACAGGTA	CTTGTAATTA	ATTAATTTAT	3240
	GCAGAAATGT	GAATTCAGTG	CAGTGCCTG	TAGTAGGCAT	TTTTACATC	ACTGAGTTTT	3300
	CCATGGCAGG	AAGGCTTGT	GTGCTTTTAG	TATTTTAGTG	AACCTGAAAT	ATCCTGCTTG	3360
	ATGGGATCT	GGACAGGATG	TGTTTGCTTT	CTGATCAAGG	CCTTATTGGA	AAGCAGTCCC	3420
	CCAAGTCTG	CCAGCTGTGC	TTATGGTACC	AGATGCAAGT	CAAGAGATCC	CAAGTAGAAT	3480
55	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
	TGRTTGTGCG	TTTCAGGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGACG	GCTCCCGGGG	3600
	ACACCTGGGA	GAATCTGGC	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
	AGGAATCTTA	AGGTGTAGCC	ACACAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
60	TGACCTGAG	CTGACAGGCC	GTGAGCATGT	TTGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
	GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTGCTG	TCTTTCTAG	AGCACTGCCA	3840
	CCAGTAGGTT	ATTTAGCTTG	GGAAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCCAGGCA	3900
	CTGCAAAACG	CCGACCTCTT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACCTGTAATA	3960
	CAATGATCCT	GTATTGAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAATA	TTTTCAGATG	4020
	TGAACCAATTA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAC	4080
65	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTATGGG	4140
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	ACCTATTTCT	TAAACACTTG	CAACCTACCT	GTGAGCATC	ACAGAATGTG	ATAAGGAAAT	4320
	CAACTGTGCT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTGAA	4380
70	CTCTTCACTC	TTCAAAATGCC	TGACTAGGGA	GCCATGTTTC	ACRAGGTCTT	TAAAGTGACT	4440
	AATGGCATGA	GAATAACAAA	AATACTCAGA	TAAAGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGTG	TTTCACTATT	GAAGACAAAT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTCTT	TGGGGTCAAC	AGTTTCTCTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GCCITCCAGA	AAACAAAAT	GCATTTCACT	TTCCGGTGTG	4680
75	TCCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CAGGTGACAC	4740
	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTTCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTATTAAAT	TCTTTAAAT	GTAAAGCCAT	GCTGGAAAT	AATAGTCTGT	4860
	AGATACATAC	AGAATTACTG	TAACTGATTA	CACCTTGGTA	TTGTACTAAA	GCCAAACATA	4920
	TATATACTAT	TAAAGAGTTT	TACAGAATTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
80	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCCT	CCAATTATAA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAAAAAA	AA				

Seq ID NO: 98 Protein sequence  
Protein Accession #: NP\_003465

1 11 21 31 41 51  
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SKNHPEVLNI RQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHY 120  
YHGHVRGYS SSVLSSTCSG LRGLIVFENE SYVLEPMKSA TNRKLPFAK KLSVSRGSCG 180  
SHRNTPLAA KNVFPFPPSQT WARRHKRETL KATKYVELVI VADNREFORQ GKDLSEVKQR 240  
LIEIANHVDK FYRPLNIRIV LVGVEVWMD DKCSVSQDPP TSLHEFLDWR KMKLLPRKSH 300  
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DTLDRGCSQ MAVKGGGIM NASTGYPFPM VFSSCSRKDL ETSLEKMGV CLFNLPEVRE 420  
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AMQCHGRGVC NNRKNCHCEA HWAPPFCDF GFGGSTDGFP IRQADNQLT IGLVLTILCL 720  
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DSYPPKNRPR RLLQCNVDI SRPLNGLNVP QPQSTQVLP PLHRAPRAPS VPAPPLPAKP 840  
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20 Seq ID NO: 99 DNA sequence  
Nucleic Acid Accession #: NM\_003714  
Coding sequence: 135..1043

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Seq ID NO: 100 Protein sequence  
Protein Accession #: NP\_003705

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ISRKCPAIRE MVSQQLRECY LKHDLCAAAQ ENTRVIVEMI HFQDLLLHEP YVDLVNLLLT 180  
CGEVKKAIT HSVQVQCEQN WSLSCILSP CTSAIQKPPT APPERQPVQD RTKLRSRAHHG 240  
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80 Seq ID NO: 101 DNA sequence  
Nucleic Acid Accession #: NM\_005940  
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Seq ID NO: 102 Protein sequence

Protein Accession #: NP\_005931

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FFPKTHREGD VHFYDETWT IGDDQGTDL LQVAHEFGHV LGLQHTTAAL ALMSAFYTFR 240  
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Seq ID NO: 103 DNA sequence

Nucleic Acid Accession #: NM\_033151.2

Coding sequence: 351..4499

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Seq ID NO: 104 Protein sequence  
 Protein Accession #: NP\_149163.2

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Seq ID NO: 105 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..4043

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Seq ID NO: 106 Protein sequence  
 Protein Accession #: Eos sequence

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   IFSEQLVLVS LMVIAVLIV SVLSPYILLM GAIIMVICPI YMMPKKAIG VFIRLENYSR 960
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Seq ID NO: 107 DNA sequence

Nucleic Acid Accession #: NM\_024022

Coding sequence: 202..1563

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35  CCATCTACAT TTTTGGGACT CGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGATGTC 180
   AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240
   TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTGTGTC ACCAGATGCA 300
   GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTCC AATCATGTC 360
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40  TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
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   AATGCGCGTC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
   AAGGTCACT ACSCAAATGT TGCTGTGCC CACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
   GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720
45  CACCTCTTGC CAGATGACAA GTGACTGCA TTACACCACT CAGTATATGT GAGGAGGGA 780
   TGTGCTCTG GCCACGTGTT TACCTTGCAG TGACAGCCCT GTGTCATAG AAGGGGCTAC 840
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70  AGATAAGCAG TATGTGACC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220
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Seq ID NO: 108 Protein sequence

Protein Accession #: NP\_076927

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   TAAWKTMCDS DWNKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFRESEFV SIDHLLPDDK 180
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15	ACAGGCATAA	AAGGCCCACT	ACCCAAACACC	AAGACACAGT	TCTTCATTCC	CTACACCATA	240
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	GGACTCCAAG	GAGAGCCAGG	GTGCCAGGA	CCACCGGGAC	CATCAGCTGT	AGGGAAACCA	420
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TGTCAGTCCA	TTCAAAAGAA	CACCCAAAGT	AAGGTATGAA	ACCCACATAC	CTGGATCCTG	1260
ACACTGACTC	AGGCCGGGGG	AGCTGTGACA	GCCCTTCCCT	TTTGTCTGAA	AAGTGTGAGG	1320
AACCCAGGCG	CAATCCCTCC	ACATTCTATG	ATCCTGAGGT	CATTGAGAAG	CCAGAGAAATC	1380
CTGAACAAC	CCACACCTGG	GACCCCACTG	GCATAAGCAT	GGAAGGCRAA	ATCCCTATT	1440
TTCATGTCTG	TGGATCCAAA	TGTTCAACAT	GGCCCTTACC	ACAGCCGAGC	CAGCACAAAC	1500
CCAGATCCTC	TTACCACAAT	ATTACTGTATG	TGTGTGAGCT	GGCTGTGGGC	CCTGCAGGTG	1560
CACCGGCCAC	TCCTGTGAAT	GAAGCAGGTA	AAGATGCTTT	AAAATCCTCT	CAAAACCATTA	1620
AGTCTAGAGA	AGAGGGAAAG	GCAACCCAGC	AGAGGGAGGT	AGAAAGCTTC	CATTCTGAGA	1680
CTGACCAGGA	TACGCCCTGG	CTGCTGCCCC	AGGAGAAAAC	CCCTTTTGGC	TCCGCTAAAC	1740
CCTTGGATTA	TGTGGAGATT	CACAAGGTCA	ACAAAGATGG	TGCATTATCA	TTGCTACCAA	1800
AACAGAGAGA	GAACAGCGGC	AAGCCCAAGA	AGCCCGGGAC	TCCTGAGAAC	AATAAGGAGT	1860
ATGCCAAGGT	TCCTGTGAAT	ATGGATAACA	ACATCCTGGT	GTTGGTGCCA	GATCCACATG	1920
CTAAAAACGT	GGCTGTCTTT	GAAGAATCAG	CCAAAGAGGC	CCCAACCATCA	CTTGAACAGA	1980
ATCAAGCTGA	GAAGGCCCTG	GCCAACTTCA	CTGCAACATC	AAGCAAGTGC	AGGCTCCAGC	2040
TGGGTGTGTT	GGATTACCTG	GATCCCGCAT	GTTTACACAT	CTCCTTTCAC	TGATAGCTTG	2100
ACTAATGGAA	TGATTGGTTA	AAATGTGATT	TTTCTTCAGG	TAACACTACA	GAGTACGTGA	2160
AATGCTCAAG	AATGTAGTCA	GACTGACACT	ACTAAAGCTC	CCAGCTCCCT	TCATGCTCCA	2220
TTTTTAACCA	CTTGCCCTCT	TCTCCAGCAG	CTGATTCCAG	AACAAATCAT	TATGTTTCTT	2280
AACGTGATT	TGTAGATTTA	CTTTTGTCTG	TAGTTATATA	AACATATGTT	TCAATGAAAT	2340
AAAAGCACAC	TGCTTAGTAT	TCTTGAGGGA	CAATGCCAAT	AGGTATATCC	TCTGGAAAAA	2400
GCTTTCTATG	TTTGGCATGG	GACAGACGGA	AATGAAATTG	TCAAAATTGT	TTACCATAGA	2460
AAGATGACAA	AAGAAATTTT	TCCACATAGG	AAATGCCAT	GAAAAATTGCT	TTTGA AAAAC	2520
AACTGCATAA	CCTTTACACT	CCTCGTCCAT	TTTATTAGGA	TTACCCAAAT	ATAACCAATT	2580
AAAGAAAGAA	TGCATTCCAG	AACAAATGTT	TTACATAAGT	TCCTATACCT	TACTGACACA	2640
TTGCTGATAT	GCAAGTAAGA	AAT				2700

Seq ID NO: 112 Protein sequence  
Protein Accession #: NP\_000940

60  
65  
70  
75

1	11	21	31	41	51	
MKENVASATV	FTLLFLNTC	LLNQQLPPGK	PEIFKCRSPN	KETFTCWWRP	GTGGGLPTNY	60
SLTYHREGAT	LMHECPDYIT	GGPNSCHFGK	QYTSWRTYI	MMVNATNQMG	SSPSDELYVD	120
VTYIVQPDPP	LELAVEVKQP	EDRKPYLWIK	WSPTLIDLK	TGWPTLLYEI	RLKPEKAAEW	180
EIHFAQQQTE	FKILSLHPGQ	KYLQVVRCKP	DHGYNSAWSP	ATFIQIPSDP	TMNDTTWNIS	240
VAVLSAVICL	IIVVAVALKG	YSMTVCIFPP	VPGPKIKGPD	AHLLEKKGSE	ELLSALGQOD	300
FPPTSDYEDL	LVEYLEVDD	EDQHLMSVHS	KEHPSQGMKP	TYLDPDTDSG	RGSNDSPSL	360
SEKCEEPQAN	PSTFYDPEVI	EKPENPETTH	TWDPQCISME	GKIPYFHAGG	SKCSTWPLPQ	420
PSQHNPRSSY	HNITDVCELA	VGPAGAPATL	LNEAGKDALK	SSQTIKSREE	GRATQOREVE	480
SFHSETDQDT	PWLLPQEKTP	FGSAKPLDVT	EIHKVNDGGA	LSLLFKQREN	SGKPKKPGTP	540
ENNKEYAKVS	GVMDNNILVL	VDPHAKNVA	CFEESAKEAP	PSLEQNQAEK	ALANPTATSS	600
KCRLQLGGLD	YLDPACTH	PH				

Seq ID NO: 113 DNA sequence  
Nucleic Acid Accession #: XM\_062811  
Coding sequence: 1..888

75  
80

1	11	21	31	41	51	
ATGTGGGCG	CTGCGGCTC	GTCCGTCTCC	TCATCTCGGA	ACGCGGCTTC	GCTCCTGCAG	60
CTGCTGCTGG	CTGCGCTGCT	GGCGGGGGGG	GCGAGGGCCA	GCGGCGAGTA	CTGCCACGGC	120
TGGCTGGAGC	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCCGAGCG	CTTGGACGGC	180
GGCGAGGCCA	CACTCTGCTG	CGGCGAGCTG	GGCTTGGCGT	ACTGCTGCTC	CAGCGCGAGG	240
GCGCGCTCG	ACGAGGGCGG	CTGCGACAAT	GACCGCCAGC	AGGGCGCTGG	CGAGCCTGGC	300
CGGGCGGACA	AAGACGGCCC	CGACGGCTCG	GCAATGCCCA	TCTACGTGCC	GTTCTCAATT	360
GTTGGCTCCG	TGTTTGTGCG	CTTTATCATC	TTGGGGTCCC	TGGTGGCAGC	CTGTTGCTGC	420

5 AGATGTCCTCC GGCTTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480  
 ATGGAGACCA TCCCCATGAT CCCCAGTGCC AGCACTCCCC GGGGGTGCTC CTCACGCCAG 540  
 TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAATCTAG GGGCCCGGGC GCCCCAACA 600  
 AGGTACACAGA CCAACTGTTG CTTGCCGGAA GGGACCATGA ACAACGTGTA TGTCAACATG 660  
 CCGACGAATT TCTGTGTGCT GAACTGTCTAG CAGGCCATCC AGATTGTGCC ACATCAGGGG 720  
 CAGTATCTGC ATCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780  
 GCTGTGCCAC CTTTTCATGGA CGGCCTGCAQ CCTGGCTACA GGCAGATTCA GTCCCCCTTC 840  
 CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

10 Seq ID NO: 114 Protein sequence  
 Protein Accession #: XP\_062811

15 1 11 21 31 41 51  
 MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60  
 GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDPDGS AVPIYVPLI 120  
 VGSVVFVPII LGSILVAACCC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180  
 SSTAAASSSS ANSGARAPPT RSQTNCLPE GTMNNVYVNM PTNFSVLWCQ QATQIVPHQG 240  
 QYLHPYVGY TVQHDSPVMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

20 Seq ID NO: 115 DNA sequence  
 Nucleic Acid Accession #: NM\_013257  
 Coding sequence: 223..1512

25 1 11 21 31 41 51  
 GGTGTCTCT TGAGGGATTA AATGCAAGA GATCACACCA TGGACTACAA GGAAAGCTGC 60  
 CCAAGTGTAA GCATTCCCAG CTCGGATGAA CACAGAGAGA AAAAGAAGAG GTTTACTGTT 120  
 TATAAAGTTC TGGTTTCAGT GGAAGAAGT GAATGGTTTG TCTTCAGGAG ATATGCAGAG 180  
 30 TTTGATAAAC TTTATAACAC TTTAAAAAAA CAGTTTCTGT CTATGGCCCT GAAGATTCTT 240  
 GCCAAGAGAA TATTGTGTGA TAATTTTGAT CCAGATTITA TTAACAAGAG ACGAGCAGGA 300  
 CTAAAGCAAT TCATTAGAA CCTAGTTAGG TATCCAGAAC TTTATAACCA TCCAGATGTC 360  
 AGAGCATTC TCAATATGGA CAGTCCAAA CACCAGTCAG ATCCATCTGA AGATGAGGAT 420  
 GAAAGAAGTT CTCAGAAGCT ACACCTTACC TCACAGAACA TCAACCTGGG ACCGTCTGGA 480  
 35 AATCCTCATG CCAAAACCAAC TGACTTTGAT TTCTTAAAG TTATTGGAAA AGGCAGCTTT 540  
 GGCAAGGTT TTTCTGCAAA ACGGAAACTG GATGGAAAAT TTTATGCTGT CAAAGTGTTA 600  
 CAGAAAAAAA TAGTTCTCAA CAGAAAAGAG CAAAAACATA TTATGGCTGA ACCTAATGTG 660  
 CTCCTGAAAA ATGTGAAACA TCCGTTTTTG GTTGATTGTC ATTATCTCTT CCAACAACCT 720  
 40 GAAAAGCTTT ATTTTGTCTT GGTATTTGTT AATGGAGGGG AGCTTTTTTT CCACCTACAA 780  
 AGAGAAGCGT CCTTTCCTGA GCACAGAGCT AGGTTTACG CTGCTGAAAT TGCTAGTGCA 840  
 TTGGGTTACT TACATTCAT CAAAATAGTA TACAGAGACT TGAACCCAGA AAATATTCTT 900  
 TTGGATTGAG TAGGACATGT TGTCTTAACA GATTTTGGGC TTTGTAAGA AGGAATTGCT 960  
 ATTTCTGACA CCACTACCAC ATTTTGTGGG ACACCAGAGT ATCTTGCACC TGAAGTAATT 1020  
 AGAAAAAGC CCTATGACAA TACTGTAGAT TGGTGGTGCC TTGGGGCTGT TCTGTATGAA 1080  
 45 ATGCTGTATG GATTGCTCC TTTTATATGC CGAGATGTTG CTGAAATGTA TGACAATATC 1140  
 CTTCAACAA CCCTAAGTTT GAGGCCAGGA GTGAGTCTTA CAGCCTGGTC CATCTGGA 1200  
 GAACCTCTAG AAAAAGACAG CAAAATCGA CTTGGTGCCA AGGAAGACTT TCTGAAATT 1260  
 CAGAATCATC CTTTTTTTGA ATCACTCAGC TGGGCTGACC TTGTACAAA GAAGATTCCA 1320  
 CCACCATTTA ATCCTAATGT GGCTGGACCA GATGATATCA GAAACTTTGA CACAGCATT 1380  
 50 ACAGAAGAAA CAGTTTCCATA TTCTGTGTGT GIATCTTCTG ACTATCTAT AGTGAATGCC 1440  
 AGTGATTGG AGGCAGATGA TGCAATCGTT GGTTCCTCT ATGCACCTCC TTCAGAAGAC 1500  
 TTATTTTGT GAGCAGTTT CCATTCAGAA ACCATTGAGC AAAATAAGTC TATAGATGGG 1560  
 ACTGAAACTT CTATTGTGT GAATATATTC AAATATGTAT AACTAGTGCC TCATTTTTAT 1620  
 ATGTAATGAT GAAAACATG AAAAAATGTA TTTTCTTCTA TGTGCAAGAA AAATAGGGCA 1680  
 55 TTCAAGAGC CTGTTTGTAT TAAAAATTAT ATTCTTGTT AATAAGCTTA TTTTAAACA 1740  
 ATTTAAAGC TATTATCTT AGCATTAACC TATTTTAA GAAACCTTT TTGCTATTGA 1800  
 CTGTTTTTC CCTCTAAGT TACACTAACA TCTACCCAAG ATAGACTGTT TTTTAAAGT 1860  
 CAATTTCAGT TCAGCTAACA TATATTAATA CCTTGTAAAC TCTTGTCTAT GGCTTTTGT 1920  
 60 ATCACACCAA AACTATGCAA TTGGTACATG GTTGTTTAA GAGAAACCGT ATTTTCCAT 1980  
 GATAAATCAC TGTTTGAAAT ATTTGGTTCA TGGTATGATC GAAATGTAAA AGCATAATTA 2040  
 ACACATTGGC TGCTAGTTAA CAATTGGAAT AACTTTATTC TGCAGATCAT TTAAGAAGTA 2100  
 ACAGGCCGGG CGCGGTGGCT CAGCCTGTGA ATCCAGCAC TTTGGGAGGC TGAGGCCGGC 2160  
 AGATCACCTC AGGTGAGGAG TTGGAGACCA GCCTGACCAA CATGGACAAA CCGCTCTCT 2220  
 65 ACTAAAATA CAAAATTGGC AGGGTGTGGT GGCACATGCC TATAATCCA GCTACTTGGG 2280  
 AGGCTAAGGC AGGAGAATCG CTTGAACCGG GGAGGCGGAG GTTGCAGTGA GCCAGATCG 2340  
 CACCATTGCA CTCCTGCTG GCAACAAGA GTGAAACTCC ATCTCCAAAA A

Seq ID NO: 116 Protein sequence  
 Protein Accession #: NP\_037389

70 1 11 21 31 41 51  
 MALKIPAKRI FGDNDPDPFI KQRRAGLNEF IQNLVRYPEL YNHPDVRAFL QMDSFKHQSD 60  
 PSEDEDERSS QKLEHSTQNI NLGPSGNPHA KPTDFDLKV IGKGSFGKVL LAKRKLDGKF 120  
 75 YAVKVLQKKI VLNRKBQKHI MAERNVLLIK VKHPFLVGLH YSFQTEKLY FVLDPVNGGE 180  
 LPFHQLQERS FPBHRARFYA AEIASALGYL HSIKIVYRDL KPENILDLSV GHVVLDTDFGL 240  
 CKEGIAISDT TTTFCGTPEY LAPEVIREQP YDNTVDWVCL GAVLYEMLYG LPPFYCRDVA 300  
 EMDYDILHQP LSLRPGVSLT AWSILEELLE KDRQNLGAK EDFLEIQNHP PFESLSWADL 360  
 80 VQKIKPPFFN FNVAGPDDIR NFDTAFTET VPYSVCVSSD YSIVNASVLE ADDAPVGPVS 420  
 APPSEDLFL

Seq ID NO: 117 DNA sequence  
 Nucleic Acid Accession #: NM\_004004.1

Coding sequence: 1..681

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5 1 11 21 31 41 51
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ATGGATTGGG GCAAGCTGCA GACGATCCTG GGGGGTGTGA ACAAACACTC CACCAGCATT 60
GGAAGATCTT GGCTCACCGT CCTCTTCATT TTGSCATTA TGATCCTCGT TGTGGCTGCA 120
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTCGCA GCCAGGCTGC 180
AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACA TCCGGCTATG GGGCTGCGAG 240
CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
GAGAAGAAGA GGAAGTTTCT CAAGGGGGAG ATAAGAGTG AATTTAAGGA CATCGAGGAG 360
ATCAAAACCC AGAAGTTCGG CATCGAAGGC TCCTGTGGT GGACCTACAC AAGCAGCATC 420
TTCTTCCGGG TCATCTTCGA AGCGGCTTC ATGTACGCT TCTATGTCAT GTACGACGGC 480
TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
TTTGTGTCCC GGCCCAACGA GAAGACTGTC TTCACAGTG TCATGATTGC AGTGTCTGGA 600
ATTGTCATCC TGCTGAATGT CACTGAATTG TGTATTATGC TAATTAGATA TTGTTCTGGG 660
AAGTCAAAAA AGCCAGTTTA A

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Seq ID NO: 118 Protein sequence  
Protein Accession #: NP\_003995.1

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20 1 11 21 31 41 51
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MDWGTLTQTL GGVNKHSTSI GKIWLTVLFI FRIMILVVAA KEVNGDEQAD FVCNTLQPGC 60
KNVCYDHYFP ISHRLNALQ LIPVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEPKDIEE 120
25 IKTKQVRIEG SLWWTYTSI PFRVIFEAAP MYVIFYMYDG FSMQRLVKCN AWPCPNTVDC 180
FVSRPTEKTV FTFVMIASVG ICILNVTEL CYLLIRYCSG KSKKPV

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Seq ID NO: 119 DNA sequence  
Nucleic Acid Accession #: XM\_061091.1  
Coding sequence: 1..2481

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35 1 11 21 31 41 51
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CACCGAGCGC TGGTGCSCGC TCTCTTCCG GTGAGTCCCA GCCCCGAGTT GGCTCTGCGG 120
CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATGGAGGT 180
CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
GTTGGGAAGC CTCCTTTTGA GGCAAAACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
ATTTAGCTTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCTGTTA 360
GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
GTCTGTGACG GTCTGGACAT CAGCCCGAG AGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
AGAATCAAGA GGATGGTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAATATC 600
CTCTGCACA GAGGTTTGGC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
GGTGTCACTG GTTTGTCTGT GGGGGTCAGG TTTCCAGGT GGGAGGAGCT GCATGCACTG 780
GCCAGGAGC CTAGAGGGCA GCACTGTCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
GGCCTCTTCA GCACCTCAG CAGCTCGGCC ATCTGTCTCA GCGCCACGCC AGCTGGGAGC 900
CCCGAGCTTG TCTTCATGGA GCGGTAAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCTC 1020
TGCCCGCTGG CCTTTGAGG GAGGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
GTGACCTTCC TCTTCTCTGT GGACAGCTCT GCGGGCACCA CTCTGGAAGG CTTCTGCGG 1140
GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCGCTGTCTG GCGAGGACTC TCGGGCCCGA 1200
GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCCGTGTGG GAGTACACAG 1260
GATGTGCTCG ACCTGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGTGTG CCCACCCCTG 1320
ACGGGCGAGT CCTTGGCGCA GCGGCGCAGG CGTGGCTTCC GGAGCGCCAC CAGGACAGGC 1380
CAGGACCCGC CAGTAGAGGT GGTGGTTTTC CTCACTGAGT CACACTCCGA GATGAGGTT 1440
GCGGGCCAGC CGCGTACGCG AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
CCGCTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
GATCCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCGCGCAG 1620
CGGCCAGGGT GCGGACACA AGCCCTGGAC CTCGTCTTCA TGTGGACAC CTCTGCCCTCA 1680
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
GAGGTGAACC CTGACGTGAC ACAGGTCCGC CTGGTGTGT ATGGCAGCCA GGTCCAGACT 1800
GCCTTCGGGC TGGACACCAA ACCCAACCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
CCCTACCTAG GTGGGGTGGG CTCAGCCGCG ACCGCCCTGC TGCAATCTA TGACAAAGTG 1920
ATGACCGTCC AGAGGGGTGC CCGGCTGGT GTCCCAAGG CTGTGGTGGT GCTCACAGGC 1980
GGGAGAGGGC CAGAGGATGC AGCCGTTCTT GCCCAGAAC TGAGGAACAA TGGCATCTCT 2040
GTCTTGTCTG TGGGGTGGG GCCTGTCTTA AGTGAGGCTC TGCGGAGGCT TGCAGGTCCC 2100
70 CSGGATTCCC TGATCCAGT GGCAGCTTAC GCGAGCTGC GGTACCACA GGAAGTGCTC 2160
ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAACC CAGCCCGTGC 2220
ATGAATGAGG GCACTGCGT CCTGCAGAA GGGAGCTACC GCTGCAAGTG TCGGGATGGC 2280
TGGAGGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
GGATGATATC TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT 2400
75 ACCCTCCCA GCAACTACAG AGAAGGCGCT GGCAGTGAAA TGGTGCCTAC CTCTGGAAT 2460
GTCTGTGCCC CAGGTCTCTA G

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Seq ID NO: 120 Protein sequence  
Protein Accession #: XP\_061091.1

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80 1 11 21 31 41 51
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MPNTSGITRI EINLLQEPFG HRALVAALLP VSPSPALALA PGYPVPAAD DRFTLFMIGG 60
QMGEKVDLW SLQVLCYEFL VGKPPFEANE VHSVKETIGK ISAASROMWC SAAVDIMFLL 120

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5 DGSNSVKGKS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQQEVKA 180  
 RIKRMVFKGG RTETELALKY LLHRGLPOGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240  
 GVTTFVAVGVR FPRWELHAL ASEPRQHVH LABQVEDATN GLFSTLSSSA ICSSATPAGS 300  
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360  
 10 VDLLFLDLSS AGTTLGGFLR AKVFKRFPVR AVLSEDSRAR VGVATYSREL LVAVPVGGEYQ 420  
 DVDPDLVWSLD GIPFRGGPTL TGSALRQAAE RGFSGATRTG QDRPRRVVVL LTESHSEDEV 480  
 AGPARHARAR ELLLLGVGSE AVRAELEET GSPEKVMVYS DPQDLFNQIP ELQGLKLSRQ 540  
 RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SPVRSALQF EVNPDVTQVG LVVYGSQVQT 600  
 15 AFGLDTKPTR AAMLRALISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660  
 GRGAEDAVP AQKLRRNGIS VLVVGVGPVL SEGRLRLAGP RDSLTHVAAY ADLRYHQDVL 720  
 IENLCEAKQ PVNLCKPSPC MNEGSCVLQV GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780  
 GWILETPLRH MAPVQEGSSR TPPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 121 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2424

20 1 11 21 31 41 51  
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 ATGCCCCCTT TCCTGTTGCT GGAGGCGCTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA 60  
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 AGCAAAATGA TGTGGTGTCT GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180  
 AGCGTCGGGA AAGGGAGCTT TGAAGAGTCC AAGCACATTG CCATCACAGT CTGTGACGGT 240  
 25 CTGGACATCA GCCCGAGAG GGTGAGAGTG GGAGCATTCC AGTTGAGTTC CACTCCTCAT 300  
 CTGGAATTCC CTTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360  
 ATGTTTTCGA AAGGAGGGCG CACGAGAGAG GAACTTGCTC TGAATACCTT TCTGCACAGA 420  
 GGGTTCCTTG GAGGAGAGAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480  
 AAGTCCACAG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540  
 TTTGCTGTGG GGGTCAGGTT TCCCAAGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600  
 30 AGAGGGCAGC ACGTGTCTGT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660  
 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720  
 CCTGTGAGC ACAGGAGCTC GGAGATGGTC CGGAGATTGG CTGGCAATGC CCTATGCTGG 780  
 AGAGGATCGC GCGGACCCCT TGCGGTGCTG GCTGCACACT GTCCTTCTA CAGCTGGAAG 840  
 AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCAGG CCCCTGTGAC 900  
 35 TCGCAGCCCT GCCAGAAATG AGGCACATGT GTTCCAGAA GACTGGAAG CTACCACTGC 960  
 CTCTGCCCGC TGGCCTTTGG AGGGAGGAGT AACTGTGCCC TGAAGCTGAG CCTGGAATGC 1020  
 AGGTGCGACC TCCTCTCTCT GCTGGACAGC TCTGCGGCA CCACTCTGGA CGGCTTCCTG 1080  
 CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140  
 CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGTGCTGCTG GGGGAGTAC 1200  
 40 CAGGATCTGC CTGACCTGGT CTGGAGCCTC GATGGCATT CCTTCCGTGG TGGCCCCACC 1260  
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 GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380  
 GTTGGCGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440  
 GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGAGGCC CAAAGCATGT GATGGTCTAC 1500  
 45 TCGGATCTCT AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCACCGTG 1560  
 CAGCGGCCAG GTGCGCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620  
 TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680  
 TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCTGTGGTG TGTATGGCAG CCAGGTGCAG 1740  
 50 ACTGCCCTTC GGCTGGACAC CAAACCCACC OGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800  
 GCCCCTTACC TAGGTGGGGT GGGCTCAGCC GGCAACGCCC TGCTGCACAT CTATGACAAA 1860  
 GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCCCA AGCTGTGGT GGTGCTCACA 1920  
 GGCGGAGAG GCGCAGAGGA TGCAGCGGTT CTGCCCCAGA AGCTGAGGAA CAATGGCATC 1980  
 TCTGTCTTGG TGTGGGGGCT GGGGCTGTG CTAAGTGAGG GTCTGCGGAG GCTTGAGGT 2040  
 55 CCCCAGGATT CCTGATCCA CGTGGCAGCT TACGCGGACC TGCGGTACCA CCAGGACGTG 2100  
 CTCATTGAGT GGCTGTGTGG AGAAGCCAG CAGCCAGTCA ACCTCTGCAA ACCAGCCCG 2160  
 TGCATGAATG AGGCGAGCTG CGTCTGTCAG AATGGGAGCT ACCGCTGCAA GTGTGGGAT 2220  
 GGCTGGGAGG GCGCCACTG CGAGAACCGT GAGTGGAGCT CTGTCTCTGT ATGTGTGAGC 2280  
 CAGGGATGGA TTCTTGAGAG GCCCCTGAGG CACATGGCTC CGGTGCAGGA GGCAGCAGC 2340  
 60 CGTACCCCTC CCAGCACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400  
 AATGTCTGTG CCCCAGGTCC TTAG

Seq ID NO: 122 Protein sequence

Protein Accession #: Eos sequence

65 1 11 21 31 41 51  
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 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SRMMWCSAV DIMFLDGSN 60  
 SVKGSGFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIK 120  
 70 MVFKGGRTET ELALKYLLER GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180  
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLPS TLSSSAICSS ATPDCRVEAH 240  
 PCERTLEMV REFAGNAPCW RGSERTLAVL AAHCPFFYSWK RVFLTHPATC YRTTCPGPCD 300  
 SQPCQNGGTC VPGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360  
 RAKVFKRFPV RAVLSEDSRV RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420  
 75 LTGSALRQAA ERGFGSATRT QDRPRRVVVL LTESHSEDE VAGPARHARA RELLLGVGS 480  
 EAVRAELEET GSPEKVMVYS SDPQDLFNQI PELQGLKCSR QRPGCRTQAL DLVFMIDTSA 540  
 VGPENFAQMQ SPVRSALQF EVNPDVTQV GLVYGSQVQ TAFGLDTPKT RAAMLRALISQ 600  
 APYLVGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVL GGRGAEDAAV PAQKLRRNGI 660  
 SVLVVGVGPV LSVLSEDSLA PRDSLTHVAA YADLRYHODV LIENLCEAK QPVNLCKPSP 720  
 80 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780  
 RTPPSNYREG LGTEMVPTFW NVCAPGP

Seq ID NO: 123 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 89..2356



	1	11	21	31	41	51	
5	GCCCCCTGGC	CCGAGCCGCG	CCCGGGTCTG	TGAGTAGAGC	CGCCCGGGCA	CCGAGCGCTG	60
	GTGCGCGCTC	TCCTTCGGTT	ATATCAACAT	GCCCCCTTTC	CTGTTGCTGG	AAGCCGCTCG	120
	TGTTTTCTCT	TTTTCCAGAG	TGCCCCCATC	TCTCCCTCTC	CAGGAAGTCC	ATGTAAGCAA	180
	AGAAACCATC	GGGAAGATT	CAGCTGCCAG	CAAAATGATG	TGGTGTCTCG	CTGCAGTGGA	240
	CATCATGTTT	CTGTAGATG	GGTCTAACAG	CGTCGGGAAA	GGGAGCTTTG	AAAGGTCCAA	300
10	GCACCTTGCC	ATCACAGTCT	GTGACGGTCT	GGACATCAGC	CCCGAGAGGG	TCAGAGTGGG	360
	AGCATTCCAG	TTCAATTCCA	CTCCTCATCT	GGAATTCCCC	TTGGATTTCAT	TTTCAACCCA	420
	ACAGGAAGTG	AAGGCAAGAA	TCAAGAGGAT	GGTTTTCAAA	GGAGGGCGCA	CGGAGACGGA	480
	ACTTGCTCTG	AAATACCTTC	TGCACAGAGG	GTTGCCTGGA	GGCAGAAATG	CTTCTGTGCC	540
	CCAGATCTCT	ATCATCGTCA	CTGATGGGAA	GTTCCAGGGG	GATGTGGCAC	TGCCATCCAA	600
15	GCAGCTGAAG	GAAAGGGGTG	TCACTGTGTT	TGCTGTGGGG	GTCAAGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTGGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TGGCCATCT	GCTCCAGCGC	780
	CACGCCAGAG	TGCAGGTCGG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTGCTG	GGCAATGCCC	CATGCTGGAG	AGGATCGCGG	CGGACCCCTG	CGGTGCTGGC	900
20	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
	TCCAGAAGGA	CTGGAGCGCT	ACCAGTGCCT	CTGCCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
	CTGTGCTCTG	AAGCTGAGCC	TGGAAATGCAG	GGTCGACCTC	CTCTTCTCTG	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGAGC	GCTTCTCTCG	GGCCAAAGTC	TTCTGTGAAG	GTTTGTGTGG	1200
25	GGCCGTGCTG	AGCGAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGTGTGGG	GTGCTGTGGG	GCGAGTACCA	GGATGTGCTT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTCCC	TTCCGTGGTG	GCCCCACCTT	GACGGGCAGT	GCCTTGGCGC	AGGCGGCAGA	1380
	GGGTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCAAGTAGAG	TGGTGGTTTT	1440
	GCTCACTGAG	TCACTCTCCG	AGGATGAGGT	TGCGGGCCCA	GCGGTGCAAG	CAAGGGCGCG	1500
30	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AGGCATGTGA	TGGTCTACTC	GGATCCTCAG	GATCTGTTCG	ACCAAATCCC	1620
	TGAGCTGAGC	GGGAAGCTGT	GCAGCCCGCA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
	CCTCGTCTTC	ATGTTGGACA	CCTCTGCCTC	AGTAGGGCCC	GAGAAATTTG	CTCAGATGCA	1740
	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
35	CTGTGTGGTG	TATGGCAGCC	AGGTGCAGAC	TGCCCTTGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TAGCCAGGCG	CCCTACCTTA	GGTGGGGTGG	GCTCAGCCGG	1920
	CACCCCGCTC	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCGCCCTGG	1980
	TGTCGCCCAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTCTC	2040
	TGCCCAGAAG	CTGAGGAACA	ATGGCATCTC	TGCTTTGGTC	GTGGGCGTGG	GGCCTGTCTT	2100
40	AAGTGAGGGT	CTGCGGAGGC	TTGCAGGTCC	CCGGGATTCC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CTGCGGGCCA	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAGCA	2220
	GCCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GGCAGCTGCG	TCTCTCAGAA	2280
	TGGGAGCTAC	GCGCTCAAGT	CTGGGATGGG	CCCACTGCGG	AGAACCGATT	2340	
	CTTGAGAGCG	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
45	AGCACTACA	GAGAGGGCCT	GGGCACTGAA	ATGGTGCTTA	CCTTCTGGAA	TGTCTGTGCC	2460
	CCAGGTCTCT	AGAAATGTCT	CTTCCCGCGG	TGGCCAGGAG	CACATTTCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCAACCCAC	2580
	AAACGATGTT	GTGAAAGAGT	TTTGATGTGT	AAGTAAATAC	CCACTTTCTG	TACCTGTCTG	2640
	GCCTTGTGTA	GGCTATGTCA	TCTGCCACCT	TTCCTTGAG	GATAAACAA	GGGTCTTGAA	2700
50	GACTTAAATT	TAGCGGCTTG	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAAATGTTG	2760
	TGACACAGTA	ATGCCACGCA	GAGGCCTTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 124 Protein sequence  
Protein Accession #: Eos sequence

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55	MPPFLLEAV	CVFLPSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVKGSFERS	KHPAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSPST	QDEVKARIKR	120
60	MVFKGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKRGVTV	180
	FAVGVRFPFW	EELHALASEP	RQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCEVEAH	240
	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGSEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
	RAKVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPDLVWSL	DGIPFRGGPT	420
65	LTGSALRQAA	ERGFGSATRT	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	EAVRAELEEI	TGSPKHMVMY	SDPQDLFNQI	PELQKGLCSR	QRPGCRTQAL	DLVFMLD TSA	540
	SVGPNFAQM	QSFVRSCALQ	FEVNPDTVQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
	APYLGGVGS	GTAALLHIYDK	VMTVQRGARP	GVPKAVVVL	GGRAEDAAV	PAQKLKRNIGI	660
	SVLVVGVGV	LSEGLRLLAG	PRDSLHVAA	YADLRYHQDV	LIEWLGEAK	QPVNLCKRPS	720
70	CWNBGSCVLQ	NGSVYRCKRD	GWE3PHCENR	FLRRP			

Seq ID NO: 125 DNA sequence  
Nucleic Acid Accession #: NM\_031942.1  
Coding sequence: 145..1260

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75	CCCGAGCCCC	GCCCCCTCGG	GCCCGGGTGG	GCGCGCCAGC	CCTGCCAGCC	GCGCTGCTGC	60
	TGCTCTCTCT	GCTGTGGGAC	CGCTGACCGC	GCGGCTGCTC	CGCTCTCCCC	GCTCCAAGCG	120
80	COGATCTGGG	CACCGGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCCGAGAA	AGATCTCAGA	180
	GTAAGAAGAA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAACAC	GAGGCTGCG	300
	TCAGTTGGGG	AAGGCTGTAG	GACCCGACGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGC	GGAGCAACCA	ACAAAAAGC	AGAGTCCCCG	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AACTCOGATT	CAGAAGATGA	AAGTGAAGT	480

5 AATTTTITGG AGAAAAGGCG TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC 540  
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 GACTCACAAAT CAAGGAGACC GCGAAGCGT ACATTCCCGG GTGTTGCTTC CAGGAGAAAC 660  
 CCTGAACCGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCCTCGG GTCCCTTGAC 720  
 GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTGTTGAG AAAGAGGAAG 780  
 ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCAGAA GCCGTGCTC CAGATCATCC 840  
 GTGACCTTTC CGCATATAAT TCGCCAGTG GAAGAAATTA CAGAGGAGGA GTTGAGAAC 900  
 GTCTGCAGCA ATTCTGAGA GAAGATATAT AACGTTTAC TGGGCTCTAC TTGTCATCAA 960  
 10 TCGCTCAGA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGGCTT 1020  
 CGAGGCCAGT TCTGTGGCCC CTGCCTTCGA AACGTTATG GTGAAGAGGT CAGGGATGCT 1080  
 CTGCTGGATC CGAACTGGCA TTGCCCGCT TGTGAGGAA TCTGCACTG CAGTTTCTGC 1140  
 CGGCAGCGAG ATGGAAGGTG TGGACTGGG GTCCTTGTG ATTTAGCCAA ATATCATGGC 1200  
 TTTGGGAATG TGCATGCCCTA CTGAAAGAG CTGAACAGG AATTGAAAT GCAAGCATAA 1260  
 15 TATCTGGAAT ATTTGCTGCC TGCTTCTAC TTCTCAAATC TTTCTGTAA AAGTTTCCAA 1320  
 TTTTCTACT GAAACCTGAG TTAATAATCT TGATGATCAG CCTGTTTCAT AAGAACTCC 1380  
 AATCAAGTAA ATCTTAGCAG ACATGTGTTT CTGGAGCATC ACAGAAGGTA TATTGCTAGT 1440  
 TACACTTTGC CCTCTGAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCC 1500  
 TCTATTTCOA ATGCTCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560  
 20 TATGAAAGCA TATTTTATTT ACTTGTGTTT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620  
 GAAACACAAAT AATAGTATTA ACTAATAGA TCTATTGAAT TTCAGAGAAG AGCCTCTAA 1680  
 CTGTGTTTACA CAAAACGAG TATGATTAG CACTCATACT AGTTGAAAT TTTAATAGAA 1740  
 TCAAGGCACA AAGTCTTAA AACCATGTG AAAAATTAG TAATTATTG AGATTGATG 1800  
 CTCTCAATCC CATGATTGC GCTTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT 1860  
 25 CTCTTAATTT CTCTGCCCC AAGGTAAGT GGTGCGTCCA GCTTACCGA TCATAATTCA 1920  
 AAGGTTGTG GGCATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGAGATT 1980  
 ATGAGTAAGC TGATTGAAAT TTTCAGTATA AAACCTTAGT ATAATTGTAG TTTGCAAGT 2040  
 TTATTTCAGT TCACATGTAA GGTATTGCAA ATAAATTCIT GGCAATTTT GTATGGAAC 2100  
 TTGATATTAA AACTAGTCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAAGCA 2160  
 30 CAAGGTTCAA GTTTAGATT TAAGCACTTT TATAACAATG ATAAGTGCTT TTTTGAGAT 2220  
 GTAACTTTTA GCAGTTTGT AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280  
 CTGTGTAGT ATTCGCCCTC CTCTTTCAT TAATCAAGG ATTTGGTAGA GGTGGAATCT 2340  
 AAGTGTGTT ATGTCCAATT TACTTGATA TGTAAACCAT TGCTGTGCA TCAATGTTT 2400  
 35 GATGCAATAT TGGACCTTGA ATCGATAAG GTAAATACAG CTTTGATCT GTAATGCTT 2460  
 TATACAAAG TTTATTTAA TAATAAATG TTTGTTCTAA AAAAAA

Seq ID NO: 126 Protein sequence  
Protein Accession #: NP\_114148.1

40 1 11 21 31 41 51  
 MDARRVPQKD LRVKKNLKKF RYVKLISMET SSSDDSCDS FASDNFANTR LQSVREGCRT 60  
 RQCRHSGL RVAMKPPARS TRGATNKKAE SRQPSNSVT DSNDSSEDES GNNFLEKRAL 120  
 NIKQNKAMLA KMSLESFPP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180  
 45 TRSRRIILGS LDALPMEEEE EEDKYLVRK RKTVDGYMNE DDLPRSRSR SSVTLPHIIR 240  
 FVEEITEEL ENVCNSREK IYNRSLGSTC HQCRQKTIIDT KTNCRNPDCW GVRGQFCGPC 300  
 LRNRGYEEVR DALLDPNWHC PPCRGICNCS FCRQRDGRCA TGVLVYLAKY HGFGNVHAYL 360  
 KSLKQEFEMQ A

Seq ID NO: 127 DNA sequence  
Nucleic Acid Accession #: AF305616.1  
Coding sequence: 1..863

55 1 11 21 31 41 51  
 ATGCACCGCT TGATGGGGGT CAACAGCACC GCGCGCGCG CCGCGGGCA GCCCAATGTC 60  
 TCTGCAAGT GCAACTGCAA ACGCTCTTTG TTCCAGAGCA TGGAGATCAC GGAGCTGGAG 120  
 TTTGTTTACA TCATCATCAT CGTGGTGGTG ATGATGGTGA TGGTGGTGGT GATCACTGTC 180  
 CTGCTGAGCC ACTACAAGCT GTCTGCAAGG TCTTTCATCA GCCGCGCAG CCAGGGGGGG 240  
 60 AGGAGAGAAG ATGCCCTGTC CTGAGAAGGA TGCTGTGGC CTGCGAGAG CACAGTGTCA 300  
 GGCAACGGAA TCCAGAGGCC GCAGGTCTAC GCGCGCCTC GCGCCACCGA CCGCTGSCC 360  
 GTGCCCGCT TCGCCAGCG GAGCGGCTTC CACCGCTCC AGCCCACTA TCGGTACCTG 420  
 CAGCAAGAGA TCGACCTGCC ACCCACTATC TCGCTGTGAG ACGGGGAGGA GCCCCACCC 480  
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 65 GAGTGGTGG GCGCACCCCC AAACAGAAC ATCTTGACA GTGACCTGAT GGATAGTGCC 600  
 AGGCTGGGG GCGCTGCCC CCGCAGCAGT AACTCGGCA TCAGCGCCAC GTGCTAAGGC 660  
 AGCGGGGGG GCATGGAGGG GCGCGCGCC ACCTACAGCG AGGTATCGG CCACTACCG 720  
 GGTCTCTCT TCCAGCACA GCAGAGCAGT GCGCGCGCT CCTTGTGGA GGGGACCCGG 780  
 70 CTCCACCACA CACATATGC GCCCTAGAG AGCGCAGCA TCTGAGCAA AGAGAAGGAT 840  
 AAACAGAAAG GACACCTCT CTAG

Seq ID NO: 128 Protein sequence  
Protein Accession #: AAL09357.1

75 1 11 21 31 41 51  
 MHRIMGVNST AAAAAGQPNV SCTCNCKRSL PQSMEITELE FVQIIIVVV MMVMVVVITC 60  
 LLSHYKLSAR SPISRHSQGR RREDALSSG CLWPSSTVS GNGIPEQVY APPRPTDLRA 120  
 VPPFAQRERF HRFQPTYPYL QHEIDLPTT SLSDGSEPPP YQGPCTQLR DPEQQLELNR 180  
 80 ESVRAPPNRT IPDSLDMSA RLGGPCPPSS NSGISATCYG SGGRMEGPPP TYSEVIGHYP 240  
 GSSFQHQSS GPPSLLEGTR LHTHIAPLE SAAIWSKEKD RQKGHPL

Seq ID NO: 129 DNA sequence  
Nucleic Acid Accession #: NM\_004952.1

Coding sequence: 1..718

1 11 21 31 41 51  
5 ATGGCGGGG CTCCGCTGCT GCTGCTGCTG CTGCTCGTGC CGTGCCGCT GCTGCGCTG 60  
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AACCAGCACC TGCGCGGAGA GGGCTACACC GTGCAGGTGA ACGTGAACGA CTATCTGGAT 180  
ATTTACTGCC CGCACTACAA CAGCTCGGGG GTGGGCCCGG GGGCGGACC GGGGCCCGGA 240  
10 GGCGGGCAGG AGCAGTACGT GCTGTACATG GTGAGCCGCA ACGGCTACCG CACCTGCAAC 300  
GCCAGCCAGG GCTTCAAGCG CTGGGAGTGC AACCGGCCCG ACGCCCGCA CAGCCCATC 360  
AAGTTCTGGG AGAAGTTCCA GCGCTACAGC GCCTTCTCTC TGGGCTACGA GTTCCAAGCC 420  
GGCCACGAGT ACTACTACAT CTCCACGCCC ACTCACAACC TGCCTGGAA GTGTCTGAGG 480  
ATGAAGGTGT TGTCTGCTG GCGCTCCACA TCGCACTCCG GGGAGAAGCC GGTCCCCACT 540  
15 CTCCCCAGT TCACCATGGG CCCCATTGTG AAGATCAACG TGCTGGAAGA CTTTGAGGGA 600  
GAGAACCCTC AGGTGCCCAA GCTTGAGAAG AGCATCAGCG GGACCAGCCC CAAACGGGAA 660  
CACCTGCCCC TGCCGTGGG CATCGCCTTC TTCCTCATGA CGTCTTGCC CTCCTAG

Seq ID NO: 130 Protein sequence  
Protein Accession #: NP\_004943.1

1 11 21 31 41 51  
20 MAAAPLLLLL LLVPVPLLLP LAQGPGGALG NRHAVYWNSS NQHLRREGYT VQVNVNDYLD 60  
IYCPHYNSSG VGPAGPGPGP GGAEQYVLYM VSRNGYRTCN ASQGFKRWEC NRPHAPHSPI 120  
25 KPSEKFORYS AFSLGYEFHA GHEYYIISTP THNLHWKCLR MKVFVCCAST SHSGEKFPVT 180  
LPQFTMGPNV KINVLDFEG ENPQVPKLEK SISGTSFKRE HPLAVGIAF FLMTFLAS

Seq ID NO: 131 DNA sequence  
Nucleic Acid Accession #: NM\_012445.1  
Coding sequence: 276..1271

1 11 21 31 41 51  
35 GCACGAGGGA AGAGGTGAT CGACCCCGGG GAAGGTGCTT GGGCAGGGCG AGTTGGGAAA 60  
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TCTGCTGGA GGCCAGGCGG TGCAAGCATG AAGACAGSAG GAAGTGGAGC CTCATTGGCC 180  
GGCCCGGGCG GCGCGCTCGG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GAGCCCGACC 240  
GCTGCGGCGC GCGCTCCGCG TGCTCTCTGC GGGTGTGGA AAACCCAGCG CCGGCGCGCG 300  
40 CCTGCGGCAA GGCCTCTGCG GCTCTCTCTC TGGCCACTCT CGGCGCGCGC GGCCAGCCTC 360  
TTGGGGGAGA GTCCATCTGT TCGCCAGAG CCGCGGCCAA ATACAGCATC ACCTTCACGG 420  
GCAAGTGGAG CAGACGCGCC TTCCCCAAGC AGTACCCCTT GTTCCGCCCC CTGCGCAGT 480  
GGTCTTCGCT GCTGGGGGCG GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCACT 540  
AGTCAGTAA CCGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCCTGGGCG CTGATGAAGG 600  
45 AGATCGAGGC GGCGGGGAGG GCGCTGCAGA GCGTGCAAGC GGTGTTTTCG GCGCCCGCGC 660  
TCCCGAGCGG CACCGGGCAG ACGTCCGCGG AGCTGGAGGT GCGCGCAGG CACTCGCTGG 720  
TCTGTTTGT GGTGCGCATC GTGCCAGGCC CCGACTGCTT CGTGGCGTGG GACAGCCTGG 780  
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CGGGAGCGGA CAGCGGCTTC ACCTTCTCCT CCCCACACTT CGCCACCATC CCGCAGGACA 900  
50 CGGTGACCGA GATAAGCTCC TCTCTCTCCA GCGACCGCGC CACTCTCTTC TACTACCCGC 960  
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GGGCTTCAT CCTCCCGGCC CAGTCTCTCG CAGCAGGGA CAATGAGATT GTAGACAGCG 1080  
CCTCAGTTCC AGAAACGCGG CTGGAAGTGG AGGTCTCCCT GTGGTCTGTC TGGGGACTGT 1140  
GGCGAGGCGA CTGTGGGAGG CTGGGAGCCA AGAGCAGGAC TCGCTACGTC GGGTCCAGC 1200  
55 CGGCCAACAA CGGAGCGGCC TGCCCGAGC TCGAAGAAGA GGCTGAGTGC GTCCCTGATA 1260  
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GGCTCCTGTG CAGGCTCATG CTGCGGCGG CCGAGGCACA GGGGTTTCG CGCTGCTCCT 1380  
GACCGCGTGT AGGCGCGCGC GACCATCTCT GCACTGAAGG GCGCTCTGCT GGCGCGCAGG 1440  
GGCATTTGGA AACAGCCTCC TCTTTCCCA ACCTTGCTTC TTAGGGGCCC CCGTGTCCCG 1500  
60 TCTGCTCTCA GCTCTCTCT CTTGAGGAT AAAGTCATCC CCAAGGCTCC AGCTACTCTA 1560  
AATTATGTC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGTCTTCTAT GGTCCAGGGG 1620  
CTTGCTCCC AGTGGTGTG AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGGCCA 1680  
CTCTCCCGAG GCGCATCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC 1740  
65 GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTGCTT TGAATAAAGA CTATCTCTGT 1800  
TGCTCAC

Seq ID NO: 132 Protein sequence  
Protein Accession #: NP\_036577.1

1 11 21 31 41 51  
70 MENPSPAAL GKALCALLA TLGAAGQPLG GESICBARAP AKYSITFTGK WSQTAPFKQY 60  
PLFRPPAQWS SLGAAHSSD YSMWRKNQYV SNGLRDPFER GEAWALKEI EAAGEALQSV 120  
HAVPSAPAVP SGTGQTSARL EVQRRLSLVS FVVRIVPSPD WFGVDSLDL CDGDRWREQA 180  
75 ALDLYPYDAG TDSGFTFSSP NFATIPQDTV TEITSSSPSH PANSFYFRL KALPPIARVT 240  
LVRLRQSPRA FIPPAVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCRLGTGS 300  
RTRYVRVQPA NNGSPCELE EAECEVPDNC V

Seq ID NO: 133 DNA sequence  
Nucleic Acid Accession #: NM\_019894  
Coding sequence: 1..1314

1 11 21 31 41 51  
80 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60

5  
10  
15  
20

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AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
CTGAGCCCTGG CGAGTATCAT CATTTGGTGT GTCTCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTCT GCGGGCAGCC TCTOCACITC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGAAGTCTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGGGCCACA 360
GGGAAGTGGT TCTCTGCTCT TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
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GATCTGGATG TTGTTGAAAT CACAGAAAC AGCCAGGAGC TTGCGCATGC GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CTGGTCTCC CTGCACGTGC TTGCTGTGGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCAGGCGAG CCCACTGCTT CAGGAAACAT AOCGATGTGT TCAACTGGAA GGTGGGGSCA 780
GGCTCAGACA AACTGGGCG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTAAG 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTCTG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGATCAT TGGATGGGCG TTTACGAAAG AGAATGGAGG GAAGATGTCT 1020
GACATATGTC TGCAGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GGGTACCAAG GGGAGTGCAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGGTGTG 1140
GACACTGCGC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
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Seq ID NO: 134 Protein sequence  
Protein Accession #: NP\_063947.1

25  
30  
35

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1 11 21 31 41 51
| | | | |
MLQDPDSQPL LNSLDVKPLR KPRIPMETFR KVGIPPIIAL LSLASIIIVV VLIKVILDKY 60
YFLCQQLPHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120
GWNFSAFCFDN FTEALAEATC RQMGYSKRP FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWFWQV SIQYDKQHVC GGSILDPHW 240
LTAHCPRKH TDVFNWKVRA GSKLGSPPS LAVAKIIIE FNPMPKMD IALMKLQFPL 300
TFSGTVRICP LPFFDEELTP ATPLWIIWGW FTQNGGKMS DILLQASVQV IDSTRCNADD 360
AYQGEVTEKM MCAGIFEGGV DTCQDSGGP LMYQSDQMHV VGIWSWGYGC GGPSTPGVYT 420
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Seq ID NO: 135 DNA sequence  
Nucleic Acid Accession #: NM\_003045  
Coding sequence: 148..2037

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CGTCATATTC CAGCTCTGAA CAGCAACATG GGGTGCAAG TCCTGCTCAA CATTTGGCAG 180
CAGATGCTGC GGGCGAAGGT GGTGGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCTCGGG GTGGGCAGCA CACTGGGTGC TGGGTCTAC 300
GTCTGGGCTG GAGCTGTGGC CGGTGAGAAT GCAGGCCCTG CCATTGTCTC CTCTCTCTG 360
ATCGCTGCGC TGGCTCTAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420
CCCAAGACGG GCTCAGCTTA CCTCTACAGC TATGTACCG TTGGAGACTC CTGGGCTTCC 480
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TGGAGCGCCA CCTTGAAGA GCTGATAGG AGACCCATCG GGGAGTTCTC ACGGACACAC 600
ATGACTCTGA ACGCCCCCGG CGTCTGGCT GAAACCCCC ACATATTGCG AGTGATCATA 660
ATTCTCATCT TGACAGGACT TTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA 720
ATATTCACTT GTATTAACTT CCTGGTCTG GGCCTCATAA TGGTGTGAGG ATTTGTGAAA 780
GGATCGGTTA AAAACTGGCA GCTCAAGGAG GAGGATTTTG GGAACACATC AGGCGTCTC 840
TGTTTGAACA ATGACACAAA AGAAGGGAAG CCGGTGTTG GTGATTATC GCCCTTGGG 900
TTCTCTGGTG TCTGTGCGG GGCAGCGACT TGCTTCTATG CCTTGGTGGG CTTTGACTGC 960
ATCGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAAG CCATCCCGT GGGGATCGTG 1020
GCGTCCCTCT TGATCTGCTT CATCGCCTAC TTTGGGGTGT CGGCTGCCCT CACGCTCATG 1080
ATGCCCTACT TCTGCTGGA CAATAACAGC CCGCTGCCCG AGCGCTTAA GCACTGGGCG 1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCCTCCCTC GCGCTCTTTC CGCCAGTCTT 1200
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ATTGTGACCG TGCTTGAAG GAGGCTCTC ACCAAGGGG CGCTGTGGGC AGTCTTCTG 1740
CTGCGAGGCT CTGCCCCCTT CTGTGCGGTG GTCAAGGGG TCATCTGAGG GCAGCCCGAG 1800
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TGGATGCTGA TAGGCTTCTT CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG 1980
TCCTTGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAAGT CAAGTGAGCG 2040
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Seq ID NO: 136 Protein sequence  
Protein Accession #: NM\_003045

1 11 21 31 41 51  
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5 MGCKVLLNIG QQMLRRKVVD CSREETRLSR CLNTFDLVAL VVGSTLGAGV YVLGAVARE 60  
 NAGPAIVISF LIAALASVLA GLCYGEFGAR VPRTGSAYLY SYVTVGELNA FITGWNLLLS 120  
 YIIGTSSVAR AMSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILITGLLT 180  
 LGVKESAMVN KIFTICINVLV LGFIMVSGFV KGSVQWQLT BEDFGNTSGR LCLMNDTKEG 240  
 KPGVGGMPFF GFSGVLSGAA TCFYAFVGF D CIATTGEEVK NPQKAIPVGI VASLLICFIA 300  
 YFGVSAALTL MHPYFCLDNN SPLPDAPKHV GWEGAKYAVA VGLKALSAS LLGSMPPMPR 360  
 VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLDV LMSIGTLLEY 420  
 SLVAACVLVL RYQPEQPNLV YQMASTDEL DPADQNELAS TNSQLGLFLP EAEMFSLKTI 480  
 LSPKNMEPSK ISGLIVNIST SLIAVLIITF CIVTVLGRE A LTKGALWAVF LLAGSALLCA 540  
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Seq ID NO: 137 DNA sequence

Nucleic Acid Accession #: NM\_032044.1

Coding sequence: 182..658

1 11 21 31 41 51  
 20 AAGATATAAA AGCTCCAGAA ACGTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60  
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 AGAAGCCGTA GTAAGGCTCTC TGAGATCCTT GCACCTAGCTA CATCTCAGG GTAGGAGGAA 180  
 GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCCTGGCCA AAACAGGAGT 240  
 CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCTCTGGA TGGTTTATAC ACAAGTCCAA 300  
 25 TTGCTATGGT TACTTCAGGA AGCTGAGGAA CTGGTCTGAT GCGAGCTCG AGTGTCACTC 360  
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 AGAGTACATA AGTGGCTATC AGAGAAGCCA GCGATATGG ATTGGCTCG ACAGCCACA 480  
 GAAGAGGCAG CAGTGGCAGT GGATGTATGG GGCCATGTAT CTGTACAGAT CCTGGTCTGG 540  
 CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTAAAC 600  
 30 TTGGAGCAGC AACGAATGCA ACAAGCGCCA ACACCTCCTG TGCAAGTACC GACCATAGAG 660  
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 GCTAAATCTG CTCATTATTT CAGAGGGGAA ACCTAGCAAA CTAAGATGA TAAGGGCCCT 780  
 ACTACACTGG CTTTTTATAG CTTAGAGACA GAAACTTTAG CATTGGCCCA GTAGTGGCTT 840  
 CTAGCTCTAA ATGTTTGGCC CGCCATCCTT TTCCACAGTA TCCTCTCTTC CTCTCCCCCT 900  
 35 GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT 960  
 CTTTGGCCAT AAGAAGTAAA GATTTGAAGA CAGAAGGAAG AACTCAGGA GTAGCTTCT 1020  
 AGACCCCTTC AGCTTCTACA CCTTCTGCC CTCTCTCCAT TGCCCTGACC CCACCCAGC 1080  
 CACTCAACTC CTGCTTGTTT TTCTTTGGC CATAGGAAGG TTTACAGTA GAATCTCTGC 1140  
 TAGGTGTATG TGGGCCATAC ATTCCTTTAA TAAACCATG TGTACATAAG AAAAAAAAAA

Seq ID NO: 138 Protein sequence

Protein Accession #: NP\_114433.1

1 11 21 31 41 51  
 45 MASRSMRLLL LLSCLAKTGV LGDIIMRSPC APGWFYHKNV CYGYFRKLNR WSDAELEQCS 60  
 YGNGAHLASI LSLKEASTIA EYISGYQRSP FIWIGLEDPO KRQWQWIDG AMYLRSWSWG 120  
 KSMGGNRHCA EMSNNNNFLT NSSNECNKRO HFLCKYRP

Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: XM\_051860.2

Coding sequence: 52..3042

1 11 21 31 41 51  
 55 GCTCACCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60  
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 GACCGGGGCA GAGCTCGCCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180  
 CCCAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTTGGAGGAT 240  
 60 AATGTACAGT CATGGAACCT TGGAGATACC CTGGTCATTG CCAGTACTGA TTAATCCATG 300  
 TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGACAGATCCT GCGCCGCCAA CCAGGTCAAA 360  
 GTGGCAGGGA AACCAATGTA CCTGCACATC GGGGAGGAGA TAGACGGGCT GGACATGCGG 420  
 GCGGAGGTTG GGTCTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480  
 TACCCTTACA GAAACCATAT CTGCAATTTC TTTGACTTGG ATACCTTTGG GGGCCACATC 540  
 65 AAGTTTGCTC TGGGATTAA GGCAGCACAC TTGGAGGGCA CGGAGCTGAA GCATATGGGA 600  
 CAGCAGCTGG TGGGTCAATA CCGATTACAT TTCCACTGG CCGGTGATGT AGACGAAAGG 660  
 GGAGGTTATG ACCCAACCCAC ATACATCAGG GACCTCTCCA TCCATCATAC ATTCTCTGCG 720  
 TGCGTCAAG TCCATGCTCT CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT 780  
 TTGGGCCACT GCTTCTTAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACTGT 840  
 70 CTGCGCTTCC TTGTCAAGTC TGGAAACCTC CTCCCTCGG ACCGTGACAG CAAGATGTGC 900  
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 GGATCTGAGG AACTCTGATT TTGTTTATT TTTCAACAG TACCAAGCGG CCTCTCGTG 1080  
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70 Seq ID NO: 140 Protein sequence  
 Protein Accession #: XP\_051860.2

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 DNRABVGLLS RNIIYVMGME DKCYPYRNHI CNPFDFTDPG GHIFKALGPK AAHLEGTLEK 180  
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 YNSLGHCFPT EDGPBERNTH DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300  
 DCMNAVSTFW ANPNRNLLNC AAAGSEETGF WPIFHHVPTG PSVGMYSPOY SEHIPLGKPY 360  
 NNRASHNYRA GMIDNGVKT TEASAKORRP FLSTIISARYS PHQDADPLKP REPAIRHFI 420  
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5 SEYPGSYLTK NDNWLVHRPD CINVPDWRGA ICSGCVYQMY IQAYKTSNLR MKIIRNDPPS 660  
 HPLYLEBALST RSTHYQQYQF VVTLOKGYTI HWDQTAPAEI AIWLINFNKG DWIRVGLCYP 720  
 RGITTFSLSD VHNRLKQTS KTGVFVRTLQ MDKVEQSYPG RSHYYWDEDS GLLFLKLLAQ 780  
 NEREKFAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLFPSQLK 840  
 TKDHFLEVKM ESSKQHFHLL WNDPAYIEVD GKXYPSSSEDG IQVVVIDGNQ GRVVSHTSFR 900  
 NSILQGIPIW LFNYVATIFD NSIVLMSKRG RYVSRGPWTR VLEKLGADRG LKLKEQMAFV 960  
 GPKGSFRPIW VTLDOTEDHKA KIPQVVPPIV VKKKRL

10 Seq ID NO: 141 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 261..2861

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 ACGTCCGGGG CCGCTGGCGT CCGTGGCCGG GAGGCGTGAC ACTGTCTCGG CTACAGACCC 240  
 20 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCTCT TTCAAGGCCA 300  
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 45 TGTACTGCA CATCGGGGAG GAGATAGACG GCGTGGACAT GCGGGCGGAG GTTGGGCTTC 1740  
 TGAGCGGAAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800  
 ACATCTGCAA TTCTTTGAC TTGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT 1860  
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Seq ID NO: 142 Protein sequence  
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ERSWGHRRVI VHVLDPKSGT VIHSDRFDY RSKKESERLV QYLNVAEDGR ILSVAVNDEG 240
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KDVVGYNSLG HCFPTEDGPE ERNTFDHCLG LLVKSGLTLP SDRDSKMKCM ITEDSYPGYI 660
PKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP 720
LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRPFLSII SARYSPHQDA DPLKPREPAI 780
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GCGTGATTTC CCAGAAGATA CTTTGAGAAA ATTCTTACAG AAGGCATATG AATCCAAAT 300
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Seq ID NO: 144 NP Protein sequence  
Protein Accession #: NP\_006008.1

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HQVTRIKRS RKLADSNFKD LRTLLNETPE QIKYILAQYN TKDKAPTDL NSINSVLGGG 240
ILDRLRPNII PVLDKESMA TAIKETKEAL ENMNSTLKS L HQQSTQLSSS LTSVKTSLRS 300
SLNDPLCLVH PSSETCNSIR LSLSQLNSNP ELRQLPPVDA ELDNVNVLRL TDLGLVQGG 360
YQSLNDIPDR VQRQTITVVA GIKRVLNSIG SDIDNVQRL PIQDILSAPS VVNMNTESYI 420
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VFLMVGVGLS FLFCWILMII VVLTFFVFGAN VEKLIPEPT SKELFRVLDL PYLLNEDWEY 540
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	ATATGATCTA	GAAGCAAAAG	CAAAACAGTT	GCCCCAGGA	AATTTGAGGA	ACTCCCTGAA	2220
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	GAATTTGTTT	TGGTTTGGCA	TAGGAAAAGC	TACTGTATTT	TTACTTCCGG	CTCTAATTTT	2640
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	AGAAACCTGC	GTAACCTCCA	CTGACAAATT	CAAAAGAGAG	AGAGAGATCT	TGAGAGAGAA	3540
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	GGTAAATATT	CATTGCTTTC	AGGAGTTTCA	TGTTGGATCT	GTCAATTATCA	AAAGTGATCA	3840
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Protein Accession #: AAH12089.1

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	IPVLDEIKSM	ATAIKETKEA	LENMNSTLKS	LHQQSTQLSS	SLTSVKTSLR	SSLNDPLCLV	300
	HPSSETQNSI	RLSLSQLNSN	PELRQLPPVD	ABLDNVNVL	RTDLGLVQQ	GQYSLNDIPD	360
	RVQRQTITV	AGIKRVLNSI	GSDIDNVQR	LPIQDILSAF	SVYVNTSEY	IHRNLPTLEE	420
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Nucleic Acid Accession #: NM\_033049.1  
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	GAAACTGCTA	GCACCAACAGC	AAATACACCT	TCTTTCCCAA	CAGCTACTTC	ACCTGCTCCC	240
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70	ACACATAGTT	CCTCCACAAAT	TCCTATACCT	ACTGCTGCAG	ACAGTGAGTC	AACCAAAAT	360
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	GTATTTGCCA	CATCTGTTTA	TGGACAGACT	GTAATTTCTA	CTGTAAGCAC	ATCTCTGTCA	840
	CCAAGATCTG	AAATGCGTGC	TGATGACAA	TTTGTTAATG	TAACAATAGT	AACAATTTTG	900
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	AACCAAGCTG	CGGATGACTG	CCTCAATGGT	TTAGCATGCG	ATTGCAAAATC	TGACCTGCAA	1080
	AGGCCTAAC	CACAGAGCCC	TTTCTGCGTT	GCTTCCAGTC	TCAAGTGTCC	TGATGCTGTC	1140
	AACGCACAGC	ACAAGCAATG	CTTAATAAAG	AAGAGTGGTG	GGGCCCTG	GTGTGCTGTC	1200
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Seq ID NO: 150 Protein sequence  
Protein Accession #: NP\_149038.1

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VASSLRKCPDA CNAQHKKCLI KSGGAPECA CVPGYQEDAN GNCQKCAFYG SGLDCKDKPQ 420
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Nucleic Acid Accession #: Eos sequence  
Coding sequence: 87..914

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CACTGAC

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Seq ID NO: 154 Protein sequence  
Protein Accession #: NP\_001423.1

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Seq ID NO: 155 DNA sequence  
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Coding sequence: 85..2466

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CAGGAGCTGT TCCACGTGGA GCCAGGCTGT CAGAGGCTGT TCTACAGGGG CAAACAGATG 240
GAGGACGGCC ATACCTCTTT CGACTACGAG GTCCGCTGTA ATGACACCAT CCAGCTCCTG 300
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	TCACAGCGGG	ACTGGGGCAA	GGGCATGGCC	TGTGTGGGCC	GCACCAAGGA	ATGTACCATC	1320
	GTCCCGTCCA	ACCACTACGG	ACCCATCCCG	GGGATCCCGG	TGGGCACCAT	GTGGCGGTTT	1380
	CGAGTCCAGG	TCAGCGAGTC	GGGTGTCCAT	CGGCCCAAG	TGGCTGGCAT	ACACGGCCGG	1440
	AGCAACGACG	GAGCGTACTC	CCTAGTCCCTG	GCGGGGGGCT	ATGAGGATGA	CGTGGACCAT	1500
	GGGAATTTTT	TCACATACAC	GGGTAGTGGT	GGTCGAGATC	TTTCCGGCAA	CAAGAGGACC	1560
	GCGGAACAGT	CTTGTGATCA	GAAACTCACC	AACACCAACA	GGGCGCTGGC	TCTCAACTGC	1620
10	TTTGCTCCCA	TCAATGACCA	AGAAGGGGCC	GAGGCCAAGG	ACTGGCGGTC	GGGGAAGCCG	1680
	GTACGGGTGG	TGCGCAATGT	CAAGGGTGGC	AAGAATAGCA	AGTACGCCCC	CGCTAGGGGC	1740
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	TTTCTCGTGT	GGCGTACCTT	TCTGCGGAGG	GACGATGATG	AGCCTGGCCC	TTGGACGAAG	1860
	GAGGGGAAGG	ACCGGATCAA	GAAGCTGGGG	CTGACCATGC	AGTATCCAGA	AGGCTACCTG	1920
15	GAAGCCCTGG	CCAAACCGAGA	GCGAGAGAAG	GAGAACAGCA	AGAGGGAGGA	GGAGGAGCAG	1980
	CAGGAGGGGG	GCTTCGCGTC	CCCCAGGAGG	GGCAAGGGCA	AGTGAAGCGG	GAAGTCGGCA	2040
	GGAGGTGGCC	CGAGCAGGGC	CGGGTCCCCG	CGCCGACAT	CCAAGAAAAC	CAAGGTGGAG	2100
	CCCTAAGATC	TCACGGCCCA	GCAGAGCAGC	CTCATCAGAG	AGGACAAGAG	CAACGCCAAG	2160
	CTGTGGAAAT	AGGTCTCTGC	GTCACTCAAG	GACCGGCGCG	CGAGCGGCAG	CCCGTCCAG	2220
20	TTGTTCCTGA	GTAAAGTGGG	GGAGACGTTT	CAGTGTATCT	GCTGTGAGGA	GCTGGTGTTC	2280
	CGGCCCATCA	CGACCGTGTG	CCAGCAACAAC	GTGTGCAAGG	ACTGCTGGGA	CAGATCCTTT	2340
	CGGGCACAGG	TGTTCAAGTG	CCCTGCCTCG	CGCTACGACC	TGGGCGGCAG	CTATGCCATG	2400
	CAGGTGAACC	AGCCTCTGCA	GACCGTCTCT	AACCAAGTCT	TCCCGGCTA	CGGCAATGGC	2460
	CGGTGATCTC	CAAGCACTTC	TCGACAGGCG	TTTTGTCTGA	AACGTGTGCG	AGGGCTCGTT	2520
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	CCTAAAAAGG	TTTGTCTTCC	TTTTTTTTTT	TTTTTTATTT	TCAATCTAT	ACATTTTCAG	2640
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30	CAACTCTCTA	AGAAGGCGAC	AGGATCAGTC	CTTCTCTAGG	GTTCTGGCCC	CCAAGGTCAG	2880
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	AAAGAGGAAA	CATCTCGGGC	CTAGTTCAAA	CCCTTGCCTC	AAAGCCATCC	CCCAACGAGC	3060
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35	CAOGCAGAAA	TGGCCTCAA	GGGACTCTGC	TCCACGTGGG	GCCAGCGGTG	TGACTGACGC	3180
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	GTCAACGAGA	TTCTAGAAAC	TGCGGTCAAT	CAGTTCTTCC	TGACACCGGA	TGGGTGCTTG	3360
	GGAAACGTTT	GAGCCTTATA	GATCAATTAC	ATTCATTTT	TTTAACTCAG	CAAGTGAGAA	3420
40	CTTACAAGAG	GGTTTTTTTT	TAATTTTTTT	TTCTCTTAAT	GAACACATT	TCTAAATGAA	3480
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	TTGTTTTTGT	ATTTTTTTTC	TTTTGAAAGG	GTTTGTTAAT	TTTTCTAATT	TTACCAAAGT	3600
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	GAGCAATGTT	ATTTTTTAAAG	GGTTTTTTTC	ACCTCCCTTAT	TCTTAGATTA	TTAATGTATT	3720
45	AGGGAAGAA	GAGACAATTT	TGTTGAGGCT	TTTTCTAAAG	TCCAGTACTT	TGTCAGGATT	3780
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Seq ID NO: 156 Protein sequence  
Protein Accession #: NP\_037414.2

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	PADEDMWDET	ELGLYKVNEY	VDARDTNMGA	WFEAQVVRVT	RKAPSRDEPC	SSTRPALKEE	180
55	DVIYHVKYDD	YPENGVVQMN	SRDVRARART	IIKWQDLEVG	QVVMNLNYPD	NPKERGFWD	240
	AEISRRKRSTR	TARELYANVV	LGDDSLNDCR	IIPVDEVFKI	ERPGESEPMV	DNPMMRKSQP	300
	SCXHCCKDDV	RLCRVCACHL	CGGRQDPDKQ	LMCDECDMAF	HIYCLDPPLS	SVPSSEDEWYC	360
	PECRNDASEV	VLGERLRES	KKAKMASAT	SSSQRDWGRG	MACVGRTKEC	TIVPSNHYGP	420
60	IGPIPVGTMW	RFRVQVSESG	VHRPHVAGIH	GRSNDGAYS	VLAGGYEDDV	DHGNFFTYTG	480
	SGGRDLSGNK	RTAEQSCDQK	LNTNRLALAL	NCFAPINDQE	GAENKWRSG	KPVRVVRNVK	540
	GGKNSKYAPA	EGNRYDGIYK	VVKYWPEKGG	SGFLVWRYLL	RRDDEPGPW	TKEGKDRIKK	600
	LGLTMQYPDG	YLEALANRER	EKENSKREEE	BQSGGFASP	RTGKGKWKRK	SAGGGPSRAG	660
	SPRRTSKRTK	VEPYSLTAQG	SSLIREDKEN	AKLWNEVLAS	LKDRPASGSP	PQLFLSKVEE	720
65	TFQCICQEL	VFRPIITVQ	HNVCCKCLDR	SFRAQVFSCE	ACRYDLGRSY	AMQVNPQLQT	

Seq ID NO: 157 DNA sequence  
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75	CTAACATGCT	GCTGCGGCTG	CTTGTGTCGG	CGGAGTCCCT	GCTGGTGGCT	CTCCTGCCCC	240
	GCCCGCCATG	CAGGGCGCTC	CTGAGCGCGG	GGCCGGTCCC	GGGAGCTCGG	CAGGCGCGGC	300
	AGCACCTCA	GCCCTTGGAT	TTCTTCCAGC	CGCCGCGCGA	GTCCGAGCAG	CCCCAGCAGC	360
	CGCAGGCTCG	GCCGGTCTCG	CTCCGATGCG	GAGAGGAGTA	CTTCTCCGCG	CTGGGGAACC	420
	TCAACAGAG	CCCGGCGGCT	CCCTTTCCGC	CCGCTCTCTC	GCTCTCGGCC	GGAGGCAGCG	480
80	GCAGCCGCC	TTCCGCCGAA	CAGGCGACCG	CCAACCTTTT	CCGCTGTGTT	CTGCAGCAGC	540
	TGCTGCTGCC	TGCGGCTCTG	CTCGACAGCC	CCGCGGCTCT	CGCGGAGCGC	GGCGCTAGGA	600
	ATGCCCTCGG	CGGCCACGAG	GAGGCACCGG	AGAGAGAGAG	GCGGTCCGAG	GAGCCTCCCA	660
	TCTCCCTGGA	TCTCACCTTC	CACCTCTCTC	GGGAAGTCTT	GGAAATGGCC	AGGGCCGAGC	720
	AGTTAGCACA	GCAAGCTCAC	AGCAACAGGA	AACATCATGA	GATTATTGGG	AAATAAAGC	780



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Protein Accession #: NP\_001191.1

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LPETSGKTTR RFFFNLSIP TEEFITSABL QVFREQWQDA LGNNSPFHR INIYIIPKA 180  
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	ATGGGTGCTC GTGGGTGTTT TTAGACACCA GAGAAACAC AGTCTCTGCT AGAGAGCACT 840
65	CCCTATTTTG TAAACATATC TGCTTTAATG GGGATGTACC AGAAACCCAC CTCACCCCG 900
	CTCACATCTA AAGGGGCGGG GCGGTGGTCT GGTCTGACT TTGTGTTTT GTGCCCTCCT 960
	GGGGACCAAG ATCTCTCTTC GGAATGAATG TTCATGGAAG AGGCTCTCT GAGGGCAAGA 1020
	GACTGTGTTT AGTGCTGCAT TCGACATGGA AAGTCTCTT TAACCTGTGC TTGCATCTCT 1080
	CTTCTCTCT CTTCTCTACA ATCCATCTCT TCTTAAGTTG ATAGTGACTA TGTCACTCTA 1140
70	ATCTCTGTT TGCCAGGTTT CCTAAATTAA TTCACITTAAC CATGATGCAA ATGTTTTTCA 1200
	TTTTGTGAAG ACCCTCCAGA CTCTGGGAGA GGCTGGTGTG GSCAAGGACA AGCAGGATAG 1260
	TGGAGTGAGA AAGGGAGGGT GGAGGGTGAG GCCAATCAG GTCCAGCAA AGTCAGTAGG 1320
	GACATTGCAG AAGCTTGAAA GGCCAATACC AGAACACAGG CTGATGCTTC TGAGAAAGTC 1380
	TTTTCTTAGT ATTTAAGAGA ACCCAAGTGA ACAGAGGAGA AATGAGATTG CCAGAAAGTG 1440
75	ATTAACCTTG CGCGTTGCAA TCTGCTCAA CCTAACCCA AACTGAAAC ATAAATACTG 1500
	ACCATCTTGA TGTTCGGACC CAAGCAAGTT AGCTAAACCA AACCACTCT TCTGCTTTGT 1560
	CCCTCAGGTG GAAAGAGAG GTAGTTTAGA ACTCTCTGCA TAGGGGTGGG AATTAATCAA 1620
	AAACCKCAGA GGCTGAATTT CCTAATACCT TTCTTTTATC GTGGTTATAG TCAGCTCATT 1680
	TCATATCCAC TATTTCCCAT AATGCTCTG AGAGCCACTA ACTTGATTGA TAAAGATCCT 1740
80	GGCTCTGCTG AGTGACCTG ACAGTAAGTC TAAAGATGAR AGAGTTTAGG GACTACTCTG 1800
	TTTTAGCAAG ARATATTKTG GGGGTCTTT TGTTTTAACT ATTGTCAGGA GATTGGGCTA 1860
	RAGAGAAGAC GACGAGAGTA AGGAAATAAA GGGRAATTGCC TCTGGCTAGA GAGTAAGTTA 1920
	GGTGTDAATA CCTGGTAGAA ATGTAAGGGA TATGACCTCC CTTTCTTTAT GTGCTCACTG 1980
	AGGATCTGAG GGGACCTGT TAGGAGAGCA TAGCATCATG ATGTATTAGC TGTTCATCTG 2040
	CTACTGGTGT GATGGACATA ACTATTGTAA CTATTCACTA TTTACTGTA GGCAGTGTCC 2100

TCTGATTAAA CTTGGCCTAC TGGCAATGGC TACTTAGGAT TGATCTAAGG GCCAAAGTGC 2160  
 AGGGTGGGTG AACTTTATTG TACTTTGGAT TTGGTTAACC TGTTCCTTC AAGCCTGAGG 2220  
 TTTTATATAC AAATCCCTTG AATACTCTTT TTGCCTTGTA TCTTCTCAGC CTCCTAGCCA 2280  
 AGTCCTATGT AATATGGAAA ACAACACCTG CAGACTTGAG ATTCACTGTC CGATCAAGGC 2340  
 5 TCTGGCATTG AGAGAACCTT TGCAACTCGA GAAGCTGTTT TTAATTCGTT TTTGTTTTGA 2400  
 TCCAGTGCTC TCCCATCTAA CAACTAAACA GGAGCCATT TCAAGGCGGA GATATTTTAA 2460  
 ACACCCAAAA TGTGTGGTCT GATTTTCAAA CTTTAAACT CACTACTGAT GATTTCTACG 2520  
 CTAGGCGAAT TTGTCCAAAC ACATAGTGTG TGTGTTTTGT ATACACTGTA TGACCCACC 2580  
 10 CCAATCTTTT GTATTGTCCA CATTCCTCAA CAATAAAGCA CAGAGTGGAT TTAATTAAGC 2640  
 ACACAAATGC TAAGGCAGAA TTTTGAGGGT GGGAGAGAAG AAAAGGGAAA GAAGCTGAAA 2700  
 ATGTAAACC ACACCCAGGA GGAAAAATGA CATTGAGAAC CAGCAACAC TGAATTTCTC 2760  
 TTGTTGTTTT AACTCTGCCA CAAGAATGCA ATTCGTGTA TGGAGATGAC TTAAGTTGGC 2820  
 AGCAGTAATC TTTCTTAGG AGCITGTACC ACAGTCTGTC ACATAAGTGC AGATTGGCT 2880  
 15 CAAGTAAAGA GAATTTCTCT AACACTAACT TCACCTGGAT AATCAGCAGC GTAACCTACC 2940  
 TAAAGCATA TCACTAGCCA AAGAGGGAAA TATCTGTCT TCTTACTGTG CCTATATTAA 3000  
 GACTAGTACA AATGTGGTGT GTCTTCCAAC TTTCATTGAA AATGCCATAT CTATACCATA 3060  
 TTTTATTCGA GTCACTGATG ATGTAATGAT ATATTTTTC ATTATTATAG TAGAATATTT 3120  
 TTATGGCAAG ATATTGTGG TCTTGATCAT ACCTATTAAA ATAATGCCAA ACACCAATA 3180  
 20 TGAATTTTAT GATGTACACT TTGTGCTTGG CATTAAGAAGA AAAAACACCA CATCTGGAA 3240  
 GTCTGTAAGT TGTTTTTTGT TACTGTAGGT CTTCAAAGTT AAGAGTGTA GTGAAAAATC 3300  
 TGGAGGAGAG GATAATTTCC ACTGTGTGGA ATGTGAATAG TTAAATGAAA AGTTATGGTT 3360  
 ATTTAATGTA ATTATTACT CAAATCCCTT GTCTACTGTG ATTTCAAGCA TGTTCCTTT 3420  
 TTCTCCTTTA TATGACTTTC TCTGAGTTGG GCAAAGAAGA AGCTGACACA CGTATGTTG 3480  
 25 TTAGAGTCTT TTATCTGCTC AGGGGAAACA AAATCTTGAC CCAAGCTGAA ATGCTTCTCT 3540  
 GAGTCAGTGC CTGAATCTTT ATTTTAAAA TTGAATGTTT CTTAAAGGTT AACATTCTCA 3600  
 AAGCAATATT AAGAAAGACT TTAATGTGTA TTTTGAAGA CTTACGATGC ATGTATACAA 3660  
 ACGAATAGCA GATAATGATG ACTAGTTCAC ACATAAAGTC CTTTAAAGGA GAAAATCTAA 3720  
 AATGAAAAGT GGATAAACAG AACATTTATA AGTGATCAGT TAATGCCATA GAGTGAAAGT 3780  
 30 AGTTCTATTG ACATCTCTCA AGATATTTAA TATCAACTGC ATTATGTATT ATGCTGCTTT 3840  
 AAATCATTTA AAAACGGCAA AGAATTATAT AGACTATGAG GTACCTTGCT GTGTAGGAGG 3900  
 ATGAAAGGGG AGTTGATAGT CTCATAAAAC TAATTGGCT TCAAGTTTCA TGAATCTGTA 3960  
 ACTAGAATTT AATTTTCAAC CCAATAATGT TCTATATAGC CTTTGCTAAA GAGCAACTAA 4020  
 TAAATTAAC CTATCTTTT AAAAAAAA

Seq ID NO: 164 Protein sequence  
 Protein Accession #: NP\_037504.1

1 11 21 31 41 51  
 MSRTAYTVGA LLLLLLTLPL AEGKKKGSQ GAIPPPDKAQ HNDSEQTQSP QPGSRNRGR 60  
 40 GQGRGTAMPG EEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120  
 QCNVFPYIPRH IRKEEGSPQS CSFCKPKRPT TMMVTLNCPE LQPPTKKIRV TRVKQCRCIS 180  
 IDLD

Seq ID NO: 165 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51  
 50 GAATTGCATC GGACAGAGCT TGGCCATGSC CGAGTTGCGC GTGGTTGTGG CACTAACACT 60  
 GCTACGTTTC CGCTGAGCG TGGACCGAAC GCGCAGAGTG CGGCGAAGC CGGAGCTCAT 120  
 ACTGCGCAGG GAGAACGGG TCTGGCTCAA G

Seq ID NO: 166 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1650

1 11 21 31 41 51  
 60 ATGCCACCTC TGCCATCCAG AATGTCTCGG GGGCCCTCCT TGGTGACAGG CAGGATGCTG 60  
 CCCATCACAG ACOGCTGCT GCACCTCCTG GGGCTGGAGA AGACGGCGTT CCGCATATAC 120  
 GCGGTGTCCA CCTTCTCCT CTCTCTGCTC TTCTCTGCTT TCGCCTGCTC GCTGCGGTTT 180  
 65 CTGAGGCTCT GCAGGAGCTT CFACATCACC TGCCGCGCGC TGCGCTGCTT CCCCCAGCCT 240  
 CCCCAGGCTA ACTGGCTGCT GGGCCACCTG GGCATGTACC TTCCAAATGA GCGGGGCTT 300  
 CAAGATGAGA AGAAGGTACT GGACAACATG CACCATGTAC TCTTGGTATG GATGGGACCT 360  
 GTCTGCGCGC TGTGGTCTT GGTGCAACCT GATTACATCA AACCCCTTTT GGGAGCCTCA 420  
 GCTGCCATCG CCCCCAAGGA TGACCTCTTC TATGGCTTCC TAAAACTTG GCTAGGGGAT 480  
 70 GGGCTGCTGC TCAGCAAAGG TGACAAGTGG AGCCGCGACC GTGCGCTGCT GACACCCGCC 540  
 TTCCACITTG ACATCCTGAA GCCTTACATG AAGATCTTCA ACCAGAGCGC TGACATTATG 600  
 CATGCTAAAT GCGGCTCTCT GGCAGAGGSC TCAGCGGTCT CCTTGTATAT GTTTAGAGCAT 660  
 ATCAGCCTCA TGACCTTGA CAGTCTTCAG AAATGTGTCT TCAGCTACAA CAGCAACTGC 720  
 CAAGAGAAGA TGAGTGATTA TATCTCCGCT ATCATTGAAC TGAGCGCTCT GTCTGTCCGG 780  
 75 CGCCAGTATC GCTTGACCCA CTACCTCGAC TTCAATTACT ACCGCTGGCG GATGGGCGG 840  
 AGGTTCCGGC AGGCTCTGTA CATGGTGAC CACTTCAACA CTGAAGTCAT CCGAGAACGG 900  
 CCGGCGGCGC TGGGTGAGG GGGGGCGGAG GCCTGGCTTA AGGCCAAGCA GGGGAAGACC 960  
 TTGACCTTTA TTGATGTGCT GCTCCTGGCC AGGATGAAG ATGGAAGAAG ACTGTCAGAC 1020  
 GAGGATATCC GAGCCGAAGC AGACACCTTC ATGTTTGAGG GTCAAGACAC AACATCCAGT 1080  
 80 GGGATCTCTT GGATGCTGTT CAATTGGCA AAGTATCCGG AATACAGGA GAAATGCCGA 1140  
 GAAGAGATTC AGGAGTCAT GAAAGGCGCG GAGCTGGAGG AGCTGGAGTG GGACGATCTG 1200  
 ACTCAGCTGC CCTTACAAC TATGTGCATT AAGGAGAGCC TGCGCAGTA CCACTCTGTC 1260  
 ACTCTGTCT CTGCGCAATG CACGAGGAC ATCAAGCTCC CAGATGGCG CATCATCCCC 1320  
 AAAGGAATCA TCTGCTTGGT CAGCATCTAT GGAACCCACC ACAACCCAC AGTGTGGCT 1380  
 GACTCCAAGG TGTACACCC CTACCGCTTT GACCCGACA ACCACAGCA GCGCTCTCCA 1440

CTGGCCTATG TGCCTTCTC TGCAGGACCC AGGAATTGCA TCGGACAGAG CTTCGCCATG 1500  
 GCGGAGTTGC GCGTGTGTG GGCCTAACA CTGCTACGTT TCGGCTGAG CGTGAGACGA 1560  
 ACGGCGAAGG TCGGCGGAA GCGGAGCTC ATACTGCGCA CGGAGAACGG GCTCTGGCTC 1620  
 AAGGTGGAGC CGCTGCTCC GCGGGCCTGA

Seq ID NO: 167 Protein sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 MPPLPSRMSR GPSLVTGRML PITDRLHLHL GLEKTAFTRIY AVSTLLFLFL FFLPRLLLR 60  
 LRLCRSFYIT CRLRCFPQP PRRNWLLGHL GMYLPNEAGL QDEKKVLNDM HHVLLVWMGP 120  
 VLPPLVLVHP DYIKPLLGAS AAIAPKDDL F YGFLKPWLG D LLLSKGDKW SRHRRLLTPA 180  
 FHFIDILKPYM KIFNQASDIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC 240  
 QEIMSDYISA IIELSALSVR RQYRLHHYLD FIYYRSADGR RFRQACDMVE HPTTEVIQER 300  
 RRALRQQGAE AWLKAQGGK LDFIDVILLA RDEDEKELSD EDIRAEADTF MFEHDTTSS 360  
 GISWMLFNLA KYPEYQSKR EEIQEVMKGR ELEELWDDL TQLPFTMC I KESLRQYPPV 420  
 TLVSRQCTED IKLEPDGRIIP KGIILVSIY GTHNPTVWP DSKVYNPYRP DPDNPQQRSP 480  
 LAYVPFSAGP RNCIGQSPAM AELRVVVALT LLRFRLSVDR TRKVRKPEL ILRTENGLWL 540  
 KVEPLPPRA

Seq ID NO: 168 DNA sequence  
 Nucleic Acid Accession #: AK058088.1  
 Coding sequence: 252..1772

1 11 21 31 41 51  
 AGGAAACCAA GGCAAGCTCC CCCTGTCAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60  
 GCCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCC AGCTCTCCTG 120  
 TAACCTCAGAG GCCAGTGTGA TGGGAGTTCC TCCACTCAGC ACACCTCCCC TGTAACACAG 180  
 CCGTGTGGTG GCAAAAGGGC TTGGAAACGG TTGCTGTCT TTTCTCTCT GGTAAATTTC 240  
 CACTTTCAAT CATGATAATG TCGAACACGC ACAAAGCTCG GCTGGAACGC CGGGTCACTG 300  
 GCTCAACCAA CCGTGGCGT TTGCCCAAAC AGCCTTTCTC TGGGGAGCTG CTCTCACTTT 360  
 CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420  
 TATGCAATTC ACAATCCAG AAGTTTTCTT TTGAGAAATT CAAGACAAG GACATCCAAA 480  
 GTGGGGAAGC AGATGTGATT CTGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540  
 GGCTTTTTCG GTCTGAGACC TTGCCCAAGC TCTACCTGAA AGCCTTGGCG CAGGGCACCA 600  
 CACACCCCTC GAGGGAGCTG GAGGAGCTTC TGCGAGCTCA ATCACTTAAG AAGACCAAAG 660  
 AAAAATCCCC TCAGGGGCGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA 720  
 AAGTGCCTCT CGCCACGGCC CTGAGAACCC TCTACATGAG TGAGGTGGAG ATTAACCTGG 780  
 AAGACCTACT GGGAGTGCTG GCTTCGCCCC ACATCCTCCA GTTCAGTGGC CTGTTTCAAA 840  
 GGTGCGTGGG TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900  
 CCGGCTGCAG GTACAAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATGTA 960  
 ACTTGTGTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCACAG GACCTGCTCC 1020  
 ACAAGATGCT GAAGTCCCCC AGGTTATTTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA 1080  
 TGCTTTGTG GGTCTTCTTG CAACTGAAC ACAAATTCA GGCAATTCGG ACTTATGAAA 1140  
 CCGTGTATGAC ATTTTTTAAG AGCTTTCTCG AGAACTGTTG CTTTCTGGAC CGGGACATAG 1200  
 GAGCGAGCTT GAGGCGGCTC TTCTCTGCT TGCGTCTGCA CGGCATCACC AAAGGCAAGG 1260  
 ATCTGGAGGT GCTCGGGCAC CTTAACCTCT TCCCAGAGTC ATGGCTCGAC CAGGTTACAG 1320  
 TCAACCATTA CCAAGCATG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380  
 CCCAGCTGTG GAGATTTGGG CTGCTCTTTA ACCAGGAGAA TACAACCTAT TCGAAAACGA 1440  
 TTGCTCTATA TGAATTCCTT TTAAAGATAA AGGGACTCAA ACATGATACT ACCTCTTATA 1500  
 GTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCCTCTGCG GTCTACGAGC 1560  
 ACAACCACTG CAGCCTGCGA GCGCACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620  
 TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACAGAT CAGCAGAAG TTTGGGTTGA 1680  
 CCAAGTCATC CTGCAAAAGC CATACCTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG 1740  
 TAAGTTTTCG ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT 1800  
 CCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATAA AAGGGAGC

Seq ID NO: 169 Protein sequence  
 Protein Accession #: BAB71658.1

1 11 21 31 41 51  
 MIMSNTHKAR LERRVTGSTN RWRLPKQPPS GDLLSLQMC KALSIDFEBA LRNPDRLCIS 60  
 QIQKFFPFEN KNKDQSGEA DVILECLGFK WELHQPRLFQ SETLAKLYLK ALAQGTTHEPL 120  
 RELEELLRAQ SPKKTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180  
 GVLASAHILQ FSGLFQRCVD VMIAHLKPST IKFYEAGCK YKEBQLTTCG EKWLMLNLPV 240  
 LGGTQIHLHK IPQDLHLKVL KSPRLPTFSE FHLKTMLLW VFLQLNYKIQ AIPTYETVMT 300  
 FPKSFFPENC FLDRDIGRSL RPLFLCLRHL GITGKDLKV LRHLNFPFES WLDQVTUNHY 360  
 HALENGDMV HLKDLNTQAV RFGLLNQEN TTYSKTIALY GPFFKIRGLK HDTTSYSFYM 420  
 QRIKHTLES PSAVYSEHNV SLRAARLVKY EIRAEALVDG KWQEPRTNQI KQKPLGLTSS 480  
 CKSHTLKIQT VGPIIVSFA FIPPAS

Seq ID NO: 170 DNA sequence  
 Nucleic Acid Accession #: NM\_007000.1  
 Coding sequence: 1...777

1 11 21 31 41 51  
 ATGGCGTCTG CGGCAGCAGC GGAGGCGGAG AAGGGATCTC CAGTTGTGGT GGGCCTGCTA 60  
 GTTGTGGGCA ATATCATGAT TCTGCTGTCA GGCGTGTCCC TGTFTGTCTA GACCATATGG 120  
 GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180  
 TTGCTGTGGT CCGTGGATTG CATCTTCTGC GGCTTCTCTC TCTCATGGT AGCCAGTTT 240

5  
10  
GGTGTGGGTG COGCACTCTG COGCCGCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG 300  
CTCATCGTCT ACATCTCTGA GTGCGCCTCC TGCATCACTG CCTACACCCA COGTGACTAC 360  
ATGGTGTCCA ACCCATCCCT GATCACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC 420  
GACCAGGGCC AGGAGCTGAC COGCTCTGG GACCGCGTCA TGATTGAGCA AGAATGCTGT 480  
GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCACTGTCG CCTTCGGGGC GGCACTCCG 540  
GAGGTGGTGT TCCCTGGGCC CCCACTGTGC TGTGCGCGGA CGGAAACTT CATCCCCCTC 600  
AACGAGGAGG GCTGCGGCTT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA 660  
CACATCGGCC ACCCCATCGA CAGCTACACG TGGGGTATCT CGTGGTTTGG GTTTGCCATC 720  
CTGATGTGGA CGCTCCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGA

Seq ID NO: 171 Protein sequence  
Protein Accession #: NP\_008931.1

15  
20  
1 11 21 31 41 51  
MASAAAAEAE KGSFVVVGLL VVGNIIILL GLSLFAETIH VTADQYRVYP LMGVSGKDDV 60  
PAGAWTAIPC GFSPFMVASF GVGAALCRRR SMVLTYLVLM LIVYIFECAS CITSYTHRDY 120  
MVSNPSLITK QMLTFYSADT DQGQELTRLV DRVMIEQECC CGSGFMDOWN FTSAFRAATP 180  
EVVFPWPLLC CRRTGNFIPL NEBGCRLGHH DYLFKGCFFE HIGHAIDSYT WGISWFGFAI 240  
LMWTLPLVMI AMYFYTML

Seq ID NO: 172 DNA sequence  
Nucleic Acid Accession #: NM\_006760.1  
Coding sequence: 39..593

25  
30  
35  
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45  
1 11 21 31 41 51  
GAAAGCCTGC CAGCACTAT TCCACCTCCC AGCCCAGCAT GGCACCCCTG CTGCCCATCC 60  
GGACCTTGCC CTGTATCTCG ATTCTGCTGG CTCTGCTGTC CCCAGGGCTC GCAGACTTCA 120  
ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCT 180  
TGCCCCCTCG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGAGA GCCAATGACA 240  
GCAAGTGGT GACGTCCAGC TTGTGGTGC CTCCGTGCCG TGGCGCAGG GAAGTGGTGA 300  
GTGTGGTGA CAGTGGTGT GGTCTCACAG TCATCTGGCT CAGTGCATAC CAGGTGACAA 360  
ACCTCGTGCC AGGAACCAA TTCTACATT CCTACCTAGT GAAGAAGGGG ACAGCCACTG 420  
AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCCATTGGGC 480  
TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCAAGGT GCTGCTCTCT GTCCCATGT 540  
TCTGCTGGT GCTGGGCTTC ATCATTGCCC TGSCACTGGG CTCGCGCAAG TAAGGAGGTC 600  
TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACCA TCCAGCTCCC CAGCCCACT 660  
GCTCCAGGC CCCAGGCTTG TGGCTCCCTT GGTGCCCTCG CCTCCTCCTC CTGCCCTCCT 720  
CTCCCTAGA GCGCTCTCCT CCGTCTGTCC CTCTCCTTGC CCGCAGTGCC TCACCTTCCA 780  
ACACTCCATT ATTCTCTCA CCGCACTCCT GTCCAGATTG ACTTTCCTCC CATTTTACCA 840  
CTTTAAACAC CCCATAACA ATTCCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG 900  
GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

Seq ID NO: 173 Protein sequence  
Protein Accession #: NP\_006751.1

50  
55  
1 11 21 31 41 51  
MAPLLPIRTL PLILILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGGNATL 60  
MVRRANDSKV VTSSFVPPC RGRRELVSUV DSGAGFTVTR LSAQVNTLV PGTKFYISYL 120  
VKKGTATBSS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLI VLGFIIALAL 180  
GSRK

Seq ID NO: 174 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2733

60  
65  
70  
75  
80  
1 11 21 31 41 51  
ATGAAAGTTG GAGTGTCTG GCTCATTCTT TTCTTCACT TCACGTACGG CCACGGTGGC 60  
TTCTGGGGA AAAATGATGG CATCAAAACA AAAAAAGAAC TCATTGTGAA TAAGAAAAAA 120  
CATCTAGGCC CAGTCTGAAGA ATATCAGCTG CTGCTTCAGG TGACCTATAG AGATTCCAAG 180  
GAGAAAAGAG ATTTGAGAAA TTTTCTGAAG CTCTTGAAGC CTCATTATT ATGGTCACAT 240  
GGGCTAATTA GAATTATCAG AGCAAAGGCT ACCACAGACT GCAACAGCCT GAATGGAGTC 300  
CTGCAGTGA CTGTGAAGA CAGCTACACC TGGTTTCTCT CCTCATGCT TGATCCCGAG 360  
AACTGCTACC TTCACACGGC TGGAGCACTC CCAAGCTGTG AATGTCTAT CAACAACCTC 420  
AGCCAGAGTG TCAATTTCTG TGAGAGAACA AAGATTGGG GCACCTTCAA AATTATGAA 480  
AGTTTACAA ATGACCTTTT GAATTCATCT TCTGCTATAT ACTCCAAATA TGCAATGGA 540  
ATTGAATTC AACTTAAAA AGCATATGAA AGAATTCAAG GTTTTGAGTC GGTTCAGGTC 600  
ACCCAAATTC GAAATGGAAG CATCGTTGCT GGGTATGAAG TTGTTGGCTC CAGCAGTGCA 660  
TCTGAACCTG TGTACAGCAT TGAACATGTT GCGAGAGAAG CTAAGACAGC CCTTCAAG 720  
CTGTTTCCAT TAGAAGACGG CTCTTTCAGA GTGTTGCGAA AAGCCAGTG TAATGACATT 780  
GTCTTTGAT TTGGGTCCAA GGATGATGAA TATACCTGCG CCTGCAGCAG TGGCTACAGG 840  
GGAACATCA CAGCCAACTG TGAGTCTCT GGGTGGCAGG TCATCAGGGA GACTTGTGTG 900  
CTCTCTCTGC TTGAAGAAGT GAACAAGAA TTCAATGATG TTGTAGGCAA TGCCACTGAG 960  
GCAGCTGTGT CATCTCTTGT GCAAAATCTT TCTGTATCA TCGGCAAAA CCGTCAAC 1020  
ACAGTGGGGA ATCTGGCTTC GGTGGTGTG ATTCTGAGCA ATATTTATC TCTGTCACTG 1080  
GCCAGCCATT TCAGGGTGTG CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAA 1140  
ATCCTTAATT CAGCCTCAGT AACCAACTGG ACAGTCTTAC TGCGGGAAGA AAAGTATGCC 1200  
AGCTCAGCGT TACTAGAGAC ATTAGAAAAC ATCAGCACTC TGGTGCTCC GACAGCTCTT 1260  
CCTCTGAATT TTTCTCGGAA ATTCAATGAC TGGAAAGGGA TTCCAGTGAA CAAAAGCCAA 1320  
CTCAAAAGGG GTTACAGCTA TCAGATTAAA ATGTGTCCCC AAAATACATC TATTCCTATC 1380  
AGAGGCCCGT TGTAAATGGG GTCAGACCAA TTCCAGAGAT CCCTTCAGA AACTATTATC 1440

5 AGCATGGCCT CGTTGACTCT GGGGAACATT CTACCCGTTT CCAAAAATGG AAATGCTCAG 1500  
 GTCAATGGAC CTGTGATATC CACGGTTATT CAAAACATTT CCATAAATGA AGTTTTCTTA 1560  
 TTTTTCCTCA AGATAGAGTC AAAACCTGAGC CAGCCTCATT GTGTGTTTGG GGATTTTCAGT 1620  
 CATTTCAGCT GGAAACGATGC AGGCTGCCAC CTAGTGAATG AAACCTCAAGA CATCGTGACG 1680  
 TGCCAAATGTA CTCACITGAC CTCTCTCTCC ATATTGATGT CACCTTTTGT CCCCTCTACA 1740  
 ATCTTCCCCG TTGTAAATATG GATCACTATAT GTGGGACTGG GTATCTCCAT TGGAAAGTCTC 1800  
 ATTTTATGCC TGATCATCGA GGCTTTGTTT TGGGAAGCAGA TTAATAAAG CCAAACTCTC 1860  
 CACACACGTC GTATTTGTCAT GGTGAACATA GCGCTGTCCC TCTTGATTGC TGATGTCTGG 1920  
 10 TTTATTGTTG GTGCCACAGT GGACACCAAG GTGAACCCCT CTGGAGTCTG CACAGCTGCT 1980  
 GTGTTCTTTA CACACTTCTT CTACCTCTCT TGTGTTCTCT GGATGCTCAT GCTTGGCATC 2040  
 CTGCTGGCTT ACCGGATCAT CCTGTGTTTC CATCACATGG CCCAGCATTT GATGATGGCT 2100  
 GTTGGATTTT GCGTGGGTTA TGGGTGCCCT CTCATTATAT CTGTCAATAC CATTGCTGTC 2160  
 ACGCAACCTA GCAATACCTA CAAAAGGAAA GATGTGTGTT GGCTTAACCT GTCCAATGGA 2220  
 15 AGCAAAACCAC TCCTGGCTTT TGTGTGCCCT GCATCGGCTA TTGTGGCTGT GAACTTCGTT 2280  
 GTGGTGTGTC TAGTTCTCAC AAAGCTCTGG AGGCGOAGCT TTGGGGAAAG ACTGAGTCGG 2340  
 GATGACAAGG CCACCATCAT CCGGTGGGG AGAGCCCTCT TCATCTGAC CCTCTGCTA 2400  
 GGGCTCACCT GGGGCTTTGG AATAGGAACA ATAGTGGACA GCCAGAATCT GGCTTGGCAT 2460  
 GTTATTTTGG CTTTACTCAA TGCAATCCAG GGATTTTTTA TCTTATGCTT TGGAAATCTC 2520  
 20 TTGGACAGTA AGCTGGGACA ACTTCTGTTT AACAAAGTGT CTGCCTTAAG TTCTTGAAG 2580  
 CAAACAGAAA AGCAAACTC ATCAGATTTA TCTGCCAAAC CCAATTTCTC AAAGCCTTTC 2640  
 AACCCACTGC AAACAAAGG CCATTATGCA TTTTCTCATA CTGGAGATTC CTCGACCAAC 2700  
 ATCATGCTAA CTCAGTTTGT CTCAATGAA TAA

Seq ID NO: 175 Protein sequence  
Protein Accession #: Eos sequence

30 1 11 21 31 41 51  
 MKVGVWLWLS FPTFTDGHGG FLGKNDGIKT KKEIIVNKKK HLGPEVEYQL LLQVTRYDSK 60  
 EKRDRLNFKL LKPPPLLSH GLIRIIRAKA TTDNSNLGV LQCTCEDSYT WFPSCLDPO 120  
 NCYLITAGAL PSCECHLNL SQSVNFCERT KIWGTFKINE RFTNDLLNSS SAIRYSKYANG 180  
 IBIQLKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSEA SELLSAIEHV AEKAKTALHK 240  
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35 CTTGCCCTGC TGACAGACCT TGAATATGTT AGGCTGGGCG ATTCTTTACA CCTACAAAA 1320  
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50 Seq ID NO: 179 Protein sequence  
Protein Accession #: NP\_001901.1

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QPSQSSTYSQ PQQSFSIQYG TGLSLGIIGA DQVSVGLTV VQQPFGESVT EPGQTFVDAB 180  
FDGLILGLVF SLAVGVVTFV FDNMMQNLV DLPMPFSVMS SNPEGAGSE LIFGGYDHS 240  
60 PSLANVVFV TKQAYWQIAL DNIQVGGTVM FCSGQALV DTGTSILITGP SDKIRQLQNA 300  
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65 Seq ID NO: 180 DNA sequence  
Nucleic Acid Accession #: NM\_018058.1  
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Seq ID NO: 181 Protein sequence  
Protein Accession #: NP\_060528.1

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PRDIASPKFS MSPSPRTVIT ADFDNDQBLE IFFNNIAYRS SSANRLFRVI RREHGDPLIE 180
ELNPGDALEP EGRGTGGVVT DFDGDMLDL ILSHGSEMAQ PLSVFRGNQG FNNNWLRVVP 240
RTRVGAPARG AKVVLVYTKS GAHLRIIDGG SYLCEMEPV AHFGLGIDEA SSVEVTWPDG 300
KMSVSNVAGS EMNSVLEILY PRDEDTLQDP APLETMPNAS SSHSCALETS PYVSTFMEAT 360
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Coding sequence: 1..1962

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GGAOGCTACT CTATCTACAT TGCCAATTAC GCTACGGTA ATGTGGGCC TGATGCCCTC 600
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CTGTCTAGGG CTGGGCTCAG CAAATATACA GGGGGCCGAG GOGTCAAGGT GGGCCCATC 720
CTCAGCAGCA GTGCTCGGA TATCTCTGCG GACATGAGA ATGGGCTTAA CTTCCTTTTC 780
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CTCGGCCAGT CACCGGGGCC CCGCCCCACC ACCCCACCG CTGCTGCTGC CACTGCGCT 1860
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Seq ID NO: 183 Protein sequence  
Protein Accession #: CAC08451

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Seq ID NO: 184 DNA sequence  
Nucleic Acid Accession #: FGENESH  
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Seq ID NO: 185 Protein sequence

Protein Accession #: FGENESHH

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KVVLTKKSG AHLRIIDGGS GYLCEMEPVA HFLGKDEAS SVEVTNPDGK MVSERNVASGE 1440
MNSVLEILYP RDEDLQDPA PLECGQGFSP QENGHOMDTN ECIQFPFVCP RDKPVCVNTY 1500
GSYRCRTNKK CSRGYEPNED GTACVGTGLG SRHTMTWKPR PKKELQLSQG ICTPVVWSFPL 1560
PGCRLLLRRA QLQAAPSTLL QKAPGIPEAQ VYBQDQE

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Seq ID NO: 186 DNA sequence

Nucleic Acid Accession #: NM\_000584.1

Coding sequence: 75..374

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65  
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1 11 21 31 41 51
AGCAGAGCAC ACAAGCTTCT AGGACAAGAG CCAGGAAGAA ACCACCGGAA GGAACCATCT 60
CACTGTGTGT AAACATGACT TCCAAGCTGG COGTGGCTCT CTTGGCAGCC TTCCTGATT 120
CTGCAGCTCT GTGTGAAGGT GCAGTTTTCG CAAGGAGTGC TAAAGAACTT AGATGTCAGT 180
GCATAAAGAC ATACTCCAAA CCTTTCACCC CCAAATTAT CAAAGAACTG AGAGTGATTG 240
AGAGTGGACC ACACTGCGCC AACACAGAAA TTATTGTAAA GCTTCTGAT GGAAGAGAGC 300
TCTGTCTGGA CCCAAGGAA AACTGGGTGT AGAGGGTTGT GGAGAAGTTT TTGAAGAGGG 360
CTGAGAATTC ATAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT 420
GAAACTTCAA GCAAACTTAC TTCAACACTT CATGTATTGT GTGGGTCTGT TGTAGGGTTG 480
CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTCA GTAAACAATG AATAGTTTTT 540
CATTGTACCA TGAATATCC AGAACATACT TATATGTAAA GTATTATTTA TTTGAATCTA 600
CAAAAAACAA CAATAATATT TTAAATATAA GGATTTTCCT AGATATTGCA CGGGAGAATA 660
TACAAATAGC AAAAATGAGC CAAGGCCCAA GAGAATATCC GAACTTTAAT TTCAGGAATT 720
GAATGGGTTT GCTAGAATGT GATATTGAA GCATCACAATA AAATGATGG GACAATAAAT 780
TTTGCCATAA AGTCAAAATT AGCTGGAATT CCTGGATTTT TTTCTGTAAA ATCTGGCAAC 840
CCTAGTCTGC TAGCCAGGAT CCACAAGTCC TTGTTCCTCT GTGCCTTGGT TTCTCCITTA 900
TTTCTAAGTG GAAAAAGTAT TAGCCACCAT CTTACCTCAC AGTGATGTTG TGAGGACATG 960
TGGAGAATCT TTAAGTTTTC TCATCATAAC ATAAATTATT TTCAAGTGA ACTTATTAAC 1020
CTATTATTAT TTTATGTATT TATTTAAGCA TCAAAATATT GTGCAAGAA TTGGAATAAT 1080
AGAAGATGAA TCATTGATTG AATAGTTATA AAGATGTTAT AGTAAATTTA TTTTATTTA 1140
GATATTAAAT GATGTTTAT TAGATAAAAT TCAATCAGGG TTTTATGATT AAACAAAGAA 1200
ACAAATGGGT ACCCAGTTAA ATTTTCATTT CAGATAAACA ACAATAAATT TTTTAGTATA 1260
AGTACATTAT TGTTTATCTG AAAGTTTAA TTGAACATAA AATCCTAGTT TGACTACTCC 1320
AGTCTGTGCA TTGCAGCTG TGTGGTAGT GCTGTGTTGA ATTACGGAAT AATGAGTTAG 1380
AACTATTAAA ACAGCCAAA CTCCACAGTC AATATTAGTA ATTTCTTGCT GGTGAAACT 1440
TGTTTATTAT GTACAAATAG ATTCTTATA TATTATTAA ATGACTGCAT TTTTAAATAC 1500

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AAGCTTTAT ATTTTAACT TTAAGATGTT TTTATGTGCT CTCCAAATTT TTTTACTGT 1560  
 TTCTGATTGT ATGGAATAT AAAAGTAAAT ATGAAACATT TAAATATATA TTGTGTGCA 1620  
 AAGTAAAAAA AAAAAAAA

5 Seq ID NO: 187 Protein sequence  
 Protein Accession #: NP\_000575.1

1 11 21 31 41 51  
 10 MTSKLAVALL AAFILISAALC EGAVLPRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH 60  
 CANTEIIVKL SDGRELCCLDP KENWVQRVVE KFLKRAENS

15 Seq ID NO: 188 DNA sequence  
 Nucleic Acid Accession #: NM\_003661.1  
 Coding sequence: 1..1152

1 11 21 31 41 51  
 20 ATGAGTGCAC TTTTCCTTGG TGTGGGAGTG AGGCGAGAGG AAGCTGGAGC GAGGGTGCAA 60  
 CAAAACCTTC CAAGTGGGAC AGATACTGGA GATCCTCAAA GTAAGCCCTT CGGTGACTGG 120  
 GCTGCTGGCA CCATGGAGCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC 180  
 AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC 240  
 GGATTCTGTG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300  
 25 GACACCTCTG CAAGACAAAT GATCATGAAA GACAAAACT GGCACGATAA AGGCCAGCAG 360  
 TACAGAAACT GGTTCCTGAA AGAGTTTCTT CGTTTGAAAA GTGAGCTTGA GGATAACATA 420  
 AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAGGCCAC CACCATCGCC 480  
 AATGTGTGTG CTGGCTCTCT CAGCATTTCCT TCTGGCATCC TGACCTCGT CGGCATGGGT 540  
 CTGGCACCTT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600  
 ATCACAGCCG CTTTGACCGG GATTACACAG AGTACCATGG ACTACGGAAA GAAGTGGTGG 660  
 30 ACACAGCCCC AAGCCCAAGA CCTGGTCATC AAAAGCCTTG ACAAAATTGA GGAGGTGAGG 720  
 GAGTTTTTGG GTGAGAACAT ATCCAACCTT CTTTCTTAG CTGGCAATAC TTACCAACTC 780  
 ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840  
 GTACCGCATG CCTCAGCCTC ACGCCCCGGG GTCACCTGAG CAATCTCAGC TGAAAGCGGT 900  
 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAA TGAGCAGAGG AGTCAAGCTC 960  
 35 AGCGATGTGG CCCCTGTAA GCTTCTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020  
 TCAGAGCACT TACATGAGGG GGCAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080  
 CAGGAGCTGG AGGAAGAGCT AAACATTCTC AACAATAATT ATAAGATTCT GCAGGCGGAC 1140  
 CAAGAAGCTG GA

40 Seq ID NO: 189 Protein sequence  
 Protein Accession #: NP\_003652.1

1 11 21 31 41 51  
 45 MSALFLGVGV RAEAGARVQ QNVPSGTDG DPQSKPLGDW AAGTMDPES IFIEDAIKYF 60  
 KEKVSTQMLL LLLTDNEAWN GFVAAELPR NEADELRKAL DNLAQIMIM DRNWHDKGQ 120  
 YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLIS SGILTLVGMG 180  
 LAPFTGGSL VLEPGMBLG ITAALTGITS STMDYGKQW TQAQHLVI KSLDKLKEVR 240  
 50 EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG 300  
 EQVERVNEPS ILERSMRGKVL TDVAPVSFPL VLDVVYLVYE SKHLHEGAKS ETAELKIVA 360  
 QELEEKLNIL NNNYKILQAD QEL

55 Seq ID NO: 190 DNA sequence  
 Nucleic Acid Accession #: NM\_014452.1  
 Coding sequence: 1..1968

1 11 21 31 41 51  
 60 ATGGGACCTT CTCCGAGCAG CAGCAACGCC CTGCTCTCTT GCAGCCGCAT CGCCCGCCGA 60  
 GCCACAGCCA CGATGATCGC GGGCTCCCTT CTCTGCTTGG GATTCTTTAG CACCACACA 120  
 GCTCAGCCAG AACAGAAAGC CTGGAATCTC ATTGGCACAT ACOGCCATGT TGACCGTGGC 180  
 ACOGGCCAGG TGCTAACCTG TGACAAGTGT CCAGCAGGAA CCTATGTCTC TGAGCATTTG 240  
 ACCAACACAA GCCTGCGCGT CTGCAGCAGT TGCCCTGTGG GGACCTTTAC CAGGCATGAG 300  
 65 AATGGCATAG AGAAATGCCA TGACTGTAGT CAGCCATGCC CATGGCCAAT GATTGAGAAA 360  
 TTACCTTTGG CTGCCCTGAC TGACCGAGAA TGCACTTGCC CACCTGGCAT GTTCCAGTCT 420  
 AACGCTACCT GTGCCCCCA TACGGTGTGT CCTGTGGGTT GGGGTGTGGG GAAGAAAGGG 480  
 ACAGAGACTG AGGATGTGCG GTGTAAGCAG TGTGCTCGGG GTACCTTCTC AGATGTGCTT 540  
 TCTAGTGTGA TGAATGCGAA AGCATACACA GACTGTCTGA GTCAGAACCT GGTGTGATC 600  
 70 AAGCOGGGGA CCAAGGAGAC AGACAAGTTC TGTGGCACAC TCCGTCCTT CTCCAGCTCC 660  
 ACCTCACCTT CCCCTGGCAC AGCCATCTTT CCAAGCCCTG AGCAGATGGA AACCCATGAA 720  
 GTCCCTTCTT CCACCTATGT TCCCAAGGCC ATGAATCAA CAGAATCCAA CTCTCTGCTC 780  
 TCTGTAGACG CAAAGGTACT GAGTAGCATC CAGGAAGGGA CAGTCCCTGA CAACACAAGC 840  
 TCAGCAAGGA GGAAGGAAGA CGTGAACAAG ACCCTCCCAA ACCTTCAGGT AGTCAACCA 900  
 75 CAGCAAGGCC CCCACACAG ACACATCTTG AAGCTGTGCG CGTCCATGGA GGCCACTGGG 960  
 GCGAGAGAGT CCAGCAGGCC CATCAAGGCC CCCAAGAGGG GACATCTTAG ACAGAACCTA 1020  
 CACAAGCACT TTGACATCAA TGAGCATTTG CCTTGGATGA TTGTCTTTT CCTGCTGCTG 1080  
 GTGCTGTGTG TGATTGTGT GTGCAGTATC CGGAAAAGCT CGAGGACTCT GAAAAGGGG 1140  
 CCCCGCAGG ATCCAGTGC CATTGTGGAA AAGGCAGGGC TGAAGAAATC CATGACTCCA 1200  
 80 ACCCAGAAAC GGGAGAAATG GATCTACTAC TGCAATGGCC ATGGTATGGA TATCTGAAG 1260  
 CTTGTAGCAG CCCAAGTGGG AAGCAGTGG AAAGATATCT ATCAGTTTCT TTGCAATGCC 1320  
 AGTGAGAGGG AGGTGTCTGC TTTCTCCAAT GGTACACAG CCGACCAOGA GCGGGCTTAC 1380  
 GCAGCTCTGC AGCACTGGAC CATCGGGGGC CCGAGGCCA GCCTGCCCCA GCTAATPAGC 1440  
 GCCCTGCGCC AGCACCGGAG AACAGATGTT GTGAGAAGA TTGTTGGGCT GATGGAAGAC 1500  
 ACCACCCAGC TGGAACCTGA CAAACTAGCT CTCCGATGA GCCCAGGCC GCTTAGCCCG 1560

5 AGCCCCATCC CCAGCCCCAA CGCGAAACTT GAGAATTCOG CTCTCCTGAC GGTGGAGCCT 1620  
 TCCCCACAGG ACAAGAACAA GGGCTTCTTC GTGGATGAGT CGGAGCCCTC TCTCCGCTGT 1680  
 GACTCTACAT CCAGCGGCTC CTCCGCGCTG AGCAGGAACG GTTCTCTTAT TACCAAGAA 1740  
 AAGAAGGACA CAGTGTTCOG GCAGGTACGC CTGGACCCCT GTGACTTGCA GCCTATCTTT 1800  
 GATGACATGC TCCACTTTCT AAATCCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG 1860  
 GCTGAGGACA AACTAGACCG GCTATTGCAA ATTATTGGAG TCAAGAGCCA GGAAGCCAGC 1920  
 CAGACCCCTCC TGGACTCTGT TTATAGCCAT CTTCCTGACC TGCTGTAG

10 Seq ID NO: 191 Protein sequence  
 Protein Accession #: NP\_055267.1

15 1 11 21 31 41 51  
 MGTSPSSSTA LASCRIARR ATATMIAGSL LLLGFLSTTT AQPBOQKASNL IGTYRHVDRA 60  
 TGQVLTCDKC PAGTYVSEHC TINTSLRVCS CPVGTPTRHE NGIEKCHDCS QPCFPWPIEK 120  
 LPCAALTDRE CTCPPGMFQS NATCAPHTVC PVGNVGRKKG TETEDVRRCQ CARGTFSQVP 180  
 SSVMKCKAYT DCLSNLVIV KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPEHMETHE 240  
 VPSSTYVPKG MNSTESNSSA SVRPKVLSSI QEGTVPDNTS SARGKEDVKN TLPLNLQVNVH 300  
 QQGPHHRHIL KLLPSMEATG GEKSSSTPIKG PKRGHPRQNL HKHFDINEHL PWMIVLFLLL 360  
 20 VLVVIVVCSII RKSSRTLKKG PRQDPSAIVE KAGLKSMTP TQNRKWIYY CNGHGIDILK 420  
 LVAAQVGSQW KDIFYFLCNA SEREVAAPSN GYTADHERAY AALQHWITIRG PEASLAQLIS 480  
 ALRQHRNDV VEKIRGLMED TTQLETDKLA LEMSPSPISP SPIPSNAPL ENSALLTVEP 540  
 SPQDKNKGF VDESEPLLR DSTSSGSSAL SRNGSFITKE KKDITVLRQVR LDPDCLQPIF 600  
 25 DDMLEHFNPE ELRVIEEIPQ AEDKLDRLFE IIGVKSQEAS QTLDSVYSH LPDLL

Seq ID NO: 192 DNA sequence  
 Nucleic Acid Accession #: XM\_044533  
 Coding sequence: 238..2751

30 1 11 21 31 41 51  
 GCTCTGCCCA AGCOCAGGCT GCGGGGCGCG CGCGGGCGCG AGGACTGCGG TGCCCCGCGG 60  
 AGGGGCTGAG TTTGCCAGGG CCGACTTGAC CCTGTTTCCC ACCTCCCGCC CCCCAGGTCC 120  
 35 GAGAGCGGGG GCGCCCGGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCGCCCGGTG 180  
 AGTCGCGCGG AGCCACCTGA GCGCGAGCGG CGGGACACCG TCGCTCCTGC TCTCCGAATG 240  
 CTGCGCACCG CGATGGGCTT GAGGAGCTGG CTCGCGCGCC CATGGGCGCG GCTGCGCGCT 300  
 CGGCCACCGC TGCTGCTGCT CCTGCTGCTG CTGCTCCTGC TGCAGCGCGC GCCTCCGACC 360  
 TGGGCGCTCA GCGCCCGGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCG ATTCTCAGCA 420  
 40 TTGGAAGCTG AACACATCTC CAACTACACA GCGCTTCTGC TGAGCAGGGA TGGCAGGACC 480  
 CTGTAGCTGG GTGCTGAGA GCGCCTCTTT GCACTCAGTA GCAACCTCAG CTCTCTGCCA 540  
 GCGCGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCGA AGAAGAAACA GCAGTGCAAG 600  
 TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAGACTACA TCAAGATCCT CCGTCGCGTC 660  
 AGCGGCAGTC ACCTGTTTCA CTGTGGCACA GCAGCCTTCA GCGCCATGTG TACCTACATC 720  
 45 AACATGGAGA ACTTACCCCT GGCAAGGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780  
 AAGGGCGGTT GTCCCTTCGA CCGGAATTC AAGTCCACTG CCCTGGTGTG TGATGCGGAG 840  
 CTCTACACTG GAACAGCTAG CAGCTTCCAA GGGAAATGACC CGGCCATCTC GCGGAGCCAA 900  
 AGCCTTGCGC CCACCAAGAC CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG 960  
 GCCTCAGCTC ACATTCCTGA GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC 1020  
 50 TTTTCTCTCA GCGAGACTGG CCAGGAATTT GAGTCTCTTG AGAACAACCAT TGTGTCCGCG 1080  
 ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC 1140  
 TCCTTCTTCA AGGCCAGCTG GCTGTGCTCA CGGCCGAGCG ATGGCTTGCC CTTCACAGTG 1200  
 CTGCAAGATG TCTTCAAGCT GAGCCCCAGC CCGCAGGACT GCGGTGACAC CCTTTTCTAT 1260  
 GGGGTCTTCA CTTCAGAGCT GCACAGGGGA ACTACAGAAG GCTCTGCGGT CTGTGTCTTC 1320  
 55 ACAATGAAGG ATGTGACAGG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CGGTGAGACA 1380  
 CAGCAGTGGT ACACCGTGAC CCACCCGGTG CCCACACCCC GGCTTGGAGC GTGCATCACC 1440  
 AACAGTGCCC GGGAAAGGAA GATCAACTCA TCCCTGCAGC TCCAGAGCGG CGTGTGAAC 1500  
 TTCTCAAGG ACCACTTCTT GATGGAAGGG CAGGTCCGAA GCGCATGCT GCTGTGAGC 1560  
 CCGCAGGCTC GCTACAGCG GGTGGCTGTA CACCGGTGCC CTGGCTGCA CACACCTTAC 1620  
 60 GATGTCTCTT TCCTGGGCAC TGGTGACGGC CGCTCCACA AGGCAGTGAG GTGGGCCCC 1680  
 CGGGTGACA TCATTAGGGA GCTGCAGATC TTCTCATCGG GACAGCCCGT GCAGAACTG 1740  
 CTCTTGAGCA CCCACAGGGG GCTGTGTAT GCGGCTCAC ACTGCGGCGT AGTCCAGGTG 1800  
 CCCATGGCCA ACTGCAGCT GTACAGGAGC TGTGGGACT GCCTCTCTCG CCGGACCCCC 1860  
 TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CAGTCAAGC TCTACCAGCC TCAGCTGGCC 1920  
 65 ACCAGGCGGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGGTCT 1980  
 TCGTTGTGT CCGGCTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTT 2040  
 CAGCCCAACA CAGTGAACAC TTTGGCCTGC CGCTCCTCT CCAACCTGGC GACCCGACTC 2100  
 TGGTACGCA AGCGGGCCCC CGTCAATGCC TGGGCTCTCT GCCAGTGCT ACCCACTGGG 2160  
 GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGTGGTC ACTAGAGGAG 2220  
 70 GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAAGGTTGG TGGAGGACGG GGTGGCAGAC 2280  
 CAAACAGATG AGGGTGGCAG TGTACCGGTC ATTATCAGCA CATCGGTGT GAGTGCACCA 2340  
 GCTGGTGAGA AGAGGCACTG GGGTGACAGC AGGTCTTACT GGAAGGAGTT CCGTGGTATG 2400  
 TGCAGGCTCT TGTGCTGAGC CGTGTGCTC CAGTTTAT TCTTGTCTTA CCGGCACCGG 2460  
 75 AACAGCATGA AAGTCTTCTT GAAGCAGGGG GAATGTGCCA GCGTGACCCC CAAGACTGTC 2520  
 CCTGTGTGTC TGCCCCCTGA GACCCGCCCC CTCAAGGCGC TAGGGCCCCC TAGCACCCCG 2580  
 CTGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640  
 GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCC TGGAGGTATC CCAAGTGTGC 2700  
 CCGCGGCCCC GGGTCCGCTT TGGCTCGGAG ATCGTGACT CTGTGTGTGT AGAGCTGACT 2760  
 80 TCCAGAGGAG GCTGCCCTGG CTTCAGGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820  
 TCCTCTCGC TCTGTCTTTC GTGGAACACG ACCGTGTTGC CCGGCCCTTG GGAGCCTTGG 2880  
 GGCCAGCTGG CCTGTGCTTC TCCAGTCAAG TAGGGAAGCT CCAACACCCC AGACACCCAA 2940  
 ACAGCGGTGG CCGCAGAGGT CTTGGCCAAA TATGGGGGCC TGCTAGGTT GGTGGAACAG 3000  
 TGCTCTTAT GTAAACTGAG CCCTTTGTTT AAAAAAAT TCCAAATGTG AAAGTGAAT 3060  
 GAGAGGGAAG AGATAGCATG GCATGCAGCA CACAGCGCTG CTCAGTTTCA TGGCCTCCCA 3120  
 GGGGTGCTGG GGATGCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAAC CCTCACCAAC 3180



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TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240
CAGGACCAGC TTGGGCTGCG TGGCTTCTGC CTGCGCAGTC AGCCGAGGAT GTAGTGTGTG 3300
CTGCCGTCGT CCCACCACCT CAGGGACCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA 3360
GGTCTTGGGC TGGGACCCAA CTCTGGAGCC TTTCAGGCT GTATCAGGCT GTGGCCACAC 3420
GAGAGGACAG CCGAGAGTCA GGAGAGATTT CGTGACAATG TACGCCCTTC CCTCAGAAAT 3480
CAGGGAAGAG ACTGTGCGCT GCCTTCTCC GTTGTGCGT GAGAACCCTG GTGCCCTTC 3540
CCACCATATC CACCTCTGCT CCATCTTTGA ACTCAAACAC GAGGAACATA CTGCACCTG 3600
GTCCTCTCCC CAGTCCCAGC TTCACCTCC ATCCCTCACC TTCCTCCACT CTAAGGGATA 3660
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGTT TTTATACATT TTTTAATAAG 3720
ATGCACTTTA TGTCAATTTT TAATAAAGTC TGAAGAATTA CTGTTT

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Seq ID NO: 193 Protein sequence  
Protein Accession #: XP\_044533.3

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1 11 21 31 41 51
| | | | |
MLRTAMGLRS WLAAPMGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120
SFKGKDPQRD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY INMENFTLAR DEKGNVLLED 180
GKGRCPDFPN FKSTALVVDG ELYTGTVSF QGNDPAISRS QSLRPTKTES SLNLQDPAP 240
VASAYIPESL GSLQGDDEKI YFPFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
TSFLKAQLLC SRPDGPPFN VLQDVPTLSP SPQDWRDTLF YGVPTSQWHR GTTEGSAVCV 360
FTMKDVQRVF SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
NFLKDHPLRV GQVRSRMLLL QPQARYORVA VHRVPLHHT YDVLPLGTGD GRLEKAVSVG 480
PRVHIIEBLQ IFSSGQPVQN LLLDTHRGLL YAASHGVVQV VPMANCSLYR SCGDCLLARD 540
PYCAWSSGSC KHVSYLQPLQ ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQVQ 600
FQPNVTNTRA CPLLSNLATR LMLENGAPVN ASASCHVLPT GDLLLVTQQL LGEPQCHSLE 660
EGFQQLVASY CEPVEDGVA DOTDEGGSVP VIISTRVSA PAGGKASWGA DRSYWKFLV 720
MCTLFVLAVL LFLVPLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNLGLPFPST 780
PLDHRGYQSL SDSPPGSRVP TESEKRPLSI QDSFVEVSPV CPRPRVRIGS EIRDSVV

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Seq ID NO: 194 DNA sequence  
Nucleic Acid Accession #: NM\_022819.1  
Coding sequence: 1..635

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1 11 21 31 41 51
| | | | |
ATGGCAGATG GGGCAAAGGC CAACCCCAAA GGGTTCAAAA AGAAGGTGCT GGATAGATGC 60
TTCTCTGGGT GGAGGGGCC ACCTCTCGGG GCCTCTCTGT CTCAAGAAC CTCAGGCTCT 120
AGCCTGGGTA TGAAGAAGTT CTTCACCGTG GCCATCCTTG CTGGCAGCGT TCTGTCCACA 180
GCTCAGCGCA GCCTGTCTCAA CCTGAAGGCC ATGGTGGAGS CCGTCACAGG GAGGAGCGCC 240
ATCCTGTCTT TCGTGGGCTA CGGTTGCTAC TGTGGGCTGG GGGGCCGTGG CCAGCCCAAG 300
GATGAGGTGG ACTGTGTGCTG CCACGCCAC GACTGCTGCT ACCAGGAACCT CTTTGACCAA 360
GGCTGTACCC CCTATGTGGA CCACTATGAT CACACCATCG AGAACACAC TGAGATAGTC 420
TGCAGTGACC TCACACAGAG AGAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG 480
GTTCTGTGCC TCATGAACCA GACGTACCGA GAGGAGTACC GTGGCTTCTT CAATGTCTAC 540
TGCCAGGGCC CCACGCCCAA CTGCAGCATC TATGAACCGC CCCCTGAGGA GGTCACTCTG 600
AGTCACCAAT CCCCAGCGCC CCCCGCCCT CCCTAG

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Seq ID NO: 195 Protein sequence  
Protein Accession #: NP\_073730

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1 11 21 31 41 51
| | | | |
MADGAKANPK GKPKKVLDRG FSGWRGPRFG ASCPSRTSRS SLGKKKFTTV AILAGSVLST 60
AHGSLNLKLA MVEAVTGRSA ILSFVGYGCV CGLGGRGQPK DEVDCCHAH DCCYQELFDQ 120
GCHPYVDHYD HTIENNTIEV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR EBYRGFLAVY 180
CQGPTFNCIS YEPFPEVTC SHQSPAPPAP P

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Seq ID NO: 196 DNA sequence  
Nucleic Acid Accession #: XM\_028196.1  
Coding sequence: 1315..1791

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1 11 21 31 41 51
| | | | |
GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
GTGTGTGTGT GTCTGAGATC ATGGCAGGCT CCCCTTCTGT CTGTCTCCTT GCTCTGCCCC 120
AGACTGGGGG CTTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
ATGGCCTGGG CTGGGCCCTT GAGGCGAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240
CTCTTGTGGG CAAGCAGGG GAGGCGCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300
CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCCTG 360
GGGTACACCT AGGCCCATG TAGCACCTTG GTTCCCTCGC CTGTAGGTGA CAGGAGCCAG 420
CCAGCCAGG TGTGCTCCTT CCCCAGGCC TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480
GGCCGCCCTT ACCTTCTCTT CCACCCACAT GCGCAAGGGT GGCCAGGCAG GCAGTGGGAC 540
GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGAATGTTT TGGCCGCTCC CAGCTGCACC 600
CTGCCCTTAC CTGACACAC CACACCTTCA TCCTCAGGCG CTGGGCGCTT GAGCCCTGCT 660
CAGGAATGCA CCTTATGCCC AGGCCCTGCT AGTGAAGTCC GCGCACAGCC AGCCCTGCTC 720
CTCCCGCAT GACCTGCGAG ACCCTCTGCG GCTTCAAGT TCCTGGGGGC TGCAGTGAAC 780
ATGCTCCACC TGCATGGCTG GCAAAACATG GTGGGCCCAA GCTGTGTGTC GTGCTGGGGT 840
AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGATATGAG TGGGACCCCC 900
AGGCAGGGCC CAGGGTCCAG GGCCAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCTGG 960
TGGAGGACGC ATCTCAAGT GGGGGCAAGG GTGCTCTGAG GTCCGTTGAA GGCAGGGACT 1020
AGGCTGCCCA GGCCTGCTT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG 1080
GCTGGGCCTG GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCTTTCAG 1140

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CTTCTGCTG CACAGAACCC TCGCCCCG CACCCCGTG CTGCTCTCTT GCCCTGGCAG 1200  
 ACCCAGCACT GGCTGCTGCT AGTCAGATGG GGTAGCCGGC AGGGGCGGGA GGGGCCACCC 1260  
 TCCCAGCTGA CCCAGCCTCC TGGGCCGCTT CTTCACAAAC AGCAGGGTAG AAAGATGGGG 1320  
 CACCCACAGC TCTCTCCAG TGCCTCCGCT CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380  
 ATTCCAGACC TTGTGCGCGG GACCCCTGT GAGTTGTGGG ATTCCCAGA GGGGTGTGGG 1440  
 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCTCTACC 1500  
 CCAGGGCCCC GCTGGGCTCT CATGCGCGGC GCCCTTGCGG CGGGCGTCTT CCTCGTCTCC 1560  
 TGCTCTCTCT GTGTGCTGCT CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGGACAAG 1620  
 GAGTCCGTGG GTCTGGGCGG TGCCCGCGGC ACCACCACCA CCCACTGGT GAGGAGCGGC 1680  
 TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740  
 GCGGAGTTCA GCCCCAGGGA TGGTTTAAAC CCCACAGAGG CAGGGGCTTG AGGACCTTCC 1800  
 TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCCAT 1860  
 GGGCCCGAGG GAGCCACAGC GGGTCTCTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920  
 TTTGGGTGGG TTTGGGCGGT CTCACAGAGC GAAGCCGAGG ATTTGTGCTT GTTGGGTGGC 1980  
 CTGGCTGGA GGGGGGGGGT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCACAGG 2040  
 CTCTGATGAG GCATGATGTC AGCACCACTT GCCCTTGTCT CCACTCACT CCAGGTGCAA 2100  
 CCTGATGTGG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCCGTGAG 2160  
 CTCTCCCTGG AGTTGCACTT TGAAGCCAG GAGGTGAAGG GCGCCGCTGC GCAGGACAG 2220  
 OGGTTCTGCG AGTTTCCGGA AAGGGTGAOC GGGGAAGGGC AGACCCCATG CCTGGGTGG 2280  
 TGGGAGCTGA ACAGGGCAGG GGCCTTGGC TGAGCCACCC CGCTGGCTC CCAGATCAGG 2340  
 GTGGGCTGAG GGCAGGCAGC CGACCTGAGG CCTGGGGGCA CGTGGAGCC CTATGCCCGG 2400  
 GTCAGCGTCT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGACCG AGGCACGCTC 2460  
 TGCCCGGTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGATGCTC GGCTGGGTGG 2520  
 GCTGCTGCGG CTGATGCGG CTGGGCTGGG TGCGCTGGG CAGCTGGGTG GGCTGGGCA 2580  
 GCTGGGTGGG CCTGAGCTAG GGCAGCAGGG CCTGGCTCAC GCGCTGCTCT CAGATCCCGC 2640  
 AGGCGGAGCT GCCAGGGGCC ACCCTGCAGG TGCACTTTT CAACTTCAAG CGCTTCTCGG 2700  
 GGCATGAGCC CCTGGGTGAG CTCGCTGCTG CACTGGGCAC CGTGGATCTG CAGCATGTTT 2760  
 TGGAGCACTG GTACCTGCTG GGCCTGCGCG CTGCCATCA GGTGAGGTGC TGGTCAACAG 2820  
 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC 2880  
 CTGATGGGCA GCATTTTCGG GGTCTGAGC CCCAACTCGG CCAGAATCAC CCTCCCGGGC 2940  
 TGAAGCCCTT CTGCTGCTCC ACAGCCCGAG CAGGTGCGGG AGCTGTGCTT CTCTCTCGG 3000  
 TACGTGCCCA GCTCAGCCG GCTGACCGTG GTGGTGTCTG AGGCTCGAGG CCTGGTCCA 3060  
 GGACTTGCAG AGCCCTACGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG 3120  
 AGAAAGACAG CCACCAAAA GGCACCGCG GCCCCTACT TCAATGAGGC CTTCACCTTC 3180  
 CTGGTGCCCT TCAGCCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GGAACGCGAG 3240  
 CTGCCGCTCC GAATCAGACC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300  
 CCCCCTGACG ACTGGGCGA CATGCTGGCC CAOCGCGGC GGCCCATTTG CCAGCGGCAC 3360  
 CCCCCTGCGC CAGCCAGGGA GGTGGACCGC ATGCTGGGCC TGACGCCCG CCTTCGCTG 3420  
 CGCTGCGCTT TGCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCGG CTGAGCCAG 3480  
 GCACCTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCTT GCC

Seq ID NO: 197 Protein sequence

Protein Accession #: XP\_028196.1

45  
 50

1 11 21 31 41 51  
 MGHPPVSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA 60  
 STPGPRWALI AGALAAGVLL VSCLLCAACC CRRHRKRPK DKESVGLGSA RGTTHLVR 120  
 SGLLTQSRE GLKSLQLSPG QRGESPRDG LTPTEAGR

Seq ID NO: 198 DNA sequence

Nucleic Acid Accession #: NM\_000612.2

Coding sequence: 553..1095

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1 11 21 31 41 51  
 TTCTCCGCA ACCTTCCCTT CGCTCCCTCC GGTCCCGCCC AGCTCCTAGC CTCGACTCC 60  
 CTCCCCCCTT CAGCCCGGCC CTCTGCGCTT CGCCGAACCA AAGTGGATTA ATTACAGCT 120  
 TTCTGTTTCT CTCGTGCTGT TTCTCTCCCG CTGTGCGCCT GCCCGCTCT CGCTGTCTCT 180  
 TCTCCCTCTT GCGCTCTCTT CGGCCCGCCC CTTTCAAGTT CACTCTGTCT CTCCACTAT 240  
 CTCTGCCCTT CTCTATCCTT GATACACAG CTGACCTCAT TTCCGATAC CTTTCCCTCC 300  
 CCGAAAGTA CACATCTGG CCGGCCCGAG CCGCAAGACA GCCGTCTCT CTTGGACAT 360  
 CAGAGCAATT CTCCTCCCTT CCCCCAAAA AAAAGCCATC CCCCCGCTT GCCCGTCTG 420  
 ACATTGCGCC CCGCGGACTC GGCAGAGGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG 480  
 CCAACGCGCG CTGTTCGGTT TGCGACAGCG AGCAGGGAGG TGGGCGGCAG CGTCCCGGC 540  
 TTCCAGACAC CAATGGGAAT CCAATGGGG AAGTGGATGC TGGTGTCTCT CACCTTCTTG 600  
 GCGTTGCGCT CGTGTGCTAT TGCTGCTTAC CGCCCCAGTG AGACCTGTG CCGCGGGGAG 660  
 CTGTTGGACA CCTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCCGCA 720  
 AGCGGTGTA GCGCTGCGAG CGTGGCATC GTTGGAGAGT GCTGTTTCCG CAGCTGTGAC 780  
 CTGGCCCTCC TGAGAGGTA CTGTGTACC CCGCCAAAGT CCGAGAGGGA CGTGTGAGC 840  
 CCTCCGACCG TGCTTCGGGA CAACTTCCCT AGATACCCCG TGGGCAAGTT CTTCAATAT 900  
 GACACCTGGA AGCAGTCCAC CCAGCGCTG CGCAGGGGCC TGCTGCTCT CTGCGTGGC 960  
 CGCGGGGCTC ACGTGTCTGC CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACCTCACCGT 1020  
 CCCCAGATTG CTCTACCCAC CCAAGACCCC GCGCCCGGGC GCGCCCGCCC AGAGATGGCC 1080  
 AGCAATCGGA AGTGAGCAAA ACTGCGCAA GTCTGCAGCC CGGCGCCAC ATCTGCAGC 1140  
 CTCCTCTGTA CCAAGGAGCT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACGT 1200  
 CCCCCTGGGG CTCTCTCTGA CCAAGTCCCC GTGCCCGGCC TCCCGGAAC AGGCTACTCT 1260  
 CCTCGGCCCC CTTCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAAACAT GTACAAAATC 1320  
 GATTGGCTTT AAACACCTT CACATACCTT CCCCC

Seq ID NO: 199 Protein sequence

Protein Accession #: NP\_000603.1

1 11 21 31 41 51

MGIPMGKSM L VLLTFLAFAS CCIAAYRPSE TLGGELVDVT LQFVCGDRGF YFSRPASRV S 60  
 RRSRGIVEEC CFRSCDLALL ETYCATPAKS ERDVSTPPTV LPDNFPRYPV GKFFQYDTWK 120  
 QSTQRLRRGL PALLRRRGH VLAKLEAFR EAKRHRPLIA LPTQDPAHGG APPENASNRK

Seq ID NO: 200 DNA sequence  
 Nucleic Acid Accession #: AK057131.1  
 Coding sequence: 61..1146

1 11 21 31 41 51  
 AGTCTGGGCG TTTAGGTCAG AACTACCCCG GTAGCCTGAC AGCAGGAGCT CGAGAGAAGC 60  
 ATGGCTCAGC GGTGCGTTTG CGTCTGGGCC CTGGTGGCTA TGCTGCTCCT AGTTTTCCTT 120  
 ACCGCTCTCA GATCGATGGG CCGAGGAGC GGGGAGCATC AAAGGGGCTC GCGAATCCCT 180  
 TCTCAGTTCA GCAAAGAGGA ACGCGTCGCG ATGAAAGAGG CGCTGAAAGG TGCCATCCAG 240  
 ATTCGAACAG TGACTTTTAG CTCTGAGAAG TCCAATACTA CAGCCCTGGC TGAGTTGCGA 300  
 AAATACATTCT ATAAAGTCTT TCCTACAGTG CTCAGCACCA GCTTTATCCA GCATGAAGTC 360  
 GTGGAAGAGT ATAGCCACT GTTCACTATC CAAGGCTCGG ACCCCAGCTT GCAGCCCTAC 420  
 CTGCTGATGG CTCACTTTGA TGTGCTGCTT GCCCTGGAAG AAGGCTGGGA GGTGCCCCCA 480  
 TTCTCTGGGT TGGAGCGTGA TGGCGTCATC TATGTTTGGG GCACACTGGA CGACAAGAAC 540  
 TCTGTGATGG CATTACTGCA GGCCTTGGAG CTCTGCTGTA TCAGGAAGTA CATCCCCGA 600  
 AGATCTTTCT TCATTCTCTT GGGCCATGAT GAGGAGTCAT CAGGGAAGG GGTCTCAGAG 660  
 ATCTCAGCCC TGCTACAGTC AAGGGGCGTC CAGCTAGCCT TCATTGTGGA CGAGGGGGG 720  
 TTCATCTTGG ATGATTTTCT TCCTAACTTC AAGAAGCCCA TCGCCTTGAT TGCAGTCTCA 780  
 GAGAAGGGTT CCATGAACCT CATGCTGCAA GTAAACATGA CTTCAGGCCA CTCTTCAGCT 840  
 CCTCCAAAGG AGACAGCAT TGGCATCCTT GCAGCTGCTG TCAGCCGATT GGAGCAGACA 900  
 CCAATGCTTC TCATATTGGG AAGCGGGACA GTGGTGAAGT TATTGCAGCA ACTGGCAAAT 960  
 GAGGTTTATG GAGAGAAATC CCTTAACCAA TGCAATAATC AGGACCAACA CGGCACTCAC 1020  
 CATATTCAAA GCAGGGGTCA AGTTCAATGT CATCCCCCA GTGGCCGAGG CCACAGTCAA 1080  
 CTTCCGGATT CACCTTGAGC AGACAGTCCA AGAGGTCTTA GAACTCAGCA AGAACATTGT 1140  
 GGCTGATAAC AGAGTCCAGT TCCATGTGTT GAGTGCTCTT GACCCCTCC CCGTCAGCCC 1200  
 TTCTGATGAC AAGGCTTGG GCTACCAGCT GCTCCGCCAG ACCGTACAGT CCGTCTCCCC 1260  
 GGAAGTCAAT ATTACTGCC CAGTTACTTC TATTGGCAAC ACAGACAGCC GATTCTTTAC 1320  
 AAACCTCACC ACTGGCATCT ACAGGTTCTA CCCCCTCTAC ATACAGCCTG AAGACTTCAA 1380  
 ACGCATCCAT GGAGTCAACG AGAAATCTC AGTCCAAGCC TATGAGACCC AAGTGAAATT 1440  
 CATCTTTAGG TTGATTCAGA ATGCTGACAC AGACAGGAGG CAGTTTCTC ACCTGCACAA 1500  
 ACTGTGAGGT CAAGGGGCTT GCTGGGTTAG GCATGCCCGA CCCCAGGACA GCACTAACCC 1560  
 AAGGGGGAAG GCTAGTGTG ATGAACTTT TGATCAAAAC CACATTGTAA AACATTGCC 1620  
 ATCTGTCTTG CTCACTCTTA AACTCTCCCA AGAACAGGC CGGGTAAGG TAAAGTCAGC 1680  
 AGAAATCTGG CTCTCTCCCT CTTCCGACA TCTGCATCCC TTGATCCACT GGCATTGCT 1740  
 GCCCTCTGTT CCCTTATCTG TCTTATGCTG GTTATTTCAC TGCTTCACCT TCCAGGCTTG 1800  
 ACTTAACAAA TGTAGATTG AGAAATCTCA ACCAGTTGTT ACCTGATAGG AGTCTTTAAT 1860  
 TTAGGGCACT CTGTCTGGGA TGCTTTCTCC AGAGCTTATA TATTCTCTCT TACTAGAACT 1920  
 TTCTTCCCCC TTTTATTTCC CTCTCTCTCT GGAGCTCATG GCTGTCTCTT CATCTCTCCT 1980  
 CTCCTCTCTG CATCTCTCCC CTTACTCTTC AATTATTCTT ACTTCTGGAC CTGCACTTAC 2040  
 CCAACTGTG ATACTACCAT AATTGTCACC ATAATCAGTC AAATAAAGTG ATCTGTGCAT 2100  
 C

Seq ID NO: 201 Protein sequence  
 Protein Accession #: BAB71368.1

1 11 21 31 41 51  
 MAQRVCVLA LVAMLLLVFP TVSRSMGPRS GEHQASRIP SQFSKEERVA MKEALKGAIQ 60  
 IPTVTPSSEK SNTTALAEPG KYIHKVFPPTV VSTSPIQHEV VEEYSHLFTI QGSDPSLQPY 120  
 LLMAHFEDVVP APEEGWEVPP FSGLERDGI YGWGTLDDKN SVMALLQALE LLLIRKYIPR 180  
 RSFFISLGHQ EBSSSGTAGR ISALLQSRGV QLAIFVDEGG FILDDFIPNF KKPIALIAVS 240  
 EKGSMMLMD VNMSTGSSSA PPKETISGIL AAASRLBQT PMPIIFGSGT VVTVLQQLAN 300  
 EVYGEKSLNQ CNNQDHHGTH HIQSRGQVQC HPPSGPGHSQ LPDSFWTDSR RGRPTREHEC 360  
 G

Seq ID NO: 202 DNA sequence  
 Nucleic Acid Accession #: NM\_004217.1  
 Coding sequence: 58..1092

1 11 21 31 41 51  
 GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTCTC TCTAAGGATG 60  
 GCCCAGAAGG AGAACTCCTA CCCCTGGCCC TAGCGCGAGC AGACGGCTCC ATCTGGCCTG 120  
 AGCACCCCTGC CCCAGCAGT CCTCCGAAA GAGCCTGTCA CCCATCTGC ACTTGTCTCTC 180  
 ATGAGCCGCT CCAATGTCCA GCCCAGAGCT GCCCTGGCC AGAAGGTGAT GGAGAAATAGC 240  
 AGTGGGACAC CCGACATCTT AACCGGCGAC TTCACAATTG ATGACTTTGA GATTGGGCGT 300  
 CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360  
 ATGCTGGGCG TCAAGGTCTT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420  
 CTGCGCAGAG AGATGGAAT CCAGGCCAC CTGACCATC CCAACATCTT CGGTCTCTAC 480  
 AACTATTTTT ATGACGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540  
 CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CAOGATCATG 600  
 GAGGATTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660  
 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTGGGCTGG 720  
 TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAAATGTGT GCACCCCTGA CTACCTGCC 780  
 CCAGAGATGA TTGAGGGGCG CATGCACAA GAGAAGGTGG ATCTGTGGTG CATTGGAGTG 840  
 CTTTGTCTATG AGCTGCTGGT GGGGAACCCA CCTTTTGA GAATCATACA CAACGAGACC 900  
 TATGCCGCA TCGTCAAGGT GGACCTAAAG TTCCCGCTT CTGTGCCAC GGGAGCCGAG 960  
 GACCTCATCT CCAAACTGCT CAGGCATAAC CCTCGGAAC GGCTGCCCTT GGCCAGGTC 1020

TCAGCCACC CTGGGTCG GGCACACTCT CGGAGGGTGC TGCCCTCCCTC TGCCCTTCAA 1080  
 TCTGTGCGCT GATGTGCCCT GTCACTTCACT CGGTGCGTGC TGTGTGTATG TCTGTGTATG 1140  
 TATAGGGGAA AGAAGGGATC CCTAAGCTGT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200  
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 203 Protein sequence  
 Protein Accession #: NP\_004208

1 11 21 31 41 51  
 MAQKENSYPW PYGRQTPSPG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60  
 SSGTPDILTR HFTIDDFEIG RPLGKGKFGN VYLAREKKSH FIVALKVLFK SQIEKEGVEH 120  
 QLRREIEIQA HLHHPNILRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI 180  
 MEELADALMY CHGKKVIHRD IKPENLLGLL KGELEKIADFQ WSVHAPSLRR KTMCGTLDYL 240  
 PPEMIEGRMH NEKVDLWICG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA 300  
 QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSWA

Seq ID NO: 204 DNA sequence  
 Nucleic Acid Accession #: AK055663  
 Coding sequence: 38..1423

1 11 21 31 41 51  
 AGAAGCGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTTCG 60  
 AAAACCACAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120  
 CGGAAGGTCC TGAAGATATC TGCTCTTTGG TGTAATAAAC TTGATATGTA CTGGCTTCCT 180  
 GCTTATGTGG TGCAGTTCTA CTAAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT 240  
 TTTTGAATCT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAAACAT TGAGGAAACC 300  
 TAGCCCTGTC TATTCATTTG GGTITGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCTCCAC 360  
 AGTCTTGCCA CAGTTGGGAG CTCCTTTTAT ATTAAAAGAA AGTGCAGAAC GCTTTTGGGA 420  
 ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 480  
 CCTGTTCAG ATGCTTTCTA TCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540  
 TAGGAGCTGG CTCAAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTAATCC 600  
 GGGACTTAGC AGTATCTTCC TTCCCCGAAT GAATCCATTT GTTTTGATTG ATCTTGCTGG 660  
 AGCATTGTCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCGTAGA 720  
 CACTGCTCTC GCTATAGCTA TTGCTTGAT GACATTTGGC ACTATGTATC CCATGAGTGT 780  
 GTACAGTGGG AAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA 840  
 ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTAGAA GTCCGAAATG AACATTTTGT 900  
 GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTGAC GAGATGCCAA 960  
 TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTAECTTAAC 1020  
 TGTTCAAATT TTCAAGGATG ACTGGATTAG GCTGCTCTTA TTGCTCGGGC CTGTTGCAGC 1080  
 CAATGTCCTA AACTTTTTCAG ATCATCACT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140  
 TGATTTGAAC CCAGTTACAT CAACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200  
 ATTTAACTCT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAAACACAC AAACAAGGCC 1260  
 TTATGTGTCT GTTCTTCAAT ATGGACACAC AOCCTACAGC AGCATGCTTA ATCAAGGACT 1320  
 TGGAGTTCCA GGAATTGGAG CAACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380  
 TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACTTATTT 1440  
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAACT TTGCATTGAC 1500  
 TGTTTAACTA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACTT TCATGAAACC 1560  
 TATGAACTA ATTTTGTGA AAATGTATTT GTGACAGTGA AATCCTGTA AATGTTAAAG 1620  
 GCTTTAATA GGCTTCTTCT AGAAAAATGTG TTTCTTTAAA TTTGATTTT GGTATCTTTG 1680  
 GTTTTGTAGT TGACTGCACT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT 1740  
 AGATCTGCTA CATTACTAAG ATACGATATT TCTTTTTTT TCGAGACGG AGTCTTGCTC 1800  
 TGCCACTGTG CCGCGCCAAT ACATTATTAT TAACTTAAGG CTGTACTTTA TTAAGGCTTC 1860  
 CTTAGTTTTT GTTTTGTITT GTTTTTTGAG ATGGAGTCTC ACTCTGTGCG CCAGGCTGGA 1920  
 ATGCAGTGGC ATGATCTCAG CTCACTGCAA CCTCTGCTCT CTGAGTTCAA ATGATTCTCC 1980  
 TGCCCTCAGC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCC AGCTAATTTT 2040  
 TGTATTTTTA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGTGCT TGAACCTCTG 2100  
 ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGTCTGG ATTAGGTGTG AGCCACCGCA 2160  
 CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT 2220  
 GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGTCTCTT TTTATAGCTT TTCCAACTT 2280  
 AATTGCTAAA TTTTCTTTG AGGTCTCTCT GAATATATGCT TTACAACTA AAAGCAAAA 2340  
 TTTTATGACG AAATTTTGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA 2400  
 GATTTTGTGTT AAGTCTCTC TCTTTAAAA ATTTTAGTAC ATTTGTAAAT

Seq ID NO: 205 Protein sequence  
 Protein Accession #: BAB70980.1

1 11 21 31 41 51  
 MGTIHLFRKP QRSFFGKLLR EFRVLAADRR SWKILLFGVI NLICTGFLLM WCSSTNSIAL 60  
 TAYTYLTIFD LFSIMTCLIS YVTLRKPSF VYSFGFERLE VLAVFASVTL AQLGALFILK 120  
 ESAERFLEQ BIHTGRLLVG TFVALCPNLF TMLSIKNKPF AYVSEAASTS WLQEHVADLS 180  
 RSLCGIIPGL SSIFLPRMNP FVLIDLAGAP ALCITYMLIE INNYFAVDTA SAIAIALMTF 240  
 GTMYFMSVYS GKVLQITPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGSLAGSVH 300  
 VRIIRDANQ MVLARVINRL YTLVSTLTQV IFKDDWIRPA LLSGPVAANV LNFSDHVVIP 360  
 MPLLLKTDLD NPVTSTPAKP SSPPEPSFN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY 420  
 SSMNLQGLGV PGIGATQGLR TGFTNIPSRY GTNNRIGQRP P

Seq ID NO: 206 DNA sequence  
 Nucleic Acid Accession #: NM\_016361.1  
 Coding sequence: 397..1662

1 11 21 31 41 51

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	GGA	ACT	CAGG		GCC	GGT	CTCT		GTT	CCT	TCAA		GAG	TGT	CTGA		GGC	AAA	ACTT		GAA	ATA	CAG	60
	TTA	ATG	TTC		CTC	GT	CGGG		AAA	AGAT	AAG		GAT	CCG	ATCT		CCC	CGG	CCCC		GGT	GTG	CAG	120
	AGG	AGC	GACC		AAC	CCG	AGCC		CGG	TTA	AAA		CTC	CC	AGGG		CTC	TTG	CTG		CTG	CC	ACT	180
	TTG	TCT	CTC		CCC	CGT	TCCC		ACT	CGG	GGTC		TCC	CT	CAGGG		CCG	GG	AGG		CAG	CGG	TCC	240
	TGCT	TGCTGA		AGGG	CTGGAT		GTAG	CGATCC		GCAG	GTCCC		GCG	GACTTG		GGG	CGCCCC		GGG	CGCCCC				300
	TGAG	CCCCGG		CGCC	CGAGA		AGACT	TGTGT		TTG	CTCTG		CAG	CTCAAC		CCG	GAGG		CAG				360	
	CGAG	GGCTA		CCAC	CATGAT		CAC	TGGTGTG		TTAG	CATGC		GCT	TGTGG		CCC	AGTGG		GGC				420	
	GTCT	GACCT		CGCT	GGCGTA		CTGC	CTGCAC		CAG	CGCGGG		TGG	CCCTGG		CGA	GCTGC		CAG				480	
	GAGG	CCGATG		GCC	AGTGTCC		GGT	OGACCG		AGC	CTGCTGA		AGT	TGAAAAT		GGT	G		CAG	GTG			540	
	GTGT	TCGAC		ACG	GGGCTCG		GAG	TCTCTC		AAG	CGCTCC		CGC	TGGAGGA		GCAG	GTAGAG						600	
	TGGA	ACCCCC		AGCT	ATTAGA		GGT	CCACCC		CAA	ACTCAGT		TTG	ATTACAC		AGT	CACCAAT						660	
	CTAG	CTGGTG		GTCC	GAAC		ATAT	TCTCCT		TAC	GACTCTC		AAT	ACCATGA		GAC	CACTCTG						720	
	AAGG	GGGGCA		TGTT	TGCTGG		GCAG	CTGACC		AAGG	TGGGCA		TGC	AGCAAT		GT	TGCTTG						780	
	GGAG	AGAGAC		CTAT	GTGGAA		GAC	ATTCCCT		TTCT	TTCAAC		AAC	CTCAAC									840	
	CCAC	AGGAGG		TCT	TATTGG		TTCC	ACTAAC		ATTT	TTGGA		ATC	TGGAGTC		CAC	CGTTGT						900	
	TTGT	TCCCC		AGCT	TTTCCA		GTGT	CAGAAA		GAAG	GAOCCA		TCAT	CATCCA		CAC	TGATGA						960	
	GCAG	ATTGAG		AAGT	CTTGTA		TCCC	AACTAC		CAA	AGCTGCT		GGAG	CCTGAG		GCAG	AGAAC						1020	
	AGAG	GGCGGA		GCC	AGACTGC		CTCT	TTACAG		CCAG	GAATCT		CAG	AGGATTT		GAAA	AGGTG						1080	
	AAGG	ACAGGA		TGGG	CATTGA		CAGT	AGTGAT		AAAG	TGGACT		TCT	TATCCT		CCT	GACAA						1140	
	GTGG	CTGCG		AGC	AGGCACA		CAA	CTCCCA		AGC	TGCCCA		TGT	GAGAG		ATT	TGACGG						1200	
	ATGAT	CGAAC		AGAG	AGCTGT		GGAC	ACATCC		TTGT	ACATAC		TGCC	CAAGGA		AGAC	AGGGAA						1260	
	AGTCT	TCAGA		TGGC	AGTAGG		CCC	ATTCTCT		CAC	ATCCTAG		AGAG	CAACCT		GCT	GAAAGCC						1320	
	ATGG	ACTCTG		CCAC	TGCCCC		CGAC	CAAGATC		AGAA	AGCTGT		ATCT	CTATGC		GGCT	CATGAT						1380	
	GTGAC	CTTCA		TACG	CTCTT		AATG	ACCCCTG		GGG	ATTTTG		ACC	CAAAATG		GCC	ACCGTTT						1440	
	GCTGT	TGACC		TGAC	CATGGA		ACT	TTACCA		CAC	CTGGAAT		CTA	AGGAGTG		GTT	TGTGAG						1500	
	CTCT	ATTACC		ACG	GGAAGGA		GCAG	GTGCG		AGAG	GTGCT		CTG	TGGCT		CTG	CCGCTG						1560	
	GACAT	GTCT		TGA	ATGCCAT		GTCA	GTTTAT		ACCT	TAAGCC		CAG	AAAAATA		CCAT	GCACTC						1620	
	TGCT	CTCAA		CTCA	GGTGAT		GGA	AGTTGA		AAT	GAAGAGT		AACT	GATTTA		TAAA	AGCAGG						1680	
	ATGT	GTGAT		TTT	AAAAATA		AGT	GCTTTA		TAC	AAAAAAA		AAAA	AAAAAA		A								

Seq ID NO: 207 Protein sequence  
Protein Accession #: NP\_057445.1

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	1	11	21	31	41	51	
	MRL	WTF	VGVL		TSL	AYCL	HQR
	LPL	EEQ	VEWN		QFD	YTV	TNLA
	GMQ	MFAL	GE		RLR	KNY	VEDI
	PII	IHT	DEAD		SEV	LYP	NYQS
	DFI	ILL	DNVA		AEQ	AHL	LPSC
	LBS	NLL	KAMD		SAT	APD	KIRK
	ESK	EFV	QLY		YHG	KEQ	VPFR
	E				CPD	GLC	PLDM
					FLN	AMSV	YTL
					SPE	KYH	ALCS
					QTV	MEV	GNVE

Seq ID NO: 208 DNA sequence  
Nucleic Acid Accession #: CAT cluster

50  
55  
60

	1	11	21	31	41	51	
	TTT	GAGG	GGG		TGGT	GGGG	GGG
	TAA	CAGC	CTG		CCCT	TGGAG	A
	TGCT	GGGG	GGC		CAGT	GTTAG	G
	TAGT	GGCAGA		GCCT	TGGAGTG		ATGAGT
	TCTG	GTGCT		CTTG	CATTTG		CATT
	GGAG	CCCTCC		GCAG	ATCAGT		CCGCT
	CGT	CTTTAT		GGCA	AATGGG		TCATT
	GCAG	GTTCCT		CTAG	CTCCT		TCACC
	TGAG	CTGGCA		GCGCAG			

Seq ID NO: 209 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..564

65  
70  
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	1	11	21	31	41	51	
	ATG	AGCCCT		GGG	CGTGG		GCAG
	TCAG	ATCOGT		TCT	CTGCGCT		GCC
	CAG	ATCACA		CAGT	TGGCCT		GACT
	GAT	CCCTTCT		ACT	ATGACTG		GAAAA
	CTGG	CAATG		CTGG	ATGCG		GGCAG
	AAG	CAGACA		GTCT	GTATCC		TGAG
	ACCT	TGGCCA		AAT	CAAAATA		ACCT
	AGCT	ACACAT		CAGT	CTTCG		AGT
	GATG	CTGCTG		CCCT	CACATC		AGG
	GGA	ACGAAG		GCTG	TACCTA		ATGA

Seq ID NO: 210 Protein sequence  
Protein Accession #: FGENESH predicted

80

	1	11	21	31	41	51	
	MEP	WAN	LQGL		KSR	PTCP	PAAS
	DPF	YD	WKNL		QLS	GLIC	GG
					LAI	AGIA	AVL
					SGK	CKCK	SSQ
					KQH	SPVP	EKA
					IPL	ITP	GRFL

TLAKSNKPLS PSTFVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSQHP SMQNMISMONT 180  
GKKGCT

5 Seq ID NO: 211 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..318

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10 1      11      21      31      41      51
    |      |      |      |      |      |
    ATGCCCGGCC ACCCGCTCTG TGAAGTGAGG AGCACCTCTG CCGGGCTGCC CGGCTGGGA 60
    AGTGAGGAGC GCCTCTGCCC GGCTGCCACC CCGTCTGTGA GTGCTGCTG CGCTGGGCCC 120
    AGGCGCGCCG TGCCCTGCCA GGCCCTCCGG CCCCCACCT TCCACCCAG GGCTGCTCC 180
    TCACCCGAGG GTTCCATCTC CTTAGTTTCC ACCAGAGACT GGGTCTTCAT TCTCACCTG 240
    CTACACAGCC CCTACCAGAA CGTTCTGAAA TGCAAACCTA ACAACTGTCT CACCCAGCA 300
    15 GGAAACTCCC CAGGGTCCCG GGCCCCCTGC GGGGTGCGAG GCCTCACTCT TCGCGCCCAT 360
    CCTCCGCCC TGACCGCCCT GAGCTCGCCC CCACTGCTGG CCTTCAOCT CCAGTTATCC 420
    CTCCAGCCTT CCAAGGTCCC CGTTACCGAA GACCGCCACC ATCAGACAT AGCGCAGCAC 480
    ATATGGGACA CTGGTGAAGG AGCAGTGAGG AACCTGCAGA GTCACACAGT TGGCCTGACT 540
    GCCTTGAAG CCAATGACCC ATTGCCAAT AAAGAAGATC CCTTCTACTA TGACTGGAAA 600
    20 AACCTGCAGC TGAGCGGACT GATCTGCGGA GGGCTCCTGG CCATTGCTGG GATCGCGGCA 660
    GTTCTGAGT GCAAAATGCAA ATGCAAGAGC AGCAGAAGC AGCAGAGTCC GTACCTGAG 720
    AAGGCCATCC CACTCATCAC TCCAGGAGCA TTCTCACCT TGGCCAAATC AATAAACCCT 780
    TTATCTCAA GCACCTTTGT CTTGGTGTGT GGCATCAGCT ACACATCAGT CTTCCGAGTG 840
    25 CCTCTTCTG CTGCTCTGTA CCTGCCATT CTTGGTGATG CTGCTGCCCT CACATCAGGC 900
    CATCCAGCA TGCAGACAT AAGCATGCAG AACACTGGAA CGAAGGGCTG TACCTAA
  
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30 Seq ID NO: 212 Protein sequence  
Protein Accession #: FGENESH predicted

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30 1      11      21      31      41      51
    |      |      |      |      |      |
    MPGHPVCEVR STSARLPRLG SEERLCPAAT PSVSACCAGP RPPVPCQALR PPTFHPRACS 60
    SPQGSISLVS TRDWVFILTL LHSFYQNLVK CKFNCLTPA GNSPGSRAPC GVAGLTLRAH 120
    35 PSALTALSSP PVLALHVLQS LPASKVPVTE DRHHHDIAQH IWDTEGAVR NLQSHTVGLT 180
    ALEANDPFAN KDDPFYDWMK NLQSLGLIC GLLAIAGIAA VLSGKCKCKS SQKQHSVPVE 240
    KAIFLITPGR FLTLAKSNKP LSPSTFVLVF GISYTSVFRV PLSASLYPAI PGDAAALTSQ 300
    HPSMQNISMQ NTGKKGCT
  
```

40 Seq ID NO: 213 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1758

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45 1      11      21      31      41      51
    |      |      |      |      |      |
    ATGATGGGGT CTCATGTTGC CCAGGCTGGT CTTGAACCTC TGGGCTCGAG TGACCTCTCT 60
    GCCTTGGCCT CCGAAAGTGC TGGGATTACA GGACTGTTAT TACAGGAATC CATAACACTG 120
    GAGGATGTGG CTGTGGACTT CACTTGGGAG GAGTGGCAAC TCCTGGGCGC TGCTCAGAA 180
    GACCTGTACC GGGATGTGAT GTTGAGAAAC TACAGCAACC TGGTGGCAGT GGGGTATCAA 240
    50 GCCAGCAAAC CGGATGCACT CTTCAAGTTG GAACAAGGAG AACAAGTGTG GACAATTGAA 300
    GATGGAATCC ACAGTGGAGC CTGTTCAGGT TCTCCAAAGG TCCCGTTCTC CATTTTCTCA 360
    TCTGTGCCCT TCACTCTTCA AAAATGCGCTT CATTCTAACA TATGGAAAGT TGATCATGTG 420
    CTGGAGCGCT TGCAGAGTGA AAGCCTGGTG AACAGAAGGA AACCATGTCA TGAACATGAT 480
    GCATTTGAAA ATATTGTTCA TTGCAGCAAA AGTCAGTTTC TGTTAGGGCA AAATCATGAT 540
    55 ATATTGACT TAAGTGGAAA AAGTTTGAAA TCCAATTAA CTTTGTGTA CCAGAGCAAA 600
    GGCTATGAAA TAAAGAACTC TGTGTAGTTT ACTGGAAATG GGGACTCTTT TCTTCATGCT 660
    AACCATGAAC GACTTCATAC TGCAATTAAA TTCCCTGCAA GTCAAAACTC CATCAGCACT 720
    AAGTCCCAT TATCATGATC CAAGCATCAG AAAACACGAA AATTAGAGAA GCATCATGTG 780
    TGCAGTGAAT GTGGGAAAGC CTTTCATCAAG AAGTCTTGGC TAACTGATCA CCAGGTAATG 840
    60 CATACAGGAG AGAAACCCCA CAGATGTAGT CTATGTGAGA AAGCCTTCTC CAGAAAGTTC 900
    ATGCTTACTG AACATCAGCG AACTCATACA GGAGAAAAC CTTATGAATG CCCTGAATGT 960
    GGCAAGCCCT TTCTCAAGAA ATCAGCGCTC AACATACATC AGAAACACCA TACCGGAGAG 1020
    AAACCCATA TATGCAATGA ATGTGGAATA GGCTTCATCC AGAAAGGAAA TCTCATTTGA 1080
    65 CACCAGCGAA TTCATACAGG TGAGAAACCT TATATATGCA ATGAATGTGG AAAAGGCTTC 1140
    ATTCAGAAGA CGTGTCTCAT AGCAGATCAG AGATTTCACA CAGGAAAGAC GCCCTTTGTG 1200
    TGCAGTGAAT GTGGAAAATC CTGTTCTCAG AAATCAGGTC TCATTAAACA TCAAGAATTT 1260
    CACACAGGAG AGAAACCCCT TGAATGTAGT GAATGTGGGA AAGCCTTTAG CACAAAGCAA 1320
    AAGCTCATTG TCCATCAAAG GACTCATACA GGAGAGAGAC CCTATGGCTG TAACGAGTGT 1380
    GGGAAAGCGT TTGCGTATAT GTGTTGCTG GTTAAGCATA AGAGAATACA CACAAGGGAG 1440
    70 AAACAAGAGG CAGCCAGGT GGAATATCCT CTTGCAGAGA GGCACAGCTC ATTACACACC 1500
    AGTGATGTCA TGCAGGAGAA AAATCTGCT AACGGGGCGA CTACACAAGT GCCTTCTGTG 1560
    GCCCTCAGA CATCATTAAT CATCAGCGGC CTCTCGCAA ACAGGAAGCT AGTCCTTGTG 1620
    GGACAGCCAG TGGTCAGATG TGCAGCCTCA GGAGATAACA GAGGATTTGT ACAGGACAGA 1680
    75 AACCTGTGA ATGCAGTGAA TGTGTTGTG CTTCCGTGA TCAATTATGT CTTATTTAT 1740
    GTTACAGAAA ACCCATAG
  
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80 Seq ID NO: 214 Protein sequence  
Protein Accession #: FGENESH predicted

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80 1      11      21      31      41      51
    |      |      |      |      |      |
    MMGSEVAQAG LELLGSSDPF ALASESAGIT GLLLQESITL EDVAVDPTWE EWQLLGAAQK 60
    DLYRDVMLEN YSNLIVAVGY ASKPDALFKL EQGEQLWTIE DGIHSGACSG SPKVPPSIFS 120
    SVPTTLQNC LHSNIWKVDHV LERLQSESLV NRRKPCHERD APENIVHCSK SQPLLQONHD 180
    IFDLRGKSLK SNLTLVNQSK GYEIKNSVEF TNGDSEFLHA NHERLHTAIK FPASQRLIST 240
  
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5 KSPFISPKHQ KTRKLEKHHV CSECGKAFIK KSWLTDHQVM HTGEKPHRCS LCEKAFSRKF 300  
 MLTEHQRTHT GEKPYBCEPC GKAFLEKSRSL NIHQRTHTGE KPYICSECGK GPIQKGNLIV 360  
 HQRIHTGEKP YICNECGKGF IQKTCLIAHQ RFHTGKTPFV CSECGKSCSQ KSLGIKHQRI 420  
 HTGKPFECES ECGKAFSTKQ KLIVHQRTHT GERPYGCNEC GKAFAYMSCL VHKRIHTRE 480  
 KQEAARKVENP PAERHSSLHT SDVMQEKNSA NGATTQVPSV APQTSNLISG LLANRNVVLV 540  
 GQPVVRCAS GDNRGFAQDR NLVNAVNVVV PSVINYVLFY VTENP

Seq ID NO: 215 DNA sequence

Nucleic Acid Accession #: NM\_032190.1

Coding sequence: 502..1332

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1	11	21	31	41	51	
GATTCGGTGT	TCTTGGCCAT	GTTAGCCATA	ATATCCTGTG	CAGTATGTTT	TTCCTGTGCA	60
GAGGCAAAAA	CATATTGGGC	ATATGTTCCC	AAGCCOCCAG	CAGTATGACC	CATACCTTGG	120
AGTGACACTC	CTCCTAAGAT	TTATCATGAT	TAAGGAGCAT	GGGCTCCAGC	ACCCCTAACT	180
CCACTGACAT	TAGAACAGTT	AGACTCTCAG	AATAATGTCA	TTAATTATAC	CGCTCCATTG	240
GAAGGACTTC	CTTTGTGTGT	CACCACAAG	ACATCACTCA	GCCATAGCTG	TCTTACAGTT	300
CAAGCTCACA	CATGGTTGAG	TCATATGGG	AAAAATCATG	ACTTATTAA	TCTTGGTTAT	360
ATTAATGTAA	CGGTTGTGCT	AACCAACCAT	TCCTGGCCCA	ATCGCCTTCA	TTGTGCTGAC	420
TATACAGAAT	GGATTCCCTT	CAATAGTTCC	TACCCOCCCT	CATAGACCCA	GTGTCTTGGC	480
CCACTGGCTA	GAACAACATC	TATGTTAACT	GGAGACATTG	TGGATTGGGG	ACCTAAAGGC	540
CAATTAGATG	GAAGAAGA	AAATCAGAAA	TCGTGGCACA	AACCTTGTCT	GCATTGGTGG	600
CAAGCTTTTA	ATGCTTCTTC	TTTATATAAC	ACTGGGATCC	AATCCAGCTG	GGCCGCCAG	660
ATTGCTTGGC	ATGGAGCAGG	CTTTAGCCCG	CCTCTTCCCT	AGTGGCATT	TCTAGGGAGG	720
AAAGGACCAA	TTCAAAGAT	GATATGGAAG	GCAGCATTC	CAITTTATGA	TGGCAACATC	780
TGGTTGCCA	TAATACTATC	CAATAATAGC	AATAGTAAGC	AACACAGTCT	TAATGTTACA	840
TTTGTAAGA	ATATCACCAC	TCAATTAC	GTGTGTGTTT	TTAATCCTTA	TGTGTTTTTG	900
GCAGCTAAGA	AGGACAGCT	CCAGGTAAC	AATACCCAAT	TGACCTGTAA	ATCTTGCCAG	960
TTATATCACT	GCATTAATCA	TAGCACATTG	CAACACATA	ATATCTCTAC	TTTGATGATT	1020
TTAGGTGCA	TCCTGGGCT	ATGATTCTCT	GTTAATCTGT	CTGAGCCATG	GGCTGCCACA	1080
ATTGCTTTAC	ATTTGTGAA	ACTTCTTCTA	ACTCAGTTTA	CTCATTGTGT	CCGTAGAGGC	1140
TTAGGCATGA	TAATTTTTC	TATGTTTAC	TTGGTCACAC	TAATAATTTT	TGTTGTGATG	1200
TCCTCTGTAG	CTTTGCATAG	TTCTATTCAA	ACAGCTCAGT	ATGTGGAGAA	CTGGACACGC	1260
ACAGTCAACC	AAGGTTGGCT	ACTTGAGAT	AAAATTAACA	CTGAGTTACA	AACTGAAAGT	1320
GCAGTGTAT	AATCCACGAT	TCTATGTTA	GGGGAACAAG	TACAAAGCTT	GCAATTGCAG	1380
CAGTAATGT	GTGTGCTTT	TAATCACT	CATATTGTG	TAACCAACTT	AGAATATAAC	1440
CAAGGTAGT	ATCCATGGGA	TCTTGTGAAA	GCCCATTTGC	AGGGAGCTTT	CACATCCGAC	1500
ATCACTTTTG	ATATTGGTGA	ATTACAAAAC	AAAATCTTGT	ATTTAAATAA	ACAAATTCCA	1560
GAGTTTCAGC	CTTCTTTAGA	AGACTGGACT	GAATTCAGC	AAGGCCTGGA	GAGCGTCAAC	1620
CCTTGGACCT	ATCTAAAGCA	CCACATTAC	ATCTTATATA	TAGTCTCTGG	AATAATGTTG	1680
TTTTGTCTCT	GTCTCTGTGT	CATAGTCTGT	AAAATCGGAT	GGACTGCCAA	TCGGAGAATG	1740
AAAGCTACCC	AGCCTGGCCT	TACATTCTTT	CACCTTAATC	ATAAACAAGA	AGGGGGAAT	1800
GTGGGAGGCC	AAAAAGGCCA	AAGGGATGGT	GACCAACTCA	GCATTCCACT	GGAGGCTACA	1860
TGATCAAAAC	GCAAACTGTT	TATCATGAAT	ACAGAATGTG	GGCAAACTCG	CTTCTGTGCC	1920
TGCCCAGAAG	GTGTGCTGAG	GGCCATGGCT	CCCTGGCCCC	GGCTCCTTGA	GTTTATCTAC	1980
TGGGACATCT	AGAGCCTATT	GTTCGAGGAA	TGCAGTCTTG	CAAGCCTACT	CTGGACCCAG	2040
CAGCTCACT	CTTCTTCCAC	ACCCCTTCTC	ACTATCTCTT	TTGCCATAA	AATATGGAGG	2100
GCTGTGAAA	GCTCAGGGCC	CTTGTCCACT	AGAGGCAAGG	TGTCCCTGTA	CCCTCTCTCC	2160
AAACAT						

Seq ID NO: 216 Protein sequence

Protein Accession #: NP\_115566.1

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 60

1	11	21	31	41	51	
MLTGDIVDWG	PRGQLDGKEE	NQKSWHLKCN	HWQAFNASS	LYNTGSIQS	AAQIAWHGAG	60
FSPPLQWHY	LGRKGPQRM	IWKAAFFPM	GNIWVAILLS	NNSNSKQSL	NVTFVKNITT	120
QFTVCFNFPY	VFLAAKRDQL	QVNTYQLTCK	SQLYHCINH	STLQENIST	LMILGCIPGL	180
WIPVNLSEFW	AATLALHFVK	LLLQTFTHCV	RRGLGMIIPA	IVYLVTLIIS	VVMSSVALHS	240
SIQTAYQVEN	WRTVWQGL	LENKINTELQ	TEVAVL			

Seq ID NO: 217 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..1566

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1	11	21	31	41	51	
ATGGTGAACC	CCAAATCCAC	TTCCCTCCCTC	TTCAGGTTAT	GTTTTTTGCT	CCTGAGGAGT	60
CAGAACCTGT	GGGTGAAGA	GCAAATCAA	TGCAAAAACA	TATTGGGCAT	ATGTTCCCAA	120
TCCOCCAGCA	GTATGGCCTA	TACTTTGGAG	CTCACTCCTC	CTGAGATTTA	TCAOGATCAG	180
GGAGAGTGGG	CTCCAGGACC	CCTAACTCCC	CGTGACATAG	AAAAGTTAGA	CTCTCAGAAC	240
AATGTCAATTA	ATTATACCAC	TCOACTGGAA	GGACTCCCTT	TGTTTATCAC	CACAAAGACG	300
TGCTCAGCG	ATGACTGTCT	TGCAATTCAA	GCTCAAAACAT	GGTTGAGTCA	CTATGGAAAA	360
ATTATGTAAT	TATTAGTCT	TGGTCTTATT	AATGTAACTG	GTGTGCTAAC	CAATCATTCC	420
CAGTTCAGT	ACCCCTAATTG	TGCTGATTAT	ACAGAATGGA	TTCCATTCAA	TAGTCTCTAC	480
CCCACTCTGT	GGACCCAGTG	TCTTGATCCA	CTGGCTAGTA	AACAATATAT	GTCAACTGAA	540
GACACTGTGG	ATTGGGAACC	TAAAGGTCAA	TTAGATGGAA	AAGGTGAAAG	TCAGAAATCA	600
TGGCACAAC	TTGCGGCA	GCTTTTAATG	CTTCTTCTTT	ATACAACAGC		660
AGAATCCAAT	CCCACTCTGC	TGCTCAGATT	GCTTGGCATG	GAGCAGGCTT	TAGCCCACT	720
CTTCTCAGT	TGCTATATCT	GGGAGGAAA	GGACCAATTC	AAGAACTAT	ATGGAAGGCA	780
GCACTCCCAT	TTATGAATGG	CAACATCTGG	ATTGGAACAC	TGTCTAATAA	TAGCAATAGT	840
AAGCAACACA	GTCTTAATGT	TGCATTGTGA	AAGAATATCA	CCACTCAGTT	TACAGTTTGT	900
GTTTTTAATC	CTTATGCCTT	TTTGGCAGCT	AAGAAGAAC	AGCTTCAGGT	GGAGAACTGG	960

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ACACGACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT 1020  
GAAGTGGCAA TGTGAAATC CATGGTTCCTG TGGTTAGGAG AACAGGTACA AAGCTTGACG 1080  
TTGCAGCAGC AATTGGCTCA TCATTTTAAT CACATTCATA TTTGCGTAAC TAACTCAGAA 1140  
TATAACCAA GTGAGTATCC GTGGGACCTT GTGAAAGCCC ATTTGCAAGG AGCTTTCACA 1200  
TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAACAAA TTATTGATTT AAATAGGCAA 1260  
ACTCAAGAAT TTCAGCCTTC TTTAGAAGAC TGGACCGAAT TCCAGGAAGG CCTGGAGAGC 1320  
CTCAACCCCTT GGACCTATCT AAGGCACCCAC ATTAACATCT TATATGTAGT TCTTGGGAATA 1380  
ATGTTGTTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG 1440  
AGAATGAGAG CCAATCCAGCC CAGCCTTACA TTCTTTCAAT TAATACATAA ACAGAAAGGG 1500  
GGATATGCAG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATTCT GCTGGAGGCT 1560  
ATATGA

Seq ID NO: 218 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
MVNPKSTSSL FRLCFLLLRS QNLWVEBQIQ CQNLIGICSQ SPSSMAYTLE LTPPEIYHDQ 60  
GEWAPGLPTP RDIEKLDSQN NVINYTTPLF GLPLFITTKT SLSSHCLAIQ AQTWLSHYGK 120  
IMYLLGLGSI NVTVGLTNHS QSSHPNCADY TEWIPFNSSY PTLWTQCLDP LASKQYMSTE 180  
DTVDWEPKQK LDGKGESQKS WHKLHWHRQ AFNASSLYNS RIQSQSAQI AWHGAGFSPP 240  
LPQLHVLGRK GPIQETIWA ALPFMNGNIW IGTLSNNSNS KQHSLSNVAPV KNITTOFTVC 300  
VFNPYAFLLA KKNQLQVENW TRTADQARLL QNKINTELQT EVAMLSKSMVL WLGEQVQSLQ 360  
LQQQLRHHFN HIHICVTNSE YNQSEYPWDL VKAHLQGAFT SNITFDIGEL QNKIIDLNRRQ 420  
TQEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLFCLCLRFI VCKIGWTTNW 480  
RMRASQPSLT FFLIHKQKG GYAGSQRPVG RDQLSILLEA I

Seq ID NO: 219 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..900

1 11 21 31 41 51  
ATGCCCGCGC GGGAGCTGAG CGAGGCGGAG CCGCCCCCGC TCGGGGCCCC GACCCCTCCC 60  
CCGCGCGCGC GTAGCGCGCC CCGAGAGCTG GGCATCAAGT GCGTGTGGT GGGCGACGGC 120  
GCCGTGGGCA AGAGCAGCCT CATGCTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180  
CGGCCCACTG CGCTGGACAC CTCTCTGTGT ACGTACGTTT AATGCGCGT GCGGCCGCGT 240  
GGCTGCGGCG GGGCTGTGCA CCGGGGAGCT GGGCGGGGCG TCTCGCGCGG AGGGCGCAGA 300  
GSACCCCGCG GAGGAGACTG GAGCAGGCCC CGAGGTGGCG CTGGTGGCGC CCAGGACGCT 360  
CTTCCTAACT CAGCTCTCC CCGCCCCCGC CTGCACTGTC AAGTCTGGT GGATGGAGCT 420  
CCGGTGGGCA TTGAGCTCTG GGACACAGCG GGCAGGAGG ATTTTGACCG ACTTCTGTCC 480  
CTTTGCTACC CGGATACCGA TGTCTCTCTG GGTGTCTTCA GGTGTGTGCA GCCCAGCTCC 540  
TTTCAAAACA TCACAGAGAA ATGGCTGCCC GAGATCCGCA CGCACAAACC CCAGGCGCCT 600  
GTGCTGCTGG TGGGACCCCA GGCAGACCTG AGGAGCATG TCAACGTACT AATTACGCTG 660  
GACCAGGAGG GCGCGGAGGG CCGCGTGCCC CAACCCAGG CTCAGGCTCT GCGCGAGAGG 720  
ATCCGAGGCT GCTGCTACCT TGAGTGTCTA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780  
TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840  
GCCAAAGGTG TGCCACCCCT CTCCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCGTTTGA

Seq ID NO: 220 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
MPPRELSEAE PPPLRAPTPP FRRRSAPPEL GIKCVLVGDG AVKSSSLIVS YTCNGYPARY 60  
RPTALDTPFG TYVQSPVRPR GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120  
LFGSGSPRPA PAVQVLVDGA FVRIELWDTA GQEDFDRLRS LCYPDTDVFL ACFSVVQFSS 180  
FQNIETKWL P EIRTHNPQAP VLLVGTQADL RDDVNLIQL DQGGREGVFP QPQAQGLAEK 240  
IRACCYLECS ALTQKVLKEV FDSAILSAT EHKARLEKKIN AKGVRTLSRC RWKKPFCFV

Seq ID NO: 221 DNA sequence

Nucleic Acid Accession #: XM\_063832.2

Coding sequence: 1..711

1 11 21 31 41 51  
ATGCCCGCGC GGGAGCTGAG CGAGGCGGAG CCGCCCCCGC TCGGGGCCCC GACCCCTCCC 60  
CCGCGCGCGC GTAGCGCGCC CCGAGAGCTG GGCATCAAGT GCGTGTGGT GGGCGACGGC 120  
GCCGTGGGCA AGAGCAGCCT CATGCTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180  
CGGCCCACTG CGCTGGACAC CTCTCTGTGT CAAGTCTGTG TGGATGGAGC TCCGCTGCGC 240  
ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTGTGTC CCTTTGCTAC 300  
CCGATACCG ATGTCTCTCT GCGGTGCTTC AGCGTGTGTC AGCCAGCTC CTTTCAAAC 360  
ATCACAGAGA AATGGCTGCC CGAGATCCGC ACACACACC CCGAGGCGCC TGTGCTGCTG 420  
GTGGGCAACC AGGCGGACCT GAGGGACGAT GTCAAGCTAC TAATTGAGCT GGACGAGGG 480  
GGCGGGAGG GCCCGTGCC CCAACCCAG GCTCAGGGT TGGCGGAGAA GATCCGAGCG 540  
TGCTGCTGCT TTAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600  
GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAACTGAA TGCCAAAGGT 660  
GTGGGCAACC TCTCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTGTGTTG A

Seq ID NO: 222 Protein sequence

Protein Accession #: XP\_063832.1

1 11 21 31 41 51

MPPRELSEAE PPPIRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIYS YTCNGYPARY 60  
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLRLCY PDTDVFLACF SVVQPSFQON 120  
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVFPQP AQGLAEKIRA 180  
 CCYLECSALT QKHLKEVFDS AILSAIEHKA RLEKLNNAKG VRTLSRCRWK KFFCFV

Seq ID NO: 223 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1161

1	11	21	31	41	51	
ATGAATCGGC	ACCATCTGCA	GGATCACTTT	CTGGAAATAG	ACAAGAAGAA	CTGCTGTGTG	60
TTCCGAGATG	ACTTCATTGC	CAAGGTGTGT	COGCGGTGT	TGGGGCTGGA	GTTTATCTTT	120
GGGCTTCTGG	GCAATGGCCT	TGCCCTGTGG	ATTTCCTGTT	TCCACCTCAA	GTCTTGGAAG	180
TCCAGCCGGA	TTTTCCTGTT	CAACCTGGCA	GTAGCTGACT	TTCTACTGAT	CATCTGCTTG	240
CCGTTCTGTA	TGACTACTA	TGTGCGGCGT	TCAGACTGGA	AGTTTGGGGA	CATCCCTTGC	300
CGGCTGGTGC	TCCTCATGTT	TGCCATGAAC	CGCCAGGGCA	GCATCATCTT	CCTCAGCGTG	360
GTGGCGGTAG	ACAGGTATTT	CCGGGTGGTC	CATCCCCACC	ACGCCCTGAA	CAAGATCTCC	420
AATTGGACAG	CAGCCATCAT	CTCTTGCCCT	CTGTGGGGCA	TCAGTGTGG	CCTAACAGTC	480
CACCTCCTGA	AGAAGAAGTT	GCTGATCCAG	AATGGCCCTG	CAAAATGTGT	CATCAGCTTC	540
AGCATCTGCC	ATACCTTCOG	GTGGCAGCAA	GCTATGTTCC	TCCTGGAGTT	CCTCCTGCCC	600
CTGGGCATCA	TCCTGTCTCG	CTCAGCCAGA	ATTATCTGGA	GCCTGCGGCA	GAGACAAATG	660
GACCGCATG	CCAGATCAA	GAGAGCCATC	ACCTTCATCA	TGGTGGTGGC	CATCGTCTTT	720
GTCACTGCT	TCCTTCCAG	CGTGGTGTG	CGGATCCGCA	TCTTCTGGCT	CCTGCACACT	780
TCGGGCACGC	AGAATGTGA	AGTGTACCGC	TCGGTGGACC	TGGCGTTCTT	TATCACTCTC	840
AGCTTCACT	ACATGAACAG	CATGCTGGAC	CCCGTGGTGT	ACTACTTCTC	CAGCCCATCC	900
TTTCCCAACT	TCCTTCCAC	TTTGATCAAC	CGCTGCCCTC	AGAGGAAGAT	GACAGGTGAG	960
CCAGATAATA	ACCGCAGCAC	GAGCGTCGAG	CTCAGAGGGG	ACCCCAACAA	AACCAGAGGC	1020
GCTCCAGAGG	CGTTAATGGC	CAACTCCGGT	GAGCCATGGA	GCCCCCTCTA	TCTGGGCCCA	1080
ACCTCAAATA	ACCATTCCAA	GAAGGGACAT	TGTCAACCAAG	AACCAGCATC	TCTGGAGAAA	1140
CAGTTGGGAT	GTGCACTCGA	G				

Seq ID NO: 224 Protein sequence  
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MNREHLQDHF	LEIDKKNCCV	PRDDPIAKVL	PPVLGLEPIF	GLLGNGLALW	IFCFHLKSWK	60
SSRIPLFNLA	VADFLLIICL	PFVMDYVRR	SDWKFGDIPC	RLVLFMPAMN	RQGSIIPLTV	120
VAVDRYFRVV	HPHHLANKIS	NWTAIIISCL	LWGITVGLTV	HLKLLKLLIQ	NGPANVCISF	180
SICHTFRWHE	AMFLEFLLE	LGIIILFCSAR	IWSLRQRQM	DRHAKIKRAI	TFIMVVAIVF	240
VICFLPSVVV	RIRIFWLLHT	SGTQNCVYR	SVDLAPFITL	SPTYMNSMLD	PVVYVFSFSS	300
FPNFFSTLIN	RCLQRKMTGE	PDNNRSTSV	LTGDPNKTRG	APEALMANS	EPWSPSYLGP	360
TSNNHSGKH	CHQEPASLEK	QLGCCIE				

Seq ID NO: 225 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1092

1	11	21	31	41	51	
ATGAATCGGC	ACCATCTGCA	GGATCACTTT	CTGGAAATAG	ACAAGAAGAA	CTGCTGTGTG	60
TTCCGAGATG	ACTTCATTGT	CAAGGTGTGT	COGCGGTGT	TGGGGCTGGA	GTTTATCTTC	120
GGGCTTCTGG	GCAATGGCCT	TGCCCTGTGG	ATTTCCTGTT	TCCACCTCAA	GTCTTGGAAG	180
TCCAGCCGGA	TTTTCCTGTT	CAACCTGGCA	GTGGCTGACT	TTCTACTGAT	CATCTGCTTG	240
CCCTTCTGTA	TGGACAACCTA	TGTGAGGCGT	TGGGACTGGA	AGTTTGGGGA	CATCCCTTGC	300
CGGCTGATGC	TCCTCATGTT	GGCTATGAAC	CGCCAGGGCA	GCATCATCTT	CCTCAGCGTG	360
GTGGCGGTAG	ACAGGTATTT	CCGGGTGGTC	CATCCCCACC	ACGCCCTGAA	CAAGATCTCC	420
AATCGACAG	CAGCCATCAT	CTCTTGCCCT	CTGTGGGGCA	TCATATTGG	CCTGACAGTC	480
CACCTCCTGA	AGAAGAAGAT	GCCGATCCAG	AATGGCGGTG	CAAAATTTGT	CAGCAGCTTC	540
AGCATCTGCC	ATACCTTCCA	GTGGCAGCAA	GCCATGTTCC	TCCTGGAGTT	CTTCTGCCCC	600
CTGGGCATCA	TCCTGTCTCG	CTCAGCCAGA	ATTATCTGGA	GCCTGCGGCA	GAGACAAATG	660
GACCGCATG	CCAAGATCAA	GAGAGCCATC	ACCTTCATCA	TGGTGGTGGC	CATCGTCTTT	720
GTCACTGCT	TCCTTCCAG	CGTGGTGTG	CGGATCCGCA	TCTTCTGGCT	CCTGCACACT	780
TCGGGCACGC	AGAATGTGA	AGTGTACCGC	TCGGTGGACC	TGGCGTTCTT	TATCACTCTC	840
AGCTTCACT	ACATGAACAG	CATGCTGGAC	CCCGTGGTGT	ACTACTTCTC	CAGCCCATCC	900
TTTCCCAACT	TCCTTCCAC	TTTGATCAAC	CGCTGCCCTC	AGAGGAAGAT	GACAGGTGAG	960
CCAGATAATA	ACCGCAGCAC	GAGCGTCGAG	CTCAGAGGGG	ACCCCAACAA	AACCAGAGGC	1020
GCTCCAGAGG	CGTTAATGGC	CAACTCCGGT	GAGCCATGGA	GCCCCCTCTA	TCTGGGCCCA	1080

Seq ID NO: 226 Protein sequence  
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MNREHLQDHF	LEIDKKNCCV	PRDDFIVKVL	PPVLGLEPIF	GLLGNGLALW	IFCFHLKSWK	60
SSRIPLFNLA	VADFLLIICL	PFLMDNYVRR	WDWKPGDIPC	RLMLFPLAMN	RQGSIIPLTV	120
VAVDRYFRVV	HPHHLANKIS	NWTAIIISCL	LWGITIGLTV	HLKLLKLLIQ	NGGANLCSS	180
SICHTFRWHE	AMFLEFLLE	LGIIILFCSAR	IWSLRQRQM	DRHAKIKRAI	TFIMVVAIVF	240
VICFLPSVVV	RIRIFWLLHT	SGTQNCVYR	SVDLAPFITL	SPTYMNSMLD	PVVYVFSFSS	300
FPNFFSTLIN	RCLQRKMTGE	PDNNRSTSV	LTGDPNKTRG	APEALMANS	EPWSPSYLGP	360
TSP						



Seq ID NO: 227 DNA sequence  
Nucleic Acid Accession #: NM\_006018  
Coding sequence: 61..1224

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      CGCCACTTTG CTGGAGCATT CACTAGGCGA GGCGCTCCAT CGGACTCACT AGCCGCACTC   60
      ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG   120
      TTCGAGATG ACTTCATTGC CAAGGTGTTG CCGCGGTGTG TGGGGCTGGA GTTTATCTTT   180
10     GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTCGGAAA   240
      TCCAGCCGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG   300
      CGGTTCTGTA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC   360
      CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG   420
      GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC   480
15     AATTGGAGC CAGGCATCAT CTCTTGCCCT CTGTGGGGCA TCACGTGTGG CCTAACAGTC   540
      CACCTCCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC   600
      AGCATCTGCC ATACCTCCG GTGGCAAGAA GCTATGTTCC TCCTGGAGTT CCTCTGCCCC   660
      CTGGGCATCA TCTCTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG   720
      GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATGCTCTTT   780
20     GTCATCTGCT TCCCTCCGAG CGTGGTTGTG CGGATCOGCA TCTTCTGGCT CCTGCACACT   840
      TCGGGCAGCG AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC   900
      AGCTTCACCT ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC   960
      TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG   1020
      CCAGATAATA ACOGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACACAGAGG   1080
25     GCTCCAGAGG CGTTAATGGC CAACTCOGCT GAGCCATGGA GCCCCTCTTA TCTGGGCGCA   1140
      ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTCAACAAG AACACGATC TCTGGAGAAA   1200
      CAGTTGGGCT GTTGACTCGA GTAATGTGAC TGGACTCGGC CTAAGGTTTC CTGGAACCTC   1260
      CAGATTGAGA GAATCTGATT TAGGGAAACT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG   1320
      GTGTGACCAC AGGAATCTCT GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAAACTTGC   1380
30     TTCACTCTG AGCTCTGCAG GACTGAAGAT GGGCAAAATG TAGGOGTTTC TGCTGAGCAG   1440
      AGTTGGAGCC AGAGATCTAC TTGTGACTTG TTGGCCTTCT TCCACATCTC GCCTCAGACT   1500
      GGGGGGGGCT CAGCTCTCTG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG   1560
      GAGAGCTGAG ATTGGAGGGA ATTGTGTTGC TCTGGAGGA AGCCAGGCA TCATTAAACA   1620
      AGCCAGTAGG TCACCTGGCT TCCGTGGACC AATTCATCTT TCAGACAAGC TTTAGAGAAA   1680
35     TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTTCCGG TGGGTGTAAT   1740
      AGGGGATTAG CCCCAGAGG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAATGGCA   1800
      TTGCTGCTTT CAACAGCGA CTAATGCAAT CCATTCCTCT CTGTGTTATA GTAATCTAAG   1860
      GGTGAGCAG TTAAGAACGG TTCAGGATAG AAGCTGTTT CCCACCTGTT TCGTTTAACT   1920
40     ATTAAGAGG AAGCTGCTCT CTGCCCAAG GGTAGAGGGG GTGCAAGTTC CTCTGCTTC   1980
      CTTCGCTTGT GTTCTGTGAC TTACCAAAAA TCTACCACCT CAATAAATTT TGATAGGAGA   2040
      CAAAAAAA A

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Seq ID NO: 228 Protein sequence  
Protein Accession #: NP\_006009.1

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45     1      11      21      31      41      51
      |      |      |      |      |      |
      MNRHHLQDHP LEIDKKNCCV FRDDPIAKVL PFVLGLEFIF GLLNGNLALW IPCFHLKSWK   60
      SSRIFLFLNA VADFLLIICL PFVMDYVVR SDWNFGDIPC RLVLFMFAMN RQGSIIFLT V   120
50     VAVDRYPRVV HPHHLLNKIS NWTAAIIISCL LWGITVGLTV HLLKKGLLIQ NGPANVCISF   180
      SICHTRFMHE AMFLLEFLLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF   240
      VICFLPSVVV RIRIFMLLHT SGTQNCVYR SVDLAPFITL SFTYMNMLD PVVYFSSPS   300
      FPNFSTLLN RCLQRMTGSE PDNNRSTSV LITGDPNKTRE APEALMANSR EPWSPSYLGP   360
55     TSNHNSKKGH CHQEPASLEK QLGCCIE

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Seq ID NO: 229 DNA sequence  
Nucleic Acid Accession #: NM\_014398.1  
Coding sequence: 64..1314

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      GGCACCGATT CGGGGCTGCG CGGACTTCTG CGCACGCTG CAGAACCTCG CCCAGOGCCC   60
      ACCATGCCCC GGCAGCTCAG CGGGGCGGCC GCGCTCTTGG CGTCCCTGGC CGTAATTTTG   120
      CACGATGGCA GTCAATAGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT   180
65     ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACGAGC TAAGCAAGCA   240
      CCTCACAAA CTTFAGCAGC AAGATTTCATG GATGTCATA TCACCTTTCA AACAGCGGCC   300
      ACAGTAAAAA TTCCAACRA CACCCAGCA ACTACAAAAC AACTGCAAC CACCAGCCCA   360
      ATTACTACA CCGTGGTCAC AACCCAGGCC ACACCCAAAC ACTCACACAC AGCTCCTCCA   420
70     GTTACTGAAG TTACAGTCGG CCTAGCTTA GCCCCTTATT CACTGCCACC CACCATCACC   480
      CCACGAGCTC ATACAGCTGG AACCACTTCA TCAACCGTCA GCCACACAAC TGGGAACACC   540
      ACTCAACCCA GTAAACAGAC CACCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC   600
      ACAACGGCTG AGAAGCCTGA TCAACCCACC CATGCCCGAG GAACAAGGCG AGCTGCCAC   660
      AATAACACCC GCACAGCTGC ACCTGCCCTCC ACGGTTCCTG GGCCACCCCT TGCACTCAG   720
75     CCATGCTCAG TCAAGACTGG AATTATCAG GTTCTAAAG GAAGCAGACT CTGTATAAAA   780
      GCAGAGATGG GGATCAGCT GATTGTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA   840
      TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CGGAAAATCC   900
      AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA   960
      TCATATTATA TCACTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC   1020
80     CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATTC CTTCAAGTGC   1080
      GTGAGTGAAC AGAGCCTCCA GTTGTCAAG CACCTGCAGG TGAATAACAA CGATGTCCAA   1140
      CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAATG TGGATGAGTG CTGCTCTGAC   1200
      TACACAAATG TGCTTCTCTG GATTGGGGCC ATCGTGGTGT GTCTCTGCCT TATGGGTATG   1260
      GGTGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTTGTT   1320
      CCGGGGGGGA ATGAATAATA TGGAATTTAG AGAACTCTTT CATCCCTTCC AGGATGGATG   1380

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5 TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440  
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT 1500  
 GTTTATTTTA TGAAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA 1560  
 GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620  
 AGCCTTCAAA TTATAAACCA AGGGTCAATT GTAACATAA CTACTGTGTG TGCAATTGAAG 1680  
 ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCTTTG TTATCAAAATG GACTTTTCAGT 1740  
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCTCTGT GTAGCACITTA 1800  
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTAGAC GGAGTTTCAC TCTTGTCCAC 1860  
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCGGCTCTC CGGGTTCAG 1920  
 TGATTCTCCT GCTTCAGCTT CCGAGTAGC TGGGATTACA GGCACACACT ACCACGCTCG 1980  
 GCTAATTTTT GTATTTTAT TATAGACGGG TTTCACCATG TTGGCCAGAC TGGTCTTGAA 2040  
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCTCCCAA GTGTGGGAT TACAGGCATG 2100  
 AGCCATTGCG CCGGCTTA AATGTTTTT TTAATCATCA AAAAGAACAA CATATCTCAG 2160  
 GTTGTCTAAG TGTTTTTATG TAAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220  
 15 CTGTAGTACT CCTAGTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280  
 CTAAACAATA AGCAAGAGAC AATAATAATG GCGCTTAATT ATTAACAAAG TGCCAGAGTC 2340  
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACA ACTTATAAGT GAATGAGTAA 2400  
 ACTGAGACTT AAGGGAACCT AATCAGCTAA ATGTCACCTG GCTAAGTATG GGCAGAGCCA 2460  
 GAGCTTGAA TCAATGTTGT CTGACATCAA GGTCTTTTGT CTCTCTCCCTA CACCAAGTTA 2520  
 20 CTTACAAGAA CAATGACACC ACACTCTGCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580  
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640  
 AGCTTTGCG ATAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700  
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTTA TGGGATTTGCT TAGCTGGGCT 2760  
 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTTTA ATTTTTTGA TAATAGAGAA 2820  
 25 ACTTGTCTAA CCAACTGTTT TTTCTTGTAG GTATAGCCCC ATCTTGTGTG AACTTGTCTG 2880  
 TTCTGCACCT CATATCCATA TTTCTTATG TTCACTTTAT TCTGTAGAGC AGCCTGCCAA 2940  
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGRAAGG AACTAAGTCA GGATGTTAAC 3000  
 AGAAAAGTCC ACATAACCCCT AGAATTTCTTA GTCAAGGAAT AATTCAGTCA AGCCTAGAGA 3060  
 30 CCATGTTGAC TTTCCTCATG TGTTCCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120  
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 230 Protein sequence

Protein Accession #: NP\_055213.1

35 1 11 21 31 41 51  
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPPARQAP 60  
 HQTLAARFMD GHITTFQTAAT VKIPTTTPAT TKNTATTSPI TYTLVTTQAT PNNSHTPPV 120  
 40 TEVTVGPSLA PYSLPPTIIP PAHTAGTSSS TVSHTTGNT QPSNQTLLPA TLSIALHKST 180  
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKGTIYQV LNSRLCIKA 240  
 EMGIQLIVQD KESVSPRRY FNIDPNATQA SGNCGTRKSN LLLNFQGGFV NLTFTKDEES 300  
 YYISEVQAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSFKCV SEQLQLSAH LQVKTIDVQL 360  
 QAFDPEDDHF GNWDECSSDY TIVLPVIGAI VVGLCLMGSG VYKIRLRCQS SGYQRI

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: NM\_005409.3

Coding sequence: 94..378

50 1 11 21 31 41 51  
 TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60  
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120  
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCCTCC CCATGTTCAA AAGAGGACGC 180  
 55 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240  
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAA 300  
 AAAGGACAAC GATGCCATAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360  
 GAAAGAAAGA ATTTTAAAAA ATATCAAAC ATATGAAGTC CTGAAAAAGG GCATCTGAAA 420  
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480  
 60 AGACTTTTCT ATGGTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540  
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTCTCTGAAT GAATGACAAT CAGAAATCCA 600  
 CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGSAA AAGCTACCTT AAGAAAGGCT 660  
 GGTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTGTATT ATACATTCT 720  
 GCATTTCTAG GCTAGAGAAC CTCTAGATT TGATGCTTAC AACTATTCTG TTTGTACTAT 780  
 65 GAGAACATTT CTGTCTTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840  
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900  
 CATCTATG TGCTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAATACAC ACTTCTTCC 960  
 CCAATATCA TGTAGCATAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020  
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080  
 TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT 1140  
 70 GATGTTTTT AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200  
 TGTACTTTTT GTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTGAAA 1260  
 TACAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAAATG TATACCTAGC 1320  
 AATCATTGTT ACTTTTGTGA ATTCGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380  
 75 TGTTCATGC CTATATCTG TAAAAATTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440  
 GTCATTTTTT TCTCAATAA ACTACACAA CCTTCTTTT TAAAAAAA AAA

Seq ID NO: 232 Protein sequence

Protein Accession #: NP\_005400.1

80 1 11 21 31 41 51  
 MSVKGMAIAL AVILCATVVQ GPFMPKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60  
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 233 DNA sequence  
Nucleic Acid Accession #: NM\_000577.1  
Coding sequence: 41..520

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5      1      11      21      31      41      51
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GGCAGCGAGG GAAGACCTCC TGTCTATCA GGCCTCCCC ATGGCTTAG AGACGATCTG 60
CGACCCCTCT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACA 120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCOGGA TACTTGCAAG GACCAATGT 180
10    CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGAGAGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGGAGGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTGGCCTT 360
CATCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCGCCTGCC CCGGTTGGTT 420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
15    CGTCATGGTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCCTGT 540
TCCCATTCTT GCATGGCAAG GACTGCAGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCG 600
GCTATGGGGT TCCCTGAGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
CCTGTGCACA GACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTCGCA CAAAGCCCTT CCATGTGGCC 780
20    TCTGCATTCA GGATCAAAAC CGACCAACTT GCCCAACTCT CTCTCTCTT GCCACTGCCT 840
CTTCTCCCTT CATTCCACTT TCCCATGCC TGGATCCATC AGGCCACTTG ATGACCCCCA 900
ACCAAGTGGT TCCCAACCTT TGTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
TTTAAGGGTT TGTGAAAAT GAAAATTAGG ATTTTCATGAT TTTTCTTTT CAGTCCCGT 1020
GAAGGAGAGC CCTTCATTG GAGATTATGT TCTTTCGGG AGAGGCTGAG GACTTAAAT 1080
25    ATTCTGCTG TGTGAAATG ATGTTGAAAG TAAGTGGTAG CTTTCCCTT CTTTCTTCT 1140
TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCATTA 1200
ATTTTCTTTT TCCTTTTAAA ACACCTCCAT AATCTGGACT CCTCTGTCCA GGCAGTCTG 1260
CCACGCTTCC AAGCTCCATC TCCACTCCAG ATTTTCTACA GCTGCTGCA GTACTTTACC 1320
TCCATACAGA AGTTTCTCAG CTCCTAAGGC TCTGAGCAA TGTGGCTCT GGGGGTCTT 1380
30    TCTTCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACCTGGAG 1440
ACTGTATGTA AAGATGGCTG TGCTCTGCC TGCTCCCCC ACCAGGCTGG GAGCTCTGCA 1500
GAGCAGGAAA CATGACTCTG ATATGCTCA GGTCCCTGCA GGGCCAAAGC CTAAGCTCTG 1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTT GGTGCAAGT TCCCTACTTC 1620
35    CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAATAT GCCTAAAAAA AAAAAAAA 1680
AAAAAAA AAAA

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Seq ID NO: 234 Protein sequence  
Protein Accession #: NP\_000568.1

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40      1      11      21      31      41      51
      |      |      |      |      |      |
MALETICRPS GRKSSRMQAP RIWDVNQKTF YLRNNQLVAG YLQGPVNMLE EKIDVPIEP 60
HALPLGIHGG KMCLSCVKSQ DETRLQLEAV NITDLSENRR QDKRFAPIRS DSGPTTSFES 120
45    AACPGWFLCT AMEADQFVSL TNMFDEGVMV TKFYFQED

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Seq ID NO: 235 DNA sequence  
Nucleic Acid Accession #: NM\_001840.1  
Coding sequence: 149..1567

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50      1      11      21      31      41      51
      |      |      |      |      |      |
GGGGACTACG GAGAGCTCTG CAGGGAGCCG AGGCCCCCGC CCGGGCCAAG GGAGCTTCTG 60
TCCCGAGGAC CAGGGGATGC GAAGGGATTG CCCCCTGTGG GTCACCTTCT CAGTCATTTT 120
GAGCTCAGCC TAATCAAGA CTGAGGTAT GAAGTCGATC CTAGATGACC TTGCAGATAC 180
55    CACCTTCGCG ACCATACCA CTGACCTCCT GTACGTGGGC TCAATGACA TTCAGTACA 240
AGACATCAAA GTTGACATGG CATCCAAATT AGGGTACTTC CCACAGAAAT TCCCTTTAAC 300
TTCTCTTAGG GGAAGTCCCT TCCAGAGAA GATGACTGCG GGAGACAACC CCCAGCTAGT 360
CCCAGCAGAC CAGGTGAACA TTACAGAAIT TTACAACAAG TCTCTCTGCT CCTTCAAGGA 420
GAATGAGGAG AACATCCAGT GTGGGGAGAA CTTTATGAGC ATAGAGTGT TCATGGTCT 480
60    GAACCCAGC CAGCAGCTGG CCATTGCAGT CCTGTCCCTC ACGCTGGGCA CTTTCAAGGT 540
CCTGGAGAAC CTCCTGGTGC TGTGCGTCAT CCTCCACTCC CGCAGCCTCC GCTGCAGGCC 600
TTCTTACCAC TTATCGGCA GCCTGGCGGT GGACAGCTCC CTGGGAGTGG TCAATTTTGT 660
CTACAGCTTC ATTGACTTCC ACGTGTTCCT CCGCAAAGAT AGCCGCAACG TGTTTCTGTT 720
65    CAACTGGGT GGGGTCAAGG CCTCTTCAC TGCTCCGTG GGCAGCTGT TCCTCACAGC 780
CATCGACAGG TACATATCCA TTCACAGGCC CCTGGCTTAT AAGAGGATTG TCACCAGGCC 840
CAAGGCCGTG GTGGCGTTT GCCTGATGTG GACCATAGCC ATTGTGATG CCGTGTCTGC 900
TCTCTGGGG TGAAGTCTGC AGAAACTGCA ATCTGTTTGC TCAGACATTT TCCACACAT 960
TGATGAACCT TACCTGATG TCTGGATCGG GGTACCCAGC GTACTGCTTC TGTTCATGCT 1020
70    GTATGOSTAC ATGTATATTC TCTGGAAGGC TCACAGCCAC GCGTCCGCA TGATTACAGC 1080
TGGCACCCAG AAGAGCATCA TCATCCACAC GTCTGAGGAT GGGAAAGGTAC AGGTGACCGC 1140
GCCAGACCAA GCCCGCATGG ACATTAGGTT AGCCAAAGAC CTGCTCCTGA TCCTGGTGGT 1200
GTGTATCATC TGCTGGGGCC CTCGCTTGC AATCATGGTG TATGATGTCT TTGGGAAGAT 1260
GAACAAGCTC ATTAAGACGG TGTTTGCATT CTGCAATATG CTCTGCTGCG TGAACCTCAC 1320
75    CGTGAACCCC ATCATCTATG CTCTGAGGAG TAAGGACCTG CGACAGCTT TCCGGAGCAT 1380
GTTTCCCTCT TGTGAAGGCA CTGCGCAGCC TCTGATTAAC AGCATGGGGG ACTCGGACTG 1440
CCTGCACAAA CACGCAACCA ATGCAGCCAG TGTTCACAGG GCGCAGAAA GCTGCATCAA 1500
GAGCAGGGTC AAGATTGCCA AGGTAACCAT GTCTGTGTCC ACAGACAGCT CTGCGAGGCC 1560
TCTGTGAGCC TGATGCCTCC CTGSCAGCAC AGGAAAAGAA TTTTCTTTT TAAGCTCAA 1620
80    ATCTAGAAGA GCTATATGTC TCCTTGGTTA TATTTTCTTA ACTTTACCAT GTCAATGAA 1680
AAGGTGATTG CCACATGTCA CTTAATTGCT TAGTTTCTGT TTGGGCTAAT CTTCGGGGT 1740
TCGTAGGAAA CCTTT

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Seq ID NO: 236 Protein sequence  
Protein Accession #: NP\_001831.1

	1	11	21	31	41	51	
5	MKSILDLGLAD	TFTRITITDL	LYVGSNDIQY	EDIKGDMSK	LGYPFQKFPFL	TSFRGSPFOE	60
	KMTAGDNPOL	VPADQVNITE	PYNKSLSSF	ENEENIQCGE	NFMDECFMV	LNPSQLAIA	120
	VLSLTLTGTF	VLENLLVLVC	ILHSRSLRCR	PSYHFIGSLA	VADLLGSVIF	VYSPIDFHP	180
	HRKDSRNVL	FKLGGVTASF	TASVGSFLT	AIDRYISIR	PLAYKRIVTR	PRAVVAFCLM	240
	WTIAIVIAVL	PLLGWNCCKL	QSVCSDFPH	IDETVLMFWI	GVTSVLLLP	VYAYMYILWK	300
10	AHSHAVRMIQ	RGTKSIIIIH	TSEDGKVQVT	RPDQARMDIR	LAKTLVLILV	VLICWGPILL	360
	AIMVYDVFGR	MNKLKIVFA	PCSMCLLNS	TWNPIIYALR	SKDLRHAFRS	MFPSCGTAQ	420
	PLDNSMGDS	CLHKHANNAA	SVHRAESCI	KSTVKIAKVT	MSVSTDTSAE	AL	

Seq ID NO: 237 DNA sequence

Nucleic Acid Accession #: NM\_016083.2

Coding sequence: 64..1482

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20	GATTGCCCCC	TGTGGGTGTC	TTTCTCAGTC	ATTTTGAGCT	CAGCCTAATC	AAAGACTGAG	60
	GTTATGAGAT	CGATCCCTAGA	TGGCCTTGCA	GATACCACT	TCCGCACTAT	CACCACTGAC	120
	CTCCTCTAGC	TGGGCTCAAA	TGACATTGAG	TACGAAGACA	TCAAAGGTGA	CATGGCATCC	180
	AAATTAGGGT	ACTTCCACACA	GAAATTCCCT	TTAACTTCCT	TTAGGGGAAG	TCCCTTCCAA	240
	GAGAAGATGA	CTGGGGGAGA	CAACCCCCAG	CTAGTCCCAG	CAGACCAGGT	GAACATTACA	300
25	GAATTTTACA	ACAAGTCTCT	CTCGTCCCTC	AAGGAGAATG	AGGAGAACAT	CCAGTGTGGG	360
	GAGAAGTCA	TGGACATAGA	GTGTTTCATG	GTCTGTAACC	CCAGCCAGCA	GCTGGCCATT	420
	GCAGTCTCT	CCCTCAGCCT	GGGCACTTTC	ACGGTCTCTG	AGAACCTCCT	GGTGTCTGTC	480
	GTCACTCTCC	ACTCCGCGAG	CCTCCGCTGC	AGGCCTTCTC	ACCACTTCAT	CGGCAGCCTG	540
	GCGGTGGCAG	ACCTCTCTGG	GAGTGTCTAT	TTTGTCTACA	GCTTCATTGA	CTTCCACGTG	600
30	TTCCACCGCA	AAGATAGCCG	CAACGTGTTT	CTGTTCAAAC	TGGGTGGGGT	CACGGCCTCC	660
	CTCACTGCTC	CCGTGGGCGA	CCTGTTCCTC	ACAGCCATCG	ACAGGTACGT	ATCCATTAC	720
	AGGCCCTCTG	CCATATAGAG	GATTGTCAAC	AGGCCCAAGG	CCGTGGTGGC	GTTTTGCCTG	780
	ATGTGACACA	TAGCCATTGC	GATGCGCTG	CTGCTCTCC	TGGGCTGGAA	CTGCGAGAAA	840
	CTGCAATCTG	TTTGCTCAGA	CATTTTCCCA	CACATTGATG	AAACCTACCT	GATGTTCTGG	900
35	ATCGGGGTCA	CCAGGCTACT	GCTTCTGTTC	ATCGTGTATG	CGTACATGTA	TATTCTCTGG	960
	AAGGCTCA	GCCAGCGCGT	CGGCATGATT	CAGCGTGGCA	CCGAGAAAG	CATCATCATC	1020
	CACACGCTG	AGGATGGGAA	GGTACAGGTG	ACCGGCCAG	ACCAAGCCCG	CATGACATT	1080
	AGGTTAGCCA	AGACCCCTGT	CCTGATCTGT	GTGGTGTGTA	TCATCTGCTG	GGGCCCTTTG	1140
	CTTGCAATCA	TGGTGTATGA	TGTCTTTGGG	AAGATGAACA	AGCTCATTAA	GACGGTGTCT	1200
40	GCATTCTGCA	GTATGCTCTG	CCTGCTGAAC	TCCACCGTGA	ACCCCATCAT	CTATGCTCTG	1260
	AGGAGTAAGC	ACCTGCGACA	CGCTTTCCGG	AGCATGTTTC	CCTCTTGTGA	AGGCACTGGG	1320
	CAGCCTCTGG	ATAACAGCAT	GGGGGACTCG	GACTGCTGTC	ACAAACACGC	AAACAATGCA	1380
	GCCAGTGTTC	ACAGGGCGCG	AGAAAGCTGC	ATCAAGAGCA	CGGTCAAGAT	TGCCAAGGTA	1440
	ACCATGTCTG	TGTCACAGCA	CACGCTGCGC	GAGGCTCTGT	GAGCCTGATG	CCTCCCTGGC	1500
45	AGCACAGGAA	AAGAAATTTT	TTTTTTAAGC	TCAAATCTA	GAGAGTCTA	TGTCTCTCTT	1560
	GGTTATATTT	TTTTAACTTT	ACCATGCTCA	ATGAAAAGGT	GATTGTCAAC	ATGATCACTT	1620
	ATCAGTTTGC	TAAATGTTCC	ATAGTTTAGG	TACTCAAACT	CCATTCTCCA	GGGGTTTACA	1680
	GTGAAGAAAG	CCGTGTTGTT	AAGTGACTGA	ACGATCTCTC	AAAGTCTCAA	TGAATAGGTA	1740
	GGGAACCTTT	TGGCTACACA	ATTGGAAGTC	TAAGAAACCA	TGGAAAAATG	CCATCAAAATG	1800
50	AATAATGCCT	TTGTAAACAC	AACTTTCACT	ATAATGTGAA	ATGTAACGTG	CCGTAGTATC	1860
	AGAGATGTCC	ATTTTACAA	GTTATAGTAC	TAGAGATATT	TTGTAATAATG	TATTATGTCC	1920
	TGTGAGATGT	GTATCAGTGT	TTATGTGCTA	TTAATATTGT	TTTAGTTTCA	CAAACTGAA	1980
	AGGTAGACTT	TTATGAGAAC	AATGGACAAG	CAGTGGATAC	GTGTCAATGT	GTGCACTTTT	2040
	TTTCTATATT	ATTGCCCATG	ATATAACTTT	AGAAATAAAC	CTTAATATTT	CTTCAAAAT	2100
55	CTCTATTATA	TTTTGACACT	GAAATAACCG	TAAAGGTTTA	TTTTTCTGTT	ACCTCAACAA	2160
	GAAGAATTGG	AAGACTTCAA	AATATTGAGC	AGAATTCATT	CTACTTAAA	AATTTATTAG	2220
	CCCTGCATTT	TCATAGGAAG	ACACATTATC	TTCTGGACTA	TAGCTGTTCT	AATGGATTAT	2280
	AATCAGAAATG	GAAGAGAGAA	AGCATATTGA	CTTTTTTTGA	GCGACATCTC	TGACTTTCTT	2340
	TAGTCTTATG	TATTACTTGG	ATCTCTTAAG	ACAGCATGTG	TTAATCTTAA	TGTATATCGT	2400
60	TATCACTGTG	CAGTTGCTGT	TTACTTGAAT	AGTATTGTGT	TCCTATATTC	CAGSTTTAAG	2460
	TAGATTTCAT	GCCTGGGTGG	CCAAACAACA	GTCTTCATT	TTTTTAATTG	AAAAGAAGTA	2520
	GTGTCTGAT	CAGTAAAAAT	ATACTGTGTG	TGAGTGTGAA	TATAAATGTG	TGTATGTGTG	2580
	TTTCTGTCCG	TAACTGTTAC	AGTAATGTCA	TAAAGTGAGA	AACTGTGAC	CAAGTATATA	2640
	CTTTTACCAC	TGCTGTCACT	CTTGCACTG	GATTCACTTT	CTAAATTTGA	GTCTCTCTGT	2700
65	TAATCTTGTT	GATAAAATA	CTGACTCCAA	CCATTCAAAA	ATTTCAACCC	ATCCCTCTCT	2760
	AAGAGATTGG	ATCAAGTATT	ACTAAATTGA	CCTTTAGGTA	TTACACAAGA	CCAGTGCTTA	2820
	GCAAAAATA	ATGACAGGCA	TCCAAGGAAG	GGATGTATTT	GTAGTGTAT	TGCCAGGAAA	2880
	GGAGAGTACT	TTGTTTCTG	AGCACCGAAT	ATTGAGCAAT	ATGTCACTCA	CTAAAAGGAA	2940
	GACAGTTCTA	CAGAAAAACA	AATGGTAACA	TTTTTCAATA	GCGTGTGTAG	ATAGTATGCA	3000
70	CTATATACAT	CACGTTAAAG	TAGGACTATC	ACACCCAGCC	CATGTGGCTA	AAAAAGCTGA	3060
	ATCAGACAGT	GGATGAGACA	CACAACGGCA	GTGAAGAACC	GATACACTTG	GCATTGAAGT	3120
	CTAGCTATGC	TGATCTGTG	CTTTGCCAC	ATGCCCTTGG	TGACAGCTGA	GCACCCAGCT	3180
	CTGTCTTGGT	AGGTTTGGGC	TAAGGAACAA	ATCTCTCTCT	TGCTGTGTGT	TAGCAAGATA	3240
	CACCTAAGCA	TGAAGATAAA	CACAGCTGCT	TTCTTCTTAC	ACCCCGGTCT	CATGCTCTCT	3300
75	AATGGCGCCA	TGGGTGCTGT	TTGGGCTTT	TTCCAGTAAG	GAATGATATT	GCTGAAGAAAT	3360
	CTACTTAAOC	CTGACAAATT	TTAATTATAA	TCTCTTCTTA	TACAGATAAA	ACATGACTCC	3420
	TACAAGGCC	CAAGGTTTAC	ATAGTCTGAA	GTGAAGTACA	GAGCTGGCAT	CTATCTGGTG	3480
	ATTCTAGCT	CTGAGATAC	CCAAGCAGCC	TGATGGGGCA	GTTCCTCTTC	TTACGTTTCA	3540
	GCCTCTAAG	CAGGATGTGG	CTTATGAGAT	ACTTTGCATT	GTCTGTCTGC	ACACCTTGAA	3600
80	TCTGCTGTCT	GGCTCCCTTA	CTTTACCTCT	CTGTCACTGT	CAGATGAAGG	CTCAGGGTGC	3660
	TAGAGGATTA	GTAAGATCTC	TTTCTAAAGA	CAGGAGAGAT	TATTTACAAG	AAGAATCTAC	3720
	CAGGGTTTAG	TTTGCAATTA	AGAATTGCCA	GTCTTTTGTG	CTGCATCATC	TTGAACATTA	3780
	ATCCACATGT	TTCAAGCTCT	ACCAGGCAGT	ACCAATGCTC	TTTTTACAGC	TATGAAGAGC	3840
	TAGAGAAATT	CTTGTATTAG	TAGAAAAATT	TCACGGTTCA	TTTTTGAAAC	TGCATTGTGT	3900
	CGTATGCACT	GTAGATTTTA	TAGTGTGTGT	TGCTTTCAAG	ATCTAAATCA	TATATAATAA	3960

5 ATTAAGGGAC AATGGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA 4020  
 TCTGTGAAAT ATCATCAAGT ATGTTATACA ACCTTCATT AAAAGGTTT AAAACTAGTT 4080  
 AGATTCACTT TGACACTTTT CATATCATTT CTTAAACCAA GTGACGAAAA CATTTGCCCC 4140  
 AATGAATATA CTCATTAGAA TTACCATTTG TTAATATCAC TCATTAATTA ACCCCATAAT 4200  
 TAGATCCATT AATTAAATG ATTTAAATTT AAGTAAGTTT TATAAGGTCT GACATCAGAG 4260  
 GTATCTTACT TTCTCTGAG GATGATGTAC TTGCCCTGAC CATGCATTTT ACCATCACAC 4320  
 ATGTTTCAGAA AGGGCCAAAT TCCCAACCTG CTCATTTTTT TTTTATCAG AGTCATGATG 4380  
 AATCAGTCTT AGAATGTTTC ATTTGCACAA GTAGGGCTGC CTCCAAGAGG AACCTCTGAT 4440  
 10 TTATTTTGTA TGAATATAT GTGAAAGGAT ATGAATCTGA GAGATGCTGT AGACATCTGT 4500  
 CCTACACTTG AGATGATTTT CAAGCCTCTC TGGCACTTTG AGTTAAGTCT ATCTGGTATT 4560  
 AAATGCCAAG GACCTTTTGC TGCTTAAATC CACTCTGCAG GAAATAGGCC CAACCCACAG 4620  
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 CATTTCATGT CCATAAAGA GACCAACCAT ATCATGCACA CAATTAGATT TCTCACTC 4740  
 TAACGTATA TTGTATGAT ATTTTAAAT CTCTAAATG CTGGGCAATG GCTATTAAAC 4800  
 15 ATTAATGTC TTGCACTGCG CTCTGATGA AATGTTAACA ATGCCTATTG TAATATAGAA 4860  
 AAAAATATTC TATCTACTGA TTTGGGCTGA ATGTATGTAA ATAGGTTTCT AAAAAGTCAG 4920  
 ATGTTTAGAC AGTGGCCTAC AAATCAGTAA TTTTGGGCTG GGAGAGTTTC TTTACATTGC 4980  
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 AGTTCCCAAG AAAGGAAACC TTTTCTGTGA TCTGGATTCA AATTATTTTC CAATGTTTCA 5100  
 20 AGCGGGAAC ATGACTCTTT ATTGTCTGTA AATCTAACAT TATTACTTTT CCTCTTAGAA 5160  
 GAATATTGTA TTGTTAGATG TTTGTTGAGC TGGTAACATC GTTGCAACCA CTGCAATATC 5220  
 TTCGTTAGTA ATCTGTATAA TACTTTGTAT ACAAGTACTG GTAAGATTGT TATTAAATGT 5280  
 AGCTTCAGTC ATTAATATAC TATAGCAAAG TAGTACTTCT TCTGTAATAT TTACAATGTA 5340  
 TTAAGCCAC AGTATATTTT ATTTCATGT AATTAAACTG TTAACTTATT CAAAGAGAAA 5400  
 25 ACATCTCATC ATGTCTATTG TCCAAAGTTA CCTGGAATCA AATAAAAAAT CTAGATTACC 5460  
 ATGAAGAACA TA

Seq ID NO: 238 Protein sequence  
 Protein Accession #: NP\_057167.1

30 1 11 21 31 41 51  
 | | | | |  
 MKSILDGLAD TPTFTITDLD LYVGSNDIQY EDIKGDMASK LGYFPQKFPPL TSFRGSPFQE 60  
 KMTAGDNPQL VPADQVNITE FYNKSLSSFK ENEENIQCGE NFMIDIECFMV LNPSQQLAIA 120  
 35 VLSLTGTFVT VLENLVLVTV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF VYSFIDFHFV 180  
 HRKDSRNVEL FKLGGVTASL TASVGSLEFLT AIDRYVSIHR PLAYKRIVTR PKAVVAFCLM 240  
 WTAIAIAVL PLLGWNCEKL QSVCSDFPHI IDETYLMFWI GVTSVLLLFV YAYMYILWK 300  
 AHSNAVRIQ RGTQKSIILH TSEDGKVQVT RPDQARMDIR LAKTLVLILV VLICWGPLL 360  
 40 AIMVYDVFGK MNKLIKTVFA PCSMLCLLNS TVNPIIYALR SKDLRHAERS MFPSCEGTAQ 420  
 PLDMSMGDSO CLHKHANNA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL

Seq ID NO: 239 DNA sequence  
 Nucleic Acid Accession #: NM\_033181.1  
 Coding sequence: 17..1252

45 1 11 21 31 41 51  
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 CTGTAGCTGG GCTCAAATGA CATTAGTAC GAAGACATCA AAGGAGAATG AGGAGAACAT 120  
 50 CCAGTGTGGG GAGAACTTCA TGGACATAGA GTGTTTCATG GTCCGTAACC CCAGCCAGCA 180  
 GCTGGCCATC GTGACTCTGT CCTCAGCTG GGGCACTTC ACGGTCCTGG AGAAGCTCCT 240  
 GGTGCTGTGC GTATCTCTCC ACTCCCGCAG CCTCGCTGCG AGGCCCTTCT ACCACTTCAT 300  
 CGGCAGCCTG GCGGTGGCAG ACCTCCTGGG GAGTGTCTAT TTTGCTACA GCTTCATTGA 360  
 55 CTTCACGCTG TTCCACGCGA AAGATAGCGG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT 420  
 CAGGGCTCTC TTCACTGCCT CGTGGGCGAG CCTGTTCTCT ACAGCCATCG ACAGGTACAT 480  
 ATCCATTCAC AGGCCCTCTG CCTATAAGAG GATTGTCTACC AGGCCCAAGG CCGTGTGTGG 540  
 GTTTTGCCCG ATGTGGACCA TAGCCATTGT GATCGCGGTG CTGCCCTCTC TGGGCTGGAA 600  
 CTGCGAGAAA CTGCAATCTG TTTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT 660  
 60 GATGTTCTCG ATCGGGGTCA CCAGGCTACT GCTTCTGTTT ATGCTGTATG CGTACATGTA 720  
 TATTCTCTGG AAGGCTCACA GCCAAGCGGT CGCATGATT CAGCGTGGCA CCCAGAAGAG 780  
 CATCATCATC CACAGCTCTG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG 840  
 CATGGACATT AGGTTAGCCA AGACCTCGGT CTGATCTCTG GTGGTGTGTA TCATCTGCTG 900  
 GGGCCCTCTG CTGCAATCA TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTA 960  
 65 GACGGTGTGT GCATTCTGCA GTATGCTCTG CCTGCTGAAC TCCACGCTGA ACCCATCAT 1020  
 CTATGCTCTG AGGAGTAAGG ACCTGCGACA CGCTTTCCGG AGCATGTTTC CCTCTGTGTA 1080  
 AGGCACTGCG CAGCCTCTGG ATAACAGCAT GGGGGAAGCG GACTGCTCTG ACACCAACGC 1140  
 AAACATGCA GCCAGTGTTC ACAGGCGCGC AGAAGCTGCG ATCAAGAGCA CGGTCAAGAT 1200  
 TGCCAAGGTA ACCATGCTCTG TGTCCACAGA CAGCTCTGCC GAGGCTCTGT GA

Seq ID NO: 240 Protein sequence  
 Protein Accession #: NP\_149421.1

70 1 11 21 31 41 51  
 | | | | |  
 MALQIPPSAP SPLTSCWNAQ MTFSTKTSKE NEENIQCGEN FMDIECFMVL NPSQQLAIAV 60  
 75 LSLTGTFTV LLENLVLVTV ILHSRSLRCR PSYHFIGSLA ADLLGSVIFV YSFIDFHFV 120  
 RKDSRNVELF KLGGVITASPT ASVGSLEFLTA IDRYISIRP LAYKRIVTRP KAVVAFCLM 180  
 TTAIVIAVL PLLGWNCEKL QSVCSDFPHI DETYLMFWIG VTSVLLLFV YAYMYILWK 240  
 80 HSHAVRMIR GTRQKSIILH SEDGKVQVTR RPDQARMDIR AKTLVLILV VLICWGPLL 300  
 IMVYDVFGKM MNKLIKTVFA PCSMLCLLNS TVNPIIYALR SKDLRHAERS MFPSCEGTAQ 360  
 LDNSMGDSO CLHKHANNA SVHRAESCI KSTVKIAKVT MSVSTDTSAE L

Seq ID NO: 241 DNA sequence  
 Nucleic Acid Accession #: NM\_003596.1

Coding sequence: 82..1194

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	TAACAAGATA	ACCACATCAA	GATGGTTTGA	AAGCTGAAGC	AGAATCTACT	ATTGGCATGT 120
	CTGGTGATTA	GTCTGTGTAC	TGTGTTTTAC	CTGGGCCAGC	ATGCCATGGA	ATGCCATCAC 180
	CGGATAGAGG	AACGTAGCCA	GCCAGTCAAA	TTGGAGAGCA	CAAGGACCAC	TGTGAGAACT 240
10	GGCTTGGACC	TCAAAGCCAA	CAAAACCTTT	GCCTATCACA	AAGATATGCC	TTTAATATTT 300
	ATTGGRGGTG	TGCTCGGAG	TGGAACCA	CTCATGAGGG	CCATGCTGGA	CGCACATCCT 360
	GACATTGCT	TGGGAGAGGA	AACCAGGTC	ATTCCCGAA	TCCTGGCCCT	GAAGCAGATG 420
	TGCTCACGGT	CAAGTAAAGA	GAAGATCCG	CTGGATGAGG	CTGGTGTAC	TGATGAAGTG 480
	CTGGATTCTG	CCATGCAAGC	CTTCTTACTA	GAAATTTACG	TTAAGCATGG	GGAGCCAGCC 540
15	CCTTATTTAT	GTAATAAAGA	TCCTTTTGCC	CTGAAATCTT	TAACTTACCT	TTCTAGGTTA 600
	TTCCCCAATG	CCAAATTTCT	CCTGATGTC	CGAGATGGCC	GGGATCATGT	ACATTCAATG 660
	ATTCTCGAA	AGTTACTAT	AGCTGGATT	GATCTGAACA	GCTATAGGGA	CTGTTTGACA 720
	AAGTGAATC	GTGCTATAGA	GACCATGTAT	AACCAAGTGA	TGGAGGTTGG	TTATAAAAG 780
	TGCATGTTGG	TTCACTATGA	ACAACTGTG	TTACATCCTG	AACGGTGGAT	GAGAACACTC 840
20	TTAAAGTTCC	TCCAGATTCC	ATGGAACCA	TCAGTATTGC	ACCATGAAGA	GATGATTGGG 900
	AAAGCTGGGG	GAGTGTCTCT	GTCAAAAGTG	GAGAGATCTA	CAGACCAAGT	AATCAAGCCA 960
	GTCAATGTAG	GAGCTCTATC	AAAATGGGTT	GGGAAGATAC	CGCCAGATGT	TTTACAAGAC 1020
	ATGGCAGTGA	TTGCTCCTAT	GCTTGCCAAG	CTTGATATG	ACCCATATGC	CAACCCACCT 1080
	AACTACGGAA	AACTGATCC	CAAAATTAAT	GAAAACACTC	GAAGGCTCTA	TAAGGGAGAA 1140
25	TTCCAACTAC	CTGACTTTCT	TAAAGAAAA	CCACAGACTG	AGCAAGTGGG	GTAGCAGAAC 1200
	CAGGAGCCTC	TTCCATACAT	GAGGAAAGAT	TGCTGCCTTT	TCAGCAGAA	GGAAATTCCT 1260
	AGGATTGGCT	GTCCCTTGCC	AAGCTTGGTG	GAGCGTCTGC	ACCTTGGCTG	CGCCGCTGCT 1320
	GCATTTGCCA	GTTTCTCTCC	ACTGAGAGGA	TGGAGGTGTC	CGCACAGCTT	TGGGCTCTGT 1380
	GAGGGATCTG	CCTCTGAGC	AAAGAGCTCT	TGATCCCGAT	TTCTATGACA	GCCTGTCAGT 1440
30	AAGGAGCCCA	GAAGGAACAT	GTGTTTCCCT	TTAAACTCCC	TCTTGTCTC	TTTTCTTACA 1500
	TTATGACGTT	TGTTTTCAG	GAGAGGTTT	AAAAATGGGA	TCCTGTAAAG	AGACTTGGGC 1560
	AGTCTCTCTT	TGAAATAGGT	TGCTGTGACA	TGTTCTAATG	TTTGTAGAA	CACGTGTGCC 1620
	TGTTTAAAGT	TATTGATGTG	AATAATATTA	AATATCTTAA	TTATTTAATT	CATGTATTTG 1680
35	TTTCTGAGAA	GTTGGGAAAT	TACCATTATA	CATTTACAAC	CTAATGACTT	TGTATTTTAA 1740
	TTTTTCAAAA	TAAAGCTTT	CAATGTGA			

Seq ID NO: 242 Protein sequence  
Protein Accession #: NP\_003587.1

1	11	21	31	41	51	
40	MVGLKQNL	LACLVISST	VFYLGQHAME	CHHRIERSQ	FVKLESTRIT	VRTGLDLKAN 60
	KTFAYHKDMP	LIFIGVPRP	GTTLMRMLD	AHPDIRGEE	TRVIPRILAL	KQMSRSSEKE 120
	KIRLDEAGVT	DEVLDAMQA	FLLEIIVKHG	EPAPYLCNKP	PFALKSLTYL	SRLFPNAKFL 180
45	LMVRDGRASV	HSMISRKVTI	AGFDLNSYRD	CLTKWNRAIE	TMYNQCMVEG	YKKCMHLVHYE 240
	QLVLHPEKWM	RTLKFLQIP	WNHSLVHHEE	MIGKAGGVSL	SKVERSTDQV	IKPVNVGALS 300
	KWVGKIPPDV	LQDMAVIAPM	LAKLGYDFYA	NPPNYGKPD	KIIENTRRVY	KGEFQLPDFL 360
	KEKPQTEQVE					

Seq ID NO: 243 DNA sequence  
Nucleic Acid Accession #: NM\_001492.3  
Coding sequence: 1395..2513

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	CGAGCGGGCG	GTATGGCGCG	GGCGGGGGCC	GCGCGGGGGC	CGACGGGGCC	CGAGCCCATG 120
	CGAGCTACG	CGCAGCTAGT	GCAGCGCGGC	TGGGGCAGCG	CGCTGGCGGC	GGCGGGGGCG 180
	TGCAGCGACT	GCGGCTGGGG	GCTGGCGCGT	CGCGGCGCTG	CTGAGCACCG	GCACCTGGCG 240
	CGCGCGAGC	TGCTGCTGCT	GGCGCTCGGC	GCGCTGGGCT	GGACCGCGCT	GCGCTCGCGG 300
60	GCCACTGCGC	GCCTCTTTCG	GCCCTGGCG	AAGCGTGCT	GCCTCCAGCC	CAGAGATGCC 360
	GCCAAGATGC	CGAGAGCGCG	TTGGAAGTTT	CTCTTCTACC	TGGGCAGCTG	GAGCTACAGT 420
	GCCTACCTGC	TGTTTGGCAC	CGACTACCCC	TTCTTCCATG	ACCCACCATC	TGCTTCTTAC 480
	GACTGGACGC	CGGGCAATGC	AGTGCCACGG	GACATTGCAG	CGGCTACCT	GCTCCAGGGA 540
65	AGCTTCTATG	GCCACTCCAT	CTACGCTACG	CTATACATGG	ACACCTGGCG	CAAGGACTCG 600
	GTGGTCAATG	TGCTCCACCA	CGTGGTCACT	CTCATCTCTA	TGCTCTCTCT	CTACGCTTTC 660
	CGGTACCACA	ATGTGGGCAT	CCTTGTGCTC	TTCTGTCACG	ATATCAGTGA	CGTGACAGCT 720
	GAGTTCAACA	AGCTCAACAT	TTACTTCAAG	TCCCGCGGCG	GCTCTTACCA	TGGCTGTCAT 780
	GCCTTGGCAG	CAGACTTGGG	CTGCTCAGC	TTGGGCTTCA	GCTGGTTCTG	GTTCCGCGCTC 840
70	TACTGGTTC	CGCTCAAGGT	CCTGTATGCC	ACCACTCACT	GCAGTCTGGG	CACGGTGCCT 900
	GACATGCCCT	TCTACTTCTT	CTTCAATGCG	CTCTGCTGCG	TGCTCACCTT	TATGAACCTC 960
	TACTGGTTC	TGTACATCGT	GGCGTTTGCA	GCCAAGGTGT	TGACAGGCCA	GGTGACAGAG 1020
	CTGAAGGACC	TGGCGGAGTA	TGACACAGCC	GAGGCCACGA	GCTGGAAGCC	CAGCAAGGCC 1080
	GAGAAAGCCAC	TAGGAAACCG	CTGGTGAAG	GACAAGCGCT	TCTGAACCCC	TGGCGCCGCG 1140
75	CCCGTGGAC	CGGCGCCAC	CCGGAATACC	CGGCGCACGC	TCCCGTCTCT	TGGCGCGCCC 1200
	TCCACCCCTT	CCAATCTCTG	TCCTCTAGGG	CGCGCGCCAC	CTCCCTGGG	ACCCGCGCCC 1260
	CTCATCTCTG	CTCCATTTCC	CGGCGACGCC	CCCGAGGACC	CCTGCCCTC	CGGCGACACC 1320
	GGCGCGCGCC	TCAGCCCATC	GGTCCCGGGC	CGCGCGGAC	CCTGCGCACT	CTCTGCTCAT 1380
	CGCTTGGGAG	GAAGATGCCA	CGCGCGCAGC	AAGGTCCCTG	CGGCGCACAC	CTCTCTCTCC 1440
80	TCCTGGCCCT	GCTGCTGCC	TGCTGCCCC	TGACCCGCGC	CCCGTGGCCC	CCAGGCCAG 1500
	CGCGCGCCCT	GCTCCAGGCT	CTAGGACTGC	GCGATGAGCC	CCAGGCTGCC	CCAGGCTCC 1560
	GGCGGTTTCC	CGCGGTTTCC	TGGCGCTGT	TTCAGCGCGG	GGACCCGACG	GAGACAGGTT 1620
	CTGGCTGCGG	GCGGAGCTCC	CCAGGGGTCA	CCCTGCAACC	GTGCCACGTC	GAGGAGCTGG 1680
	GGGTGCGCGG	AAACATCGTG	CGCACATCC	CGGACCGCGG	TGCGCCACAC	CGGCGCTCGG 1740
	AGCCTGTCTC	GGCGCGGGG	CATTGCCCTG	AGTGACAGT	CGTCTTGGAC	CTGTGGGCTG 1800

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TGGAACCCCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGG GCGGCGGCGG 1860  
 CGGCAGCCCC GGAGGGCGGC TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GGCGCGGGCG 1920  
 CGGACCCCGG GCGGTGCTG CTCCGCCAGT TGGTGCCCGC CTGGGGCCCG CCAGTGGCGG 1980  
 CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCTCATG GCGCGCAGC CTCGCGCTGG 2040  
 CGCTGGCGCT AGCCCCCGG GCCCTGCGG CCTGCGCGCG CCTGGCCGAG GCCTCGCTGC 2100  
 TGCTGGTGAC CCGTGGACCG CGCTGTGACC ACCCCCTGGC CGGGCGCGCG CGCGAGCGCG 2160  
 AACCCTGTT GGGCGCGGC CCGGGGGGCG CTTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220  
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCGCG CGGCTTCCTG GCCAACTACT 2280  
 GCCAGGTCA GTGCGCGCTG CCGCTGCGCG TGTGCGGGTC CGGGGGCGCG CGCGCGCTCA 2340  
 ACCAGCGCTG GCTGCGCGCG CTGATGACG CGGCCGCCCG GGGAGCGCGC GACCTGCCCT 2400  
 GCTGCGTGCC CGCGCGCGCT TCGCCCATCT CCGTGTCTTT CTTTGACAA AGCGACAAAG 2460  
 TGGTGTGCG CGAGTATGAG GACATGGTGG TGAACGAGTG CGGCTGCGCG TAACCGGGGG 2520  
 CGGGCAGGGA CGCGGGCCA ACAATAAATG CCGGTGGTTC TGCTC

Seq ID NO: 244 Protein sequence  
 Protein Accession #: NP\_001483.2

1 11 21 31 41 51  
 20 MPPFPQGGPCG HLLLLLLALL LPSLPLTRAP VPPGPAAALL QALGLRDEPQ GAPRLRPVPP 60  
 VMWRLFRRRD PQETRSRGR TSPGVTLQPC HVEELGVAGN IVRHI PDRGA PTRASEFVSA 120  
 AGHCPEWTVV FDLSSAVEPAE RPSRARLELR FAATAAAPE AGWELSVQA GQAGADPGP 180  
 VLLRLQVLPAL GPPVRAELLG AAWARNASWP RSLRLALALR PRAPAACARL AEASLLLVTL 240  
 DPRLCHPLAR FRRDAEPVLG GPPGGACRAR RLYVSPREVG WHRWIAPRG FLANYCQGC 300  
 25 ALPVALSGSG GPPALNHAVL RALMHAAAPG AADLPCCVPA RLSPISVLFF DNSDNVVLQ 360  
 YEDMVVDECG CR

Seq ID NO: 245 DNA sequence  
 Nucleic Acid Accession #: NM\_021267.1  
 Coding sequence: 17..1125

1 11 21 31 41 51  
 35 ACGGCGGGCG CGGGGCTCCG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCAAGGCGGG 60  
 CGAGCGGGCG GTATGGCGCG GCGGGGGCCC GCGGCGGGCG CGAGCGGGCC CGAGCCCATG 120  
 CCGAGCTACG CGCAGCTAGT GCAGCGCGCG TGGGCGACCG CGCTGGCGCG GCGCGGGGCG 180  
 TGCACGAGCT GCGGCTGGGG GCTGGCGCGT CGCGGCTTGG CTGAGCACGC GCACCTGGCG 240  
 CGCGCGGAGC TGCTGCTGCT GCGGCTCGCG GCGCTGGGCT GGACCGCGCT CGCTCGCGCG 300  
 40 GCCACTGGCG GCCTCTTTCG GCCCTGGGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360  
 GCCAGATGC CCGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCGAGTG GAGCTACAGT 420  
 GCCTACCTCG TGTGTCGCAC GCACTACCCC TTCTTCCATG ACCCAACATC TGTCTTCTAC 480  
 GACTGGACCG CGGGCATGCG AGTGCCACCG GACATTGCAG CGGCTACCT GCTCCAGGGA 540  
 AGCTTCTATG GCGACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600  
 45 GTGGTCAATG TGTCCACCA CGTGGTCACT CTCTCTCTCA TGTCTCTCTC CTACGCTTTC 660  
 CGGTACCACA ATGTGGGCGT CCTTGTGCTC TTCTGCAAG ATATCAGTGA CGTGCACTT 720  
 GAGTTCACCA AGCTCAACAT TTACTTCAAG TCCCGGGCG GCTCTTACCA TGGGCTGCAT 780  
 GCCTTGGACG CAGACTTGGG CTGCTCAGC TTGGCTTCA GCTGTTCTG GTTCCGCTC 840  
 TACTGTTCC GCGTCAAGT CTTGTATGCC ACCAGTCACT CGAGTCTGCG CAGGCTGCT 900  
 50 GACATCCCTT TCTACTTCTT CTCTCAATCG CTCTGCTGCG TGCTCACCTT TATGAACCTC 960  
 TACTGTTCC TGTACATCGT GCGGTTTGCA GCCAAGGTGT TGACAGGCGA GGTGCACGAG 1020  
 CTGAAGGAGC TGCGGGAGTA TGACACAGCC GAGGCGGAGA GCCTGAAGCC CAGCAAAGCC 1080  
 GAGAAGCCAC TGAGGAACCG CCTGTTGAAG GACAAAGCGT TCTGAACCCC TGGGCGGCGC 1140  
 CCGGTTGAGC CGGCGCCAC CCGGAATACC CCGGCGGCGC TCCCGTCTCT TGGCGGCGCC 1200  
 55 TCCACCCCTT CCAACTCTGC TCCCTTAGGG CCGCGGCCAC CTCCCTGGG ACCCGGCCCC 1260  
 CTCATCTGCG CTCCTATTTC CGGCGCGGCC CCGGAGGACC CTGCGGCTTC CGGGGACACC 1320  
 GGCGCGGCCC TCGCCCACT GGTCCCGGGC CGCGCGGCGC CCGGCGGCTC CTCTGGTCT 1380  
 CGCTGGGAG GAGGATGCCA CCGCGCGGCG AAGGTCCTGT CGGCGGCGCC CTCTCTCTTC 1440  
 60 TCCGCGGCTT GCTGCTGCCC TGCTGCCCC TGAACGCGCG CCGGCTGCCC CAGGCGGCG 1500  
 CGCGCGGCTT GCTCAGGCT CTAGGACTGC GCGATGAGCC CCAGGCTGCC CCCAGGCTCC 1560  
 GCGCGGTTCC CCGGCTCATG TGGCGGCTGT TTGAGCGCG GAGCCCGCAG GAGACAGGT 1620  
 CTGGCTCGCG CGGGAACGTC CCAGGGGTCA CCTGCAACC GTGCCACGTC GAGGAGCTGG 1680  
 GGGTCCGCGT AAACATCGTG CGCCACATCC CGGACCGCGG TGGCGGCGCC CGGCGCTCGG 1740  
 AGCTGCTCTC GCGCGCGGGG CATTGCGCTG AGTGGACAGT GGTCTTGGAC CTGTGCGCTG 1800  
 65 TGGAACCCCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGG GCGGCGGCGG 1860  
 CGGAGCCCC GAGGGGCGCG TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GGCGCGGGCG 1920  
 CGGACCCCGG GCGGCTGCTG CTCCGCCAGT TGGTGGCGCG CCGGGGCGCG CAGTGGCGCG 1980  
 CGGAGCTGCT GGGCGCGGCT TGGGCTCGCA ACGCTCATG GCGCGCAGC CTCGCGCTGG 2040  
 CGCTGGCGCT ACGCCCCCGG GCCCTGCGCG CCTGCGCGCG CCTGGCGGAG GCCTCGCTGC 2100  
 70 TGCTGGTGAC CCGGACCGCG CGCCTGTGCC ACCCCTTGGC CGGCGCGCGG CGCGAGCGCG 2160  
 AACCGGTGTT GGGCGGCGCG CCGGGGGGCG CTTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220  
 TCGCGAGGTT GGGCTGGCAC CGCTGGGTCA TCGCGCGCG CGGCTTCTCT GCCAACTACT 2280  
 GCCAGGTGTA GTGCGCGCTG CCGTGGCGCG TGTGCGGGTC CGGGGGCGCG CGGCGGCTCA 2340  
 ACCAGCTGTT GCTGCGCGCG CTGATGACG CGGCGGCCCC GGGAGCGGCG GACCTGCCCT 2400  
 75 GCTGCGTGCT CGCGCGCTG TCGCCCATCT CCGTGTCTTT CTTTGACAA AGCGACAAAG 2460  
 TGGTGTGCG CGAGTATGAG GACATGGTGG TGAACGAGTG CGGCTGCGCG TAACCGGGGG

Seq ID NO: 246 Protein sequence  
 Protein Accession #: NP\_067090.1

1 11 21 31 41 51  
 80 MAAAGPAAGP TGPEPMPSYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60  
 LLLALGALGW TALRSAATAR LFRPLAKRCC LQPRDAARKP ESANKFLPYL GWSYSAYLL 120  
 FGTIDYPPFHD PPSVPYDWTG GMVPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML 180

LHHVVTLLILI VSSYAFRYHN VGILVFLHD ISDVQLEFTK LNIYFKSRGG SYHRLHALAA 240  
 DLGCLSPFGS WFWRLYWFP LKVLATSHC SLRTVPDIPF YFFFNALLLL LTLNLYWFL 300  
 YIVAFAAKVL TGQVHELKDL REYDTAAQS LKPSKAERPL RNLGVKDKRF

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Seq ID NO: 247 DNA sequence  
 Nucleic Acid Accession #: NM\_002081.1  
 Coding sequence: 222..1898

10 1 11 21 31 41 51  
 | | | | |  
 GGCTGCCGA GCGAGCGTTC GGACCTCGCA CCGCGCGCGC CCGCGCGCGC CGCCGCCGCC 60  
 GGCTTTTGT GTCTCCGCTT CCTCGGCGCG CGCGCGCTCT GGACCGCGAG CGCGCGCGCG 120  
 CGGAGCTTGG GCTCTGCCCT TCGCGGCGCG GAACTGCGCA GGACCGCGCC AGGATCCGAG 180  
 AGAGGCGCGG GCGGGTGGCC GGGGCGCGCG CGGCGCCCGC CATGGAGCTC CGGCGCCGAG 240  
 15 GCTGGTGGCT CTTATGTGCG CCGCGAGCGC TGGTGGCTTG CGCCCGCGGG GACCGCGCCA 300  
 GCAAGAGCGG GAGCTGCGCG GAGGTCCGCG AGATCTAAGG AGCCAAGGGC TTCAGCCTGA 360  
 CGAAGCTGGC CCAGGCGGAG ATCTCGGGTG AGCACTGCGG GATCTGTCCC CAGGGCTACA 420  
 CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480  
 CCGCGCTCCG GGACAGCAGC CGGTCTCTGC AGGCCATGCT TGCCACCCAG CTGCGCAGCT 540  
 20 TOGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GAGCTGCGAG GCCACCTTCC 600  
 CCGCGCGCTT CCGAGAGCTG TACACGACAG ACGCGAGGGC CTTCCGGGAC CTGTACTCAG 660  
 AGCTGCGCCT GTACTACCGC GGTGCCAACC TGCACCTGGA GGAGAAGCTG CGCGAGTTCT 720  
 GGGCCCGCCT GCTCGAGCGC CTCCTCAAGC AGCTGCACCC CCAGCTGCTG CTGCGCTGATG 780  
 25 ACTACCTGGA CTGCTCGGCG AAGCAGGCGG AGCGCGCTGG GCCCTTCGGG GAGGCGCCGA 840  
 GAGAGCTGGC CTTGCGGGCG ACCCGTGCCT TCGTGGCTGC TCGCTCCTTT GTGCGAGGCC 900  
 TGGGCGTGGC CAGCGAGCTG GTCCGGAAAG TGGCTCAGGT CCGCTTGGGC CCGGAGTGTCT 960  
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCTT GGGAGTCCCG GCGCGCAGGC 1020  
 CCTGCCCTGA CTATTGCGCA AATGTGCTCA AGGGCTGCTT TGCCAAACAG CCGGACCTGG 1080  
 30 ACGCGAGTGT GAGGAACTCT CTGGAATCCA TGGTGTCTAT CACCGACAGG TTCTGGGGTA 1140  
 CATCGGGTGT GAGAGAGTGT ATCGGAGCGG TGCAACAOTG GCTGGCGGAG GCCATCAACG 1200  
 CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTGAT CAGGGGCTGC GGGAAACCCA 1260  
 AGGTCAACCC CCAGGGCCCT GGGCCTGAGG AGAAGCGGGC CCGGGGCAAG CTGGCCCCGC 1320  
 GGGAGAGGCC ACTTCAGGCG ACGCTGGAGA AGCTGGTCTC TGAAGCCAGG GCCCAGCTCC 1380  
 35 GCGAGCTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGAGTGAAG AAGATGGCCC 1440  
 TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGATGGC CAGAGGCGCG TACCTCCCGC 1500  
 AGGTGATGGG TGACGGCTGT GCCAACCAGA TCAACAACCC CGAGGTGGAG GTGGACATCA 1560  
 CCAAGCCGGA CATGACCATC CGGAGCAGGA TCATGCACTT GAAGATCATG ACCAAGCGGC 1620  
 TGCGCAGCGC CTACACCGGC AACGACGTGG ACTTCAGGGA CGCCAGTGAC GACGGCAGCG 1680  
 40 GCTCGGGCAG CCGTGATGGC TGTCTGATGT ACCTCTGGGG CCGGAAGGTC AGCAGGAAGA 1740  
 GCTCCAGCTC CCGGACGCCCT TTGACCCATG CCTTCCACAG CCGTGTACAG CAGGAAGGAC 1800  
 AGAAGACCTC GGCTGCCAGC TGCCCCAGCG CCCGACCTT CCTCTGCCCG CTCTCTCTCT 1860  
 TCCTGGCCCT TACAGTAGCC AGGCCCCGCT GCGGTAATCT GCCCAAGGC CCCAGGGACA 1920  
 45 GAGGCGAAGG ACTGACTTTG CCAAAAATAC AACACAGAGC ATATTTAATT CACCTCAGCC 1980  
 TGGAGAGGCC TGGGTGGGA CAGGGAGGGC CGGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040  
 GTCCCGAGCC CAGGCGTGGC CTGCGCTGCC TTCTGCTCTT TTAATTTTGT ATGAGGTCTT 2100  
 CAGGTCAAGT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGAGCT CAGGGGACCC 2160  
 TCCGCTGCCC TAGCCCTCCC CCCAGCTCCC TGCAACCGCG CAGAAGCAGC CCCTCGAGGC 2220  
 50 CTACAGAGGA GGCTTCAAGG CAACCGCGTG GAGCCACAG CGAGCCTGTG CCTTCTCTCC 2280  
 CGCTCTCTCC CACTGGGACT CCCAGCAGAG CCCACACAGC AGCCCTGCGC CACCCCCAG 2340  
 CCTCCAGAGA AGCCCGGAC GGGCTGTCTG GGTGTCCGCC ATCCAGGCTC TGGCAGAGCC 2400  
 TCTGAGATGA TGCATGATGC CCTCCCTCA GCGCAGGCTG CAGAGCCCGG CCCACCTCC 2460  
 CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGAAGCG TGAGACAGCA CCACTGTCTA 2520  
 55 GGAGCTCAG GACTGTCTCT CCACAGACCC TGCACTGAGG GGCCCTCCAT GCGCAGATGA 2580  
 GGGGCCACTG ACCCACTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCAG 2640  
 GGAGGCGAGC TGGGCTCTGC CAATGTGGGC TGCCCTCTGC ACACAGGGCT CACAGGGCAG 2700  
 GCCTTGTCTG GGTCCAGGGC TGTGAGGGA CCGGAGGGC TGAGGAGCAG CCAGGACCGG 2760  
 CCTGTCTCCA TCCTCACCCA GATCAGGAAC CAGGGCCTCC CTGTTACCGG TGACACAGGT 2820  
 CAGGGCTCAG AGTGACCTTC GGCTGTCACT TGCTCACAGG GATGCTGGTG GCTGGTGA 2880  
 60 CCGCGCACTG CACACGGGAA TGCTTAGGTC CCTTCCCGAC CCAGCCAGCT GCACTGCAGG 2940  
 GCACCGGGAC CTGGATAGTT AAGGCTTTT CCAACATGCG ATCCATTAC TGACACTTCC 3000  
 TGTCTTGTG CATGGAGAGC TGTGCTCTCC TCCAGATGCG CTTGGAGGCG CCGCAGGGCC 3060  
 CACCTTGGAC CCGTGTGACC TCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCGAGGC 3120  
 CTGSAAGGCG CCTCTTCCC TCTGTGCCCG CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180  
 65 TGTGGTGTG GGAAGGGGTC CTGAGGGGG AGGAGGACTT GGAGGCTG GGGGCGAGCT 3240  
 TCTTGAACCG ACTGACCTTG AGGAGGCGCG TTAGTGTGCG TTGCTTTTC ATCAAGGTCC 3300  
 OGCACAGTGG ACGGAGGTCC CCGGTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360  
 CTGACTTTAG ATGTTTGGG ATCAGGAGCC CCAACACAG GCAAGTCCAC CCTAATAA 3420  
 CCCTGCCAGT GCCAGGGTGG GCTGGGAGCT CTGGCACAGT GATGCGGGC GCCAGGACAG 3480  
 70 CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTAGCTCA 3540  
 TCTCTGGAAG GGGCAGCCCT GAGTGGTCACT TGGTCAGGCG AGTGGCCAAG CCTGTGTGT 3600  
 CTTCTCTCCA CAAGGTCCCC CCAACGCTCA GTGTCAAGCG GTGAGTGTG TTTCTTTGAG 3660  
 TCCTTGTATG AATAAAGGC TGAACCTA AA

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Seq ID NO: 248 Protein sequence  
 Protein Accession #: NP\_002072.1

80 1 11 21 31 41 51  
 | | | | |  
 MELRARGWWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSVDP QAEISGEHLR 60  
 ICPQGTTCCT SEMEENLANR SHABLETALR DSRVLQAML ATQLRSFDH FQHLNDSE 120  
 TLQATPPGAG GELTYQARA FRDLYSELRL YVRGANLHLE ETLAEPWALR LERLLFKQLHP 180  
 QLLLPDDYLD CLGKQABALR PFGEAPREL RLRATRAFVA RSPVQGLGVA SDVVRKVAQV 240  
 PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVLKGL ANQADLDAEW RNLLDSMVL 300  
 TDKFWGTSGV ESVGSVHTW LAEAINALQD NRDTLTAKVI QGQGNKYNP QGPGPEEKRR 360



RGKLAPRPRP PSGTLEKLVS EAKAQLRDVQ DFWSLPGTL CSEKHALSTA SDDRCWNGMA 420  
 RGRYLPEVMG DGLANQINNP EVEVDITKPD MTRQQIMQL KIMTNRLRSA YNGNDVDFPD 480  
 ASDDGS GSGS

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Seq ID NO: 249 DNA sequence  
 Nucleic Acid Accession #: NM\_001492.3  
 Coding sequence: 8..1864

10 1 11 21 31 41 51  
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 GAAGGCCATG GTCTCCOCAC GGAATGTCGG GTCCTCTCC CAGACTGTGA TCCTAGOGCT 60  
 CATTTTCCCT CCCACAGACAC GGCCCGCTGG CGTCTTCGAG CTGCAGATCC ACTCTTTCGG 120  
 GCGGGGTCCA GGCCCTGGGG CCGCGGGTTC CCGCTGCAGC GCGCGGCTCC CCTGCGGCT 180  
 15 CTCTCTCAGA GTCTGCTGA AGCCTGGGCT CTCAGAGGAG GCGCGGAGT CCCGCTGGC 240  
 CTGCGGCGAC GCGCTGAGTG CGCGCGGACC GGTCTACACC GAGCAGCCCG GAGCGCCCGC 300  
 GCCTGATCTC CCACTGCGCG ACGGGCTCTT GCAGGTGCCC TTCGGGAGC CCTGGCTGG 360  
 CACCTTCTCT TTCACTATCG AACCTGGAG AGAGGAGTTA GGAGACCAGA TTGGAGGGCC 420  
 CGCTGGAGC CTGCTGGGCG GCGTGGCTGG CAGCGGGCGC TTGGCAGCGG GAGGCCCGTG 480  
 20 GGCCCGGGAC ATTACAGCGG CAGGCGGCTG GAGCTGCGC TTCTCGTACC GCGCGGCTG 540  
 CGAGCGGCTT GCGCTCGGGA CGCGTGCAC GCGCTCTGC CGTCCGCGCA GCGCCCGCTC 600  
 GCGGTGGCGT CCGGACTGCG GCGCTGCGC ACGCTCGAG GACGAATGTG AGGCGCGCT 660  
 GGTGTGCGGA GAGGCTGCA GCGCTGAGCA TGGCTTCTGT GAACAGCCCG GTGAATGCG 720  
 ATGCTAGAG GCGTGGAGTG GACCCCTCTG CACGCTCCCT GTCTCCACCA GCAGCTGCT 780  
 CAGCCCGAGG GCGCGTCTCT CTGCTACCAC CGGATGCCTT GTCCCTGGGC CTGGGCGCTG 840  
 25 TGACCGGAGC GCGTGTGCGA ATGAGGCGAG CTGTAGTGAG ACACCCAGGT CCTTTGAATG 900  
 CACCTGCGCG CTGTGGTCTT ACGGGCTGCG GTGTGAGGTG AGCGGGGTGA CATGTGCGA 960  
 TGGACCTGCG TTCAACGCGG GCTTGTGTGT CCGGGGTGCA GACCTGACT CTGCTACAT 1020  
 CTGCCACTGC CCACTGGGTT TCCAAGGCTC CAACTGTGAG AAGAGGGTGG ACCGGTGCAG 1080  
 30 CTGCGAGCCA TGCCGCAATG GCGGACTCTG CCGGACCTG GGCCAAGCCC TGCGCTGCG 1140  
 CTGCGCGGCG GCGTTCGCGG GTCTCGCTG CGAGCACGAC CTGGAAGACT GCGCGGGCG 1200  
 CGCTGCGCT AACGCGGCGA CGTGTGTGGA GCGCGGGCG GCGCACCGCT GCTCTGCGC 1260  
 GCTGGGCTTC GCGCGCGCG ACTGCGCGCA GCGCGCGGAC CCGTGGCGCG CCGCGCCCTG 1320  
 TGCTCACGGC GCGCGCTGCT ACGCCCACTT CTCGCGGCTC GTCTGCGCTT GCGCTCCCG 1380  
 35 CTACATGGGA GCGCGGTGTG AGTTCCAGT GCACCCGAGC GCGCAAGCG CCTTGCCCG 1440  
 GGCCCGCGCG GCGCTCAGCG CCGGGGACCC TCAGCGCTAC CTTTTCCTC CGGCTCTGG 1500  
 ACTGCTCGTG GCGCGGGCG TGGCGGGCG TCGCTCTTG CTGCTCCAG TGGCGGGCG 1560  
 TGCCCACTCC CAGGATGCTG GTCTCGCTT GCTGGCTGGG ACCCGGAGC CGTCAGTCCA 1620  
 CGCACTCCCG GATGCACTCA ACAACCTAAG GAOCAGGAG GGTTCGGGG ATGGTCCGAG 1680  
 40 CTGCTCCGTA GATTGGAATC GCGCTGAAGA TGTAGACCTT CAAGGGATTT ATGTATATC 1740  
 TGCTCCTTCC ATCTAOGCTC GGGAGGTAGC GACGCCCTT TTCCCGCGC TACACACTGG 1800  
 GCGCGCTGG CAGAGGCAGC ACCTGCTTTT TCCCTACCTT TCCTGATTC TGTCCGTGA 1860  
 ATGAATTGGG TAGAGTCTCT GGAAGGTTT AAGCCATTT TCAGTTCTAA CTTACTTTCA

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Seq ID NO: 250 Protein sequence  
 Protein Accession #: NP\_058637.1

1 11 21 31 41 51  
 | | | | | |  
 MVSPRMSGLL SQTIVILALIF LQTRPAGVF ELQIHSFGPG PGPGAPRSPC SARLPCLRF 60  
 50 RVCLKPLGSE EAESPICALG AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDAMPGT 120  
 SFIIETWREE LSGQIGGPAPW SLLARVAGRR RLAAGGFWAR DIQRAGAWEL RFSYRARCEP 180  
 PAVGTACTRL CRPRSAFSPC GPGLRPAFPL EDECEAPLVC RAGCSPEHGF CEQPGECRCL 240  
 EGWTGPLCTV PVSTSSCLSP RGPSSATTGC LVPGEPCDG NPCANGGSCS ETFRSFECTC 300  
 55 PRGFYGLRCE VSGVTADGP CFNGGLCVGG ADPDSAYICH CPPPGQGSNC EKRVRCSLQ 360  
 PCRNGLCLLD LGHALRCRER AGFAGPRCEH DLDDCAGRAC ANGGTCVEGG GAHRCSCALG 420  
 FGGRDCRERA DPCARFPCAH GGRCYAHFSG LVCACAPGYM GARCEFPVHP DGASALPAAP 480  
 PGLRPGDPQR YLLFPALGLL VAAGVAGAA LLVHVRRGH SQDAGSRLLA GTPEPSVHAL 540  
 60 PDALNLRITQ EGSDDGSSS VDWNRPEVDV PQGIYVISAP SIYAREVATP LFPPLHTGRA 600  
 GQRQHLLFPY PSSILSVK

60

Seq ID NO: 251 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

65 1 11 21 31 41 51  
 | | | | | |  
 GAAATATAAC CATTGCAATT AGAAAAATATC CAAAAATAGCC TGTATCTTC CAOGTGGCCT 60  
 AGATATATGA CAATCCCAAA TATACAAATT TTCTTTAAAA GTAGTACAAT TTCTTTGTA 120  
 GCTCAATTC CTTATATGAC TTCAGACTGG AGAAGCCTGT TAAACCACTG TTAGTTTCAG 180  
 70 TTAGAAAGTC TGAGAGACTT TATACATAAA TTCTCAATT GGCTGCTGTA CAOGTGCCAG 240  
 AGTTTACTA CTGTAGTGAC CGTTGAGAAG ACCCTTGTTT ATTACATTT GAAGCACTGT 300  
 TTGTGCAAAAC AACCTTTCTT TGTAAAGTGC CTGTATTCCT TTCAATTACT TCATGTCCAG 360  
 GGGTGCTATT TACCTAGAAC CATTGTCTAC TACAATTAAC ATTACATTA CAAAGTGTGT 420  
 75 GGTTTTCTTT TTCAAGGAGG TTCAATTAAG GCAATAAGAT GTTGTCTGGA GAAACCTATT 480  
 GTTACTGAA AGCACTCAAT GAAGTCAAA TACTGAAGCT TTTGCTACA TCTTGTCTT 540  
 TTATGTAAT ATGTTAAATA TAACATCTAA GGAAAAATAA CAATATTATA ATTATGTGT 600  
 TGCCATTGTC ATATCAACT TGCTTTGTAT CATACTAATG TTACATACT TATCGATCAA 660  
 TAAAAATACA TTTCAATGTT AAAAAAAAAA AAAAAAAA

80

Seq ID NO: 252 DNA sequence  
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | | |  
 AGGTACTGCC AGAAAGGATC AGGACCTGGA GTCTGGCAAG AGGAAGACAG AGGCCTGTGT 60

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GGGAAGCGAG TTGTTATCTT TGGTTATCTA GCTGTATGAG TGTATTGGTC TTCATAAAGC 120  
TAGATAAACC AGAAGTAAAA CTCTCTCAAG ATCGCGGGG AGCGTGTGAG AATGAAAGAC 180  
TACAGCCGAG AGACAGATAA AACCCAGAAAG GTCCAGGAATA CTTATTGAAT CTAACCTTTGT 240  
TTTTGTTTGT TTTTCTTCTT TATGATTAAA GGTGGGATGA GAGAAAATTA AATGACACAC 300  
ACATGCTAAA ATATCAAGGT TCCAGATATG TCTTGAGAGG GGTGTGTGCA GCTGCAAAAG 360  
AGAAGTGTAT AGTGATAATG AGTAAAGATG CATGTGCAGT TTGTTCTATT TTAAGGCCAA 420  
AGTTATATCA GGGATTTTTT TCTTAGAAAG GTGTGCGAGA GATGTCTGGT ACCTAGTTTA 480  
AAAATGATTC CATATATATG AGACTTGGGC AGTTCCTTTG GGAGGCACCT CCCTCTCAAA 540  
ATTTGAAGAT TGTGCTTGGG AATTACTTTA CATGTATTGT GGCTGTATGT CAATTGTGAC 600  
GAAATTAGAC TTTCAGAAAA GTTTATACTG GAAGGTTAAT AATTGTATC TACTGAGGAC 660  
TTAGAGCTAG CAGGCAAAAT GAAAAAARAG CAAGGGCTGA TTTTATTCTT 720  
TCTATTCAA ATACAAGGAC AGATGCTTCT CTGTTCCAAG AGGGTTTCTT TGAGGAAGCT 780  
ACTGAAGCAG AAAGACATGA TGGAGACGAG ATCGCCTCCC CTCTGTGCAA AGTGTAAAA 840  
AAATGTTCTG TCTTACTCTG CGCCTAGCAT TGGAAATGAA AGTGACATTT AOGCCACAAC 900  
CCACGTGTGC GCCTCCTCTC TTTTGTTTTA AGGATGATCA GGTCTATCCA GGAAACAGCT 960  
CTGGCATCCC AAATGAAAT AATTAGGACG TATATAGACC TGACAAAAAT GGAAAGGGGG 1020  
TGGGGAATCT GAGGGTCTGT CTGCTTAAT TGATTCCGCT AAACGGAATG CAGGAGATGT 1080  
GAACGGCAGG AGCTCCGAT TCCCACGCTC GGGGGCAAGT GATAAAGCGG GGCCGGGCAG 1140  
CCTATGACAG ACAGCCCTGT TGGGGGGTGG GGGTATGAAA AAAACATCAA GTGCACACAC 1200  
CATACTCAATC TCATCGCTT AAGAAAGTAA AGGCATTTC CACCCACAGC CATCTGCAGC 1260  
TTCCCAATG GCAGACCAA CTGGTCTGTA GCTGCTACAT AGTCTGCTTC TGTAAATTTT 1320  
TTAACCATCT TTTAATCTGG CCATAATTAA GTTGGCTTT CTTCGTTGTT TGAGATTTTC 1380  
AGAATTCAAG GCAAGCTAGT AGAAAGCAAT TCCAAGAAAG TCCCATGACT GCCTGCCCTT 1440  
AATGTCAAAA TCTCAGTCCA TGAGATTATG GCCTTGTGAC CACATTTTGT CTTTGTGTTT 1500  
GGGTGGGCAA ATGTGTATAG AGATAAATA CATATCTCTA TATAACAGTC GTTATTATAA 1560  
TTTCATGAGG CTTTAACTCT CTTAACATGA TACATCTAGG AACTTGGTCT AATTGTGCTA 1620  
GTAGATATAC ACTAGAAGTA AAACATATAA GTCATTAGCC TGTAGAAAGT TGATTATGAT 1680  
AACAATATGA TAAAAAGTTT GTTTTGGAAAT AGTCTCAGCT AGATGGGTCT AAATAGCCAT 1740  
TTTAATGTAA TCTAAAAATA ACACATATGCC TAGCAGAAAC TTTGGCGCTT TGGAGGTCCC 1800  
CATTGTGCGC TCTTCATAAA AGTCCCTAAG TTTTCCATAT GTCACCAAGC AAACATTTGT 1860  
ATAGGCATT TACACAGAAAT ATAACCATG CAATTAGAAA ATATCCAAAA TAGCCTGTTA 1920  
TCTTCCACGT GGCCTAGATT ATTGACAATC CCAATATAC AATTTTCTT TAAAGTAGT 1980  
ACAATTTCTT TTGTAGCTTC AATTCCTTAT ATGACTTCAG ACTGGAGAAG CCTGTTAAAC 2040  
CACTGTAGT TCCAGTTAGA AAGTCTGAGA GACTTTATAC ATAAATCTC AATTGGCTG 2100  
CTGTACACTC GTCAGAGTTT TACTACTGTA GTGACCGTTG AGAAGACCTT TGTATTATTA 2160  
CATTGAAGC ACTGTTGTG CAAACAACCT TTCAATTGTA AGTGCTGTA TTCCTTTCAT 2220  
TTACTTCATG TCCAGGGGTG CTATTTACCT AGAACCATG TCTACTACAA TTAACATTTA 2280  
CATTACAAAG TGTGTGGTTT TCTTTTCAA GGAGGTTCAA TTAAGGCAAT AAGATGTTG 2340  
CTGGAGAAAC CTATTGTTTA CTGAAAGCAC TCAATGAAGT CAAATTACTG AAGCTTTTGC 2400  
CTACACTTGT GTCTTTTATG TAAATATGTT AAATATAACA TCTAAGGAAA ATAAACAATA 2460  
TTATAATTAT GTGTTTGCCA TTGTATATC AAACCTGCTT TGTATCATAC TAATGTTACA 2520  
TAACCTATCG ATCAATAAAA ATACATTTCA ATGTT

45 Seq ID NO: 253 DNA sequence  
Nucleic Acid Accession #: NM\_001650.2  
Coding sequence: 40.1011

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GGGGTCTGGA CTCAGCTTTT CTGGAAAGCA GTCCAGCGG AATTCTCTGC CATGCTTATT 180  
TTTGTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240  
GTGACATGG TTCTCATCTC CTTTGTCTT GGACTCAGCA TTGCAACCAT GGTGCAAGTC 300  
TTTGGCCATA TCAGCGGTGG CCACATCAAC CTGTCAGTGA CTGTGGCCAT GGTGTGCACC 360  
AGGAAGATCA GTCTGCGCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420  
ATTGGAGCAG GAACTCTCTA TCTGTGCACA CCTCCAGTG TGTGGGAGG CTTGGGAGTC 480  
ACCATGGTTC ATGGAAATCT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540  
TTTCAATTGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACGGACTGA TGTCACTGGC 600  
TCAATAGCTT TAGCAATTGG ATTTTCTGTT GCAATTGGAC ATTTATTGTC AATCAATTAT 660  
ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720  
GAAAACCATT GGAATATATG GGTGGGCCC ATCATAGGAG CTGTCTCGC TGGTGGCCTT 780  
TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840  
AAAGCTGCCC AGCAACAACA AGGAAGCTAC ATGAGGTTGG AGGACAACAG GAGTCAGGTA 900  
GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCAATG TGATTGACGT TGACCGGGGA 960  
GAGGAGAAGA AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTCAATATG ACTAGAAGAT 1020  
CGCACTGAAA GCAGACAGA CTCCTTAGAA CTGTCTCAG ATTTCTCTCC ACCCATTAAG 1080  
GAAACAGATT TGTATATAAT TAGAAATGTG CAGGTTTGT GTTTCATGTC ATATTACTCA 1140  
GTCTAAACAA TAAATATTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200  
TCCAAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAATATATG ACCTATTTTA 1260  
TCTAGTTACC TTTCATTAC AACCAATTTT AACOGTGTG CAAGATTGG TTAAGCTTGT 1320  
CCTGACAGAA CTCAAAGACA CGTCTATCAG CTTATTCCTT CTCTACTGGA ATATTGTTAT 1380  
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75 Seq ID NO: 254 Protein sequence  
Protein Accession #: NP\_001641.1

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1 11 21 31 41 51  
MSDRPTARRW GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EPLAMLIPVL LSLGSTINWG 60  
GTEKPLPVDV VLISLCFGLS IATMVQCFGR ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120  
AQCLGAIIGA GILYLVTPPS VVGJLVTMV HGNLTAGHGL LVELIITFQL VFTIFASCD 180  
KRTDVTGSIA LAIGFSVAIG HLPAINYGA SMNPARSPFG AVIMGNWEKH WIYVVGPIIG 240  
AVLAGGLYEX VFCPDVEFKR RFKEAFSKAA QQTKGSYMEV EDNRSQVETD DLILKPGVVH 300

VIDVDRGEEK KGKQDSGEVL SSV

Seq ID NO: 255 DNA sequence

Nucleic Acid Accession #: U26742.1

Coding sequence: 325..1449

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GGCAGCGGAC	CCGGCACTTC	CAACATTATT	AAATAATAAG	AAAGCGGCTC	CTACTCCAGG	120
CTCAAACTCT	CCTGCAGACC	AATGGACACC	TTCTAAGAGT	TTGGCGAGTC	AGTGACTGAA	180
GGGCCCCGTC	ATTCCAAGAT	AAATAGGATT	TACCAATCCT	TGGATGAAGT	GCTTGGGAAG	240
TCCTTAAAGT	CCATAATCAA	CTGCCATTTC	AAAGAATATA	GATGGTTTTC	AAAAGTTCAT	300
GCTGTCCTCT	CATTGAATTT	TAGAATGATT	GAAGATAGTG	GGAAAAGAGG	AAATACCATG	360
GCAGAAAGAA	GACAGCTGTT	TGCAGAGATG	AGGGCTCAAG	ATCTGGATCG	CATCOGACTC	420
TCCACCTACA	GAACAGCATG	CAAGCTTAGG	TTTGTTTACA	AGAAATGCAA	TTTGCACTCG	480
GTGGACATAT	GGAATGTGAT	AGAAGCATTC	CGGGAATAAT	CTCTGAACAA	CCTGGACCCA	540
AACACTGAAC	TCAACGTGTC	COGCTTAGAG	GCTGTGCTCT	CCACTATTTT	TTACCAGCTC	600
AACAAACGGA	TGCCAACACC	TCACCAAAATC	CATGTGGAGC	AGTCCATCAG	CCTCCTCCTT	660
AACCTTCCTG	TTGCAGCGTT	TGATCCGGAA	GGCCATGGTA	AAATTTTCAGT	ATTTGCTGTC	720
AAATATGGCTT	TAGCCACATT	GTGTGGAGGG	AAGATCATGG	ACAAATTAAG	ATATATTTTC	780
TCAATGATTT	TGACTCCAG	TGGGGTGATG	GTTTATGGAC	GATATGACCA	ATTCCTTCGG	840
GAAGTCTCA	AACATACCCAC	GGCAGTTTTT	GAAGGTCCCT	CATTGTGGTA	CACAGAACAG	900
TCAGCCAGAT	CCGTGTTCTC	CCACAGAGAA	AAAGTCACGT	TAAATGGTTT	CTTGACACCG	960
CTTATGTCAG	ATCCTCCCCC	GCACTGTCTG	GTCTGGTTGC	CTCTCTGCA	TCGACTAGCA	1020
AATGTGGA	ATGCTCTCCA	TCCGGTTGAG	TGTTCCCTACT	GCCACAGTGA	GAGTATGATG	1080
GGATTTGCT	ACCGATGCCA	ACAGTGTAC	AATTACCCAGC	TCTGTCAGGA	CTGCTTCCTG	1140
AGGGGACATG	CCGGTGGTTT	TCATAGCAAC	CAGCACCAAA	TGAAAGAGTA	CAOGTCATGG	1200
AAATCACCTG	CTAAGAACCT	GACTAATGCA	TTAAGCAAGT	CCCTGAGCTG	TGCTTCCAGC	1260
CGTGAACCTT	TGCACCCCAT	GTTCCAGAT	CAGCCTGAGA	AGCCACTCAA	CTTGGCTCAC	1320
ATGTTGATA	CTTGGCCTCC	CAGACCTGTA	ACCAGCATGA	ACGACACCTT	GTTCTCCAC	1380
TCGTGTTCCCT	CCTCAGGAAG	TCCTTTTAT	ACCAGGAGCT	CGGACGGTGC	TTTGTGGA	1440
TGCGTCTAGA	TGGATAACAT	GACTTCTTCT	ACCTTAAAT	ATTCTATATA	TACTTTGAGC	1500
TGTTCTGGTT	CCTCCAGGGT	GCAATGTAAC	CATTAAACCA	AAATATGATT	ATTTCCCTTT	1560
TTTCCCATTT	TCAGTCATTT	TGGAATGTTT	TCTGTGAACC	ACAGTTGGGT	TGTTTAAAGC	1620
TCACATTTCT	TTCTGTCAAC	ACAGAGATTG	GCCTACGGTT	TCTGTTTGA	GGGTGCTGTT	1680
CAATAAGCT	GTGTACACTA	AATGTCC				

Seq ID NO: 256 Protein sequence

Protein Accession #: AAC50424.1

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MIEDSGKGRN	TMAERRQLFA	EMRAQDLDR	RLSTYRTACK	LRFVQKKCNL	HLVDIWNVIE	60
ALRENALNNL	DPNELNVS	LEAVLSTIFY	QLNKRPMTTH	QIHVEQSISL	LINFLAAFD	120
PEGHGKISVF	AVKMLATLC	GGKIMDKLRY	IFSMISDSSG	VMVYGRYDQF	LRVLEKLFPA	180
VFEQSPFGYT	EQSARSCFSQ	QKVTNLGFL	DTLMSDPPFQ	CLVWLPPLHR	LANVENVFHP	240
VECSYCHSES	MMGFYRQDC	CHNYQLQDC	FWRGHAGGSH	SNQHQMKEYT	SNKSPAKILT	300
NALSKSLSCA	SSREPLHMP	PDQPEKPLNL	AHIVDTWPPR	PVTSMNDTLF	SBSVPSSGSP	360
FITRSSDGAF	GGCV					

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Seq ID NO: 257 DNA sequence

Nucleic Acid Accession #: NM\_004172.1

Coding sequence: 179..1807

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CACCCCTTAC	AAAATCAGAA	AAGTTGTGTT	TTCTAATACC	AAAGAGGAGG	TTTGGCTTTC	120
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GACTAAAAGC	AATGGAGAAG	AGCCCAAGAT	GGGGGGCAGG	ATGGAGAGAT	TCCAGCAGGG	240
AGTCCGTAAA	CGCACACTTT	TGGCCAAGAA	GAAAGTGAG	AACATTACAA	AGGAGGATGT	300
TAAAGCTTAA	CTGTTTGGGA	ATGCTTTTGT	GCTGCTCACA	GTCAACGCTG	TCATTGTGGG	360
TACAATCCTT	GGATTTACCC	TCCGACCATA	CAGAATGAGC	TACCGGGAAG	TCAAGTACTT	420
CTCCTTTCTT	GGGGAACCTC	TGATGAGGAT	GTTACAGATG	CTGGTCTTAC	CACCTATCAT	480
CTCCAGTCTT	GTCAACAGAA	TGGCGGCGCT	AGATAGTAAG	GCATCAGGGA	AGATGGGAAT	540
GCGAGCTGTA	GTCTATTATA	TGACTACCA	CATCATTGCT	GTGGTGATG	GCATATCAT	600
TGTCATCATC	ATCCATCCTG	GGAAGGGCAC	AAAGGAAAAC	ATGCACAGAG	AAGGCAAAAT	660
TGTAOGAGTG	ACAGCTGCAG	ATGCCCTTCT	GGACTTGATC	AGGAACATGT	TCCCTCCAAA	720
TCTGGTAGAA	GCCTGCTTTA	AACAGTTTAA	AAOCCAACTA	GAGAAGAGAA	GCTTTAAAGT	780
GCCCATCCAG	GCCACGAGAA	CGCTTGTGGG	TGCTGTGATA	AACAATGTGT	CTGAGGCCAT	840
GGAGACTCTT	ACCCGAATCA	CAGAGGAGCT	GGTCCCACTT	CCAGGATCTG	TGAATGGAGT	900
CAATGCCCTG	GCTCTAGTTG	TCTTCTCCAT	GTGCTTCGGT	TTTGTGATTG	GAAACATGAA	960
GGAAACAGGG	CAGGCCCTGA	GAGAGTCTTT	TGATTCCTTT	AACGAAGCCA	TCATGAGACT	1020
GGTAGCAGTA	ATAATGTGTT	ATGCCCCCGT	GGGTATTCTC	TTCTGATTG	CTGGGAAGAT	1080
TGTGGAGATG	GAGACATG	GTGTGATTGG	GGGGCAGCTT	GCCATGTACA	CGTGACTGT	1140
CATTGTTGGC	TTACTCATTC	ACGCACTCAT	CGTCTTGCCA	CTCCTCTACT	TCITGGTAAC	1200
ACGGAAAAAC	CCTTGGGTTT	TTATTGGAGG	GTGTGTCGAA	GCACTCATCA	CGCTCTGGG	1260
GACCTCTTCA	AGTTCTGCCA	CCCTACCCAT	CACCTTCAAG	TGCTGGAAG	AGAACAATGG	1320
CGTGGACAAG	CGGCTACCCA	GATTGCTGCT	CCCGTAGGGA	GCCACCAATTA	ACATGGATGG	1380
GACTGCCCTC	TATGAGGCTT	TGGCTGCCAT	TTTCATTGCT	CAAGTTAACA	ACTTTGAAC	1440
GAACCTCGGA	CAAATTATTA	CAATCAGCAT	CACAGCCACA	GCTGCCAGTA	TTGGGGCAGC	1500
TGGAATTCTT	CAGGGGGGCC	TGGTCACTAT	GTCATTGTTG	CTGACATCTG	TGGGCTGCC	1560
CACAGACGAC	ATCAAGCTCA	TCATCGGGT	GGACTGGTTC	CTGGATGCC	TCCGACCA	1620

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 GGAATCCCAT TTATCAATC ATTCAAAAT TTCACTGGA GTGGGGTTTG CTTTGTGTTT 3240  
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 TTAATTTTAA CCCCTAAGG AATATCCAGT CAAAGACGCT GAGTGGGAGC TGTCAAGGCA 3420  
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 GAGGCTCTAT TTCGGAATA CACTACAAAT GTTAAAGTAC GTGGCTGTCC TCTTAAGACA 3660  
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 CACAGGCTCT GCATACACAT GCACCTAGTG TGGACTGGGA AGCATTACTT TGTAGATGTA 3840  
 TTTCAATAA AGAAAAAAT AGTTTATACAT T

Seq ID NO: 258 Protein sequence  
 Protein Accession #: NP\_004163.1

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1 11 21 31 41 51  
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 MRAYVYMTT TIIAVVIGII IVIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFPP 180  
 NLVEACQKQF KTNYEKRSFK VPIQANETLV GAVINNVSEA METLTRITE LVPVPGSVNG 240  
 VNALGLVVPF MCFPGVIGNM KEQGQALREF FDSLNEAIMR LVAVIMMYAP VGILFLIAGK 300  
 IVEMEDMGVI GGQLAMYTVT VIVGLLIHAF IVLPLLYFLV TRKNPWVFIG GLLQALITAL 360  
 GTSSSSATLP ITFKCLEENN GVDKRVTRFV LPVGATINMD GTALYEALAA IPIAQVNIFE 420  
 LNFQGIIITIS ITATAASIGA AGIPQAGLVT MVIVLTSVGL PTDDITLIIA VDWFLDRLRT 480  
 TTNVLGDSLG AGIVEHLRSR ELKRNDRVEMG NSVIEENEMK KPYQLIAQDN ETEKPIDSET 540  
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Seq ID NO: 259 DNA sequence  
 Nucleic Acid Accession #: NM\_021948.1  
 Coding sequence: 48..2783

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 TGAAGGAGA CAGCTCAGAG GACCGGCTT TCGCGTGGC CATCGCGGGC GACCGGCCAC 180  
 TGCAAGGCGT GCTCGGCGGC GGCCTCACA TCCCTTGCCA CGTCCACTAC CTGCGGCCAC 240  
 CGCGGAGCCG CGGGGCTGTG CTGGGCTCTC CGCGGGTCAA GTGGACTTTC CTGTCCCGGG 300  
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 GGTTCGCGCT GGCACCTGCC GCGTACCCAG CGTGGCTCAC CGAGCTCTCC CTGGCGCTGA 420  
 GCGAGCTGCG CCCCAACGAC TCAGGTATCT ATCGCTGTGA GGTCCAGCAC GGCATCGATG 480  
 ACAGCAGGGA CGCTGTGGAG GTCAAGGTCA AAGGGGTGCT CTCTCTCTAC CGAGAGGGCT 540  
 CTGCGCGCTA TGCTTTCTCC TTTCTTGGG CCGAGGAGGC CTGTGCGCGC ATTGGAGCCC 600  
 ACATCGCCAC CCGGAGCAG CTCTATGCCG CCTACCTTGG GGGCTATCAG CAATGTGATG 660  
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 ACGGAGACAT GGTAGGCTTC CCCGGGGTCC GGAACATAGG TGTGTGGAG CCGGATGACC 780  
 TCTATGATGT GTACTGTTAT GCTGAAGACC TAAATGGAGA ATTGTTCTCT GGTGACCCCT 840  
 CAGAGAAGCT GACATTGGAG GAAGCACGGG CGTACTGCCA GGAGCGGGGT GCAGAGATTG 900  
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 GCTTGGCTCG TGTCAAGCAT CTCTTCTCTT TCCCCAACCA GACTGGGCTT CCCAATAAGC 1080  
 ACAGCGCCTT CAACGTCTAC TGCTTCCGAG ACTCGGCCCA GCCTTCTGCC ATCCCTGAGG 1140  
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 CAGAGGCCCC TAGGACGCTC CTAGAAATTG AAACACAATC CATGGTACCG CCCACGGGGT 1380

5	TCTCAGAAGA	GGAAGGTAAG	GCATTGGAGG	AAGAAGAGAA	ATATGAAGAT	GAAGAAGAGA	1440
	AAGAGGAGGA	AGAAGAAGAG	GAGGAGGTGG	AGGATGAGGC	TCTGTGGGCA	TGGCCAGCG	1500
	AGCTCAGCAG	CCCGGGCCCT	GAGGCCTCTC	TCCCACTGA	GCCAGCAGCC	CAGGAGGAGT	1560
	CACCTCTCCA	GGGCCAGCA	AGGGCAGTCC	TGCAGCCTGG	TGCATCACA	CTTCTGATG	1620
	GAGAGTCAGA	AGCTTCCAGG	CCTCCAAGGG	TCCATGGACC	ACCTACTGAG	ACTCTGCCCA	1680
	CTCCACGGGA	GAGGAACCTA	GCATCCCAT	CACCTTCCAC	TCTGGTTGAG	GCAAGAGAGG	1740
	TGGGGGAGGC	AACTGGTGGT	CCTGAGCTAT	CTGGGTGCC	TGAGGAGAG	AGCGAGGAGA	1800
	CAGGAAGCTC	CGAGGGTGCC	CCTTCCCTGC	TTCCAGCCAC	ACGGGCCCC	GAGGGTACCA	1860
10	GGGAGCTGGA	GGCCCCCTCT	GAAGATAATT	CTGGAAGAAC	TGCCACGCA	GGGACCTCAG	1920
	TGCAGGCCCA	GCCAGTGTCT	CCCACTGACA	GCGCCAGCCG	AGGTGGAGTG	GCCGTGGTCC	1980
	CGCATCAGG	TGACTGTGTC	CCAGCCCCCT	GCCACAAATG	TGGGACATGC	TTGGAGGAGG	2040
	AGGAAGGGGT	CCGCTGCCCTA	TGCTCTGCTG	GCTATGGGG	GGACCTGTGC	GATGTTGGCC	2100
	TCGCTTCTG	CAACCCCGGC	TGGGACGCTT	TCCAGGGGCG	CTGCTACAAC	CACCTTTCCA	2160
15	CAOGAAGGAG	CTGGGAGGAG	GCAGAGACCC	AGTGCCGGAT	GTAOGGCGOG	CATCTGGCCA	2220
	GCATCAGCAC	ACCOGAGGAA	CAGGACTTCA	TCAACAACCG	GTACCGGAG	TACCACTGGA	2280
	TCGGACTCAA	CGACAGGACC	ATCGAAGGCG	ACTTCTTGTG	GTCCGATGGC	GTCCCCCTCG	2340
	TCTATGAGAA	CTGGAACCTT	GGGCAGCCTG	ACAGCTACTT	CCTGTCTGGA	GAGAACTCGG	2400
	TGGTCAATGT	TGGCATGAT	CAGGGACAAT	GGAGTGAOGT	GCCCTGCAAC	TACCACTGT	2460
20	CCTACACCTG	CAAGATGGGG	CTGGTGTCTT	GTGGGCCGCG	ACCGGAGCTG	CCCCCTGGCTC	2520
	AAGTGTTCGG	CCGCCCAOGG	CTGGGCTATG	AGGTGGACAC	TGTGCTTGGC	TACCGGTGCC	2580
	GGGAAGGACT	GGCCAGGCGC	AATCTGCGCG	TGATCOGATG	CCAAGAGAAC	GGTCTGTTGG	2640
	AGGCCCCCCA	GATCTCTCTG	GTGCCAGAA	GACCTGCCCG	AGCTCTGCAC	CCAGAGGAGG	2700
	ACCCAGAGAG	ACGTCAAGGG	AGGCTACTGG	GACGCTGGAA	GGCGTGTGTG	ATCCCCCTTT	2760
25	CCAGCCCCAT	GCCAGGTCCC	TAGGGGCCAA	GGCCTTGAAC	ACTGCGGGCC	ACAGCACTGC	2820
	CCTGTACACC	AAATTTTCCC	TCACACCTG	CGCTCACCAC	AGGAAGTGAC	AACATGAC	

Seq ID NO: 260 Protein sequence  
Protein Accession #: NP\_068767.1

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Protein Accession #: Eos sequence

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   |      |      |      |      |      |
CCCCCTTGTC ATTAATACAT TAAAAAGATT CAATCITTAC CTGAGGTAA TTTTGGCCAG 60
TTGTACACCG ATTATACCA AATAATGGA CTGATTGTG ATTCAAACCA AGATATGTG 120
GACGGTTACC AGAGGAGAAG GACTCAGTCC TATTGAAAGC TGTGAAGGAT TGGGAGATCC 180
TGCTTGCTTT TATGTTCGCT TAATTTTTAT TTTAAATGGA CTAATGATGG CATTATTCIT 240
CATATATGGC ACATATTAA GTGGCAGCCG ATTAGGAGGC CTGGTTACAG TGTGTGCTT 300
CTTTTCAAT CATGGAGAGT GTACCCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT 360
CTCATATCCA TTCTTGTTT TCCAGATGTT GCTAGTGACT CATATTCTCA GGGCTACAAA 420
ACTTTATAGA GGAAGCTTGA TTGACTCTG CATTTCGAAT GTATTTTCA TGCTTCCTTG 480
CGAGTTGCTT CAGTTTGCTC TTCTTACTCA GATTGCATCA TTATTGCGAG TATATGTGT 540
CGGGTACATT GATATATGTA AATTACGGAA GATCATTIAT ATACACATGA TTTCTCTTG 600
35 ACTTTGTTTT GTTTGTATGT TTGGGAACCT AATGTTATTA ACTTCITATT ATGCTTCTC 660
TTTGGTAATT ATTTGGGGTA TTCTGGCAAT GAAACCACAT TTCTGAAAA TAAATGTATC 720
TGAACCTAGT TTATGGGTTA TTCAAGGATG TTTTGGTTA TTTGGAAGCT TCATACTTAA 780
ATACTTGACA TCTAAATTT TTGGTATGCG AGATGACGCT CATATTGGCA ACTTACTAAC 840
ATCAAAATTC TTTAGTTATA AGGATTTTGA TACTTTATTG TATACCTGTG CAGCGGAGTT 900
40 TGACTTTATG GAAAAAGAGA CTCACCTGAG ATACACAAAG ACATTATTGC TTCCAGTTGT 960
TCTTGTAGTG TTTGTTGCTA TTGTTAGAAA GATTATTAGT GATATGTGGG GTGTCTTAGC 1020
TAAACAACAG ACACATGTAA GAAAAACCA GTTTGATCAT GGAGAGCTGG TTTACCATGC 1080
ATTGCAATGT TTAGCATATA CAGCCCTTGG TATTTTAATT ATGAGACTAA AACTCTCTCT 1140
GACACCACAC ATGTGTGTTA TGGCATCACT GATCTGCTCA AGACAGCTAT TTGGATGGCT 1200
45 CTTTGTCAAA GTACATCCTG GTGCTATTGT GTTTGCTATA TTAGCAGCAA TGTCAATACA 1260
AGGTTACGCA AATCTGTCAA CCGAGTGGAA TATTGTAGGG GAGTTACGCA ATTTGCCCCA 1320
AGAAGAACTT ATAGAAATGA TCAAAATATG TACTAAACCA GATGCACTGT TTGGGGGTGC 1380
CATGCCACG ATGGCAAGTG TTAAGCTCTC TGCACTTCGG CCCATTGTGA ATCATCCACA 1440
50 TTATGAAGAC GCAGGCTTGA GAGCCAGAAC AAAAATAGTA TACTCAATGT ATAGTCGGAA 1500
AGCAGCCGAA GAAGTGAAGC GAGAACTGAT AAAGTTAAAA GTGAACATAT ACATTCTAGA 1560
AGAGTCAATG TGTGTAAGAA GATCCAAGCC TGGTTGCAGT ATGCCCTGAA TTTGGGATGT 1620
AGAAGATCCT GCCAATGCTG GAAAACTCC CTTATGTAAC CTCTTGGTGA AGGATTCCAA 1680
ACCTCAATTC ACCACTGTAT TCCAGAACAG TGTTTACAAA GTCCATAAGG TTGTAAAGA 1740
55 ATGACTGCTA CATGACCTGC TGCTACGGA GAACTACATC TGTAATGGTT TTAATGTTTT 1800
GCTAAGTCAAT GTGTGTTTCA TATCCCAAAA ACTTTTATAG GTAAGTGT TCAATAGAAA 1860
AACGTTTTAT TTGGTCAATT TGAATGTCT TCTAATTATA AAAATGACTT ACACCTTTAT 1920
CAATTGGTTA CTATTTCAT GCACCCCTTA AAATTTGCTA TGCAATGAG TATATGCTTG 1980
TACTTGACTT TAATATTGT GCTAAAGTGA GCAAGCTAC CTGTATAAG AAAACACAGT 2040
60 GGGTTGTGAC AAGGATGACA TGAAAAATCA GGACAATTCT GACAAATGAG GGGCTGATTT 2100
TATAGTGTA GAACTATTAA TGCCCTTTC TTCTTTTTC TGCCCTTTC TCTGTCTTT 2160
TGGACATTT AGTGATTGTA AGTTCTTGG TCAATGTCAGC COCTGTCTAT AACTTGAGTT 2220
ACAGTAGATG GGGCAGACAT GGAGTGTTG CTATATAAAA CTATCTGTT GTTTTACTTC 2280
CTTGTCGCT TTTTGTCTC TGTCTCTTG TTAATGAAGC TTTTCCCTCC CATTATTAT 2340
65 CCAAACTCTT GGACCTTGTG GTTAGGAAAT TCCTTAACT TCCAGCCATA TGGCATTATC 2400
GTGCTCTTT CTCTCTCTCT CTGCTCTCT CTCTCTCTCT CTCTCCATA TTTTCTGTCA 2460
AATAAGTACT GTTTACTCAT TTAGTTGCTT ATCAAGTACT TATTCTTGGT TTTAAAAAAA 2520
ATTAATGGTA ACTGTATTT TCTCATTTT AGCATTATTC AAATGTTTAT ATTTAATAC 2580
CTTAAACCA CTTTAAAGTT TTTTCATGTT TAATTATAGT TTTAAGAAAA ACTATTTTGA 2640
70 ACAACCCCAA ATATAGTGCA TCTAGAACT AATGTATATT TGATTAGACA TCATTATAG 2700
TGGAACAGTA GACTGTAGTA CATGTAATT TTTCTTTTAC TATTAAGATA CAATAAAACA 2760
TGACTAATTT TGTGTCAAA AATGTAAAGA ATAATGATA ATGGAGTTTT TTAATTTT 2820
CTTTAAGAT TGCTGTCTT TAATAAGACA AAGCCTTAAG CTTATGTTA TAATTTTGGT 2880
TCTAAAAACC ATCATTTTCA TATAAGGAAT AAGTATATTT CGTCTCTCTC TTTAGTTTTT 2940
TTCTTCTTAT TTCTTTTAT TTTGAAAAAT TTCTACACCT TCTTTGAATT CTTGTATGA 3000
75 ATTTTGTGTT CTAGAAGTT AATTGTGTG AAATGAGATT CTTCAAAACG ATGAACCTTC 3060
ATAGCTCTGA GAAAAGGTT TAGGGTTTT AATTCTAAGC AAAGCGTGAC TATGGCTGAC 3120
AGACTACACA TTTAATTATA CAGCTTCTCT TTCTTAACCA CAGGCAGATT AACCTCATTG 3180
TGGATTGTCC TTACAGCCTT AGTCTCTCAG CATGTTTCT GGTGCCACT CCTGGAAGCC 3240
GCTGTTCCCT TCTACCTCT TTACCAGAGC CCAAGGGCAG GCCTGTGCCC GGGGAAGCAG 3300
80 CAGCTTGCTG ACATAAGTCA GCTGCAAGG CTGAGGAGTG TGCCCTCAGA GAAGCACGCG 3360
CCCCAGTCT TGTGCCAGCG CCTAGAGCCG CAGCTCCAGC GGATGCTCCT TCCTGGAGG 3420
CAGCCAGGA GAGGAGCTCT GGCAGGTTT TTCAGATTG TGCCCACTGT TTCTCATTTG 3480
CTGTTGACT GTTTTATTT CTAGGCTTT TGCTAGTTT AGAAAATAGG GAAGCAGCCC 3540
TTGATTTGTG GATTAAAGC AACATTTGAG CGATGATGCA CAACAGTCCA GGAATAATGG 3600

```



5 CGGTGGACAC TTGAGGCTGA GGATGGGAGT TGACATGAGC AGGGAGAGGG AGGTGCGCGC 3660  
 TGCTTATCTG TGATTGTTGC TCACCTGAGT GTGGCTGATT GTGTACATCC AGCAGTTACA 3720  
 ATTTTAAAAA ATTATACCTT TACATTTATT TTATATTTT CTCACCCCA GTAATTTCTT 3780  
 10 TCCAAAGAAG TCACATGTA ATAAGTAGAA ATCTGTATA GGAAAAAGC ATTAATAATA 3840  
 CTATTATAAC TGCTTCATT GCTGGGAACC ATTAAGAATA ATATAAATA GCTTTTCCA 3900  
 GAAGGATCCT TTTGTAGCAG TGTTTATGAA TGTAAACCC AGCAAAATAT GGCTATATAT 3960  
 TAGGGGAGCC AGTTTGGAGC AGAGGCTGA AGGTCCCTGC TATGCAGCCG TGGCCACAGC 4020  
 TCGCAGCCCA AGCACTGTGG AGCATCCACA CCTTTGATGG CAATGCAGAT TGGTAGCAGG 4080  
 15 TTCCATAGGC GTACAAACA GTATTAAAGC TCAGTGTTTT GCATATTGTT AGCATTACA 4140  
 AATATTTTGT CTTTAGTATG AGGAAAGTAA GGATGGGCAA AGAAGCGATC AAAATAGCTA 4200  
 TTGCTACAAC ATTTTCGAAA ACAGAGTTGG GGCTGTATTT CTTTAAAAAG ATAAGCCTCT 4260  
 AAAAAATGCTT GGCAAAAAA ATATAGTGTT AAAATAGGCC AGTGATATTA ATGAGAAAT 4320  
 GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATGTATTTT TATGAATTT 4380  
 20 ATGCCAGTGT TTTACATGTA CTATATATGT TAAATTAATA AAAATCATGA GAAATG

Seq ID NO: 266 Protein sequence

Protein Accession #: BAA74900.1

20 1 11 21 31 41 51  
 | | | | |  
 PLVINTLKRF NLYPEVILAS WYRIYTKIMD LIGIQTKICW TVTRGEGLSF IESCEGLGDP 60  
 ACPYVAVIFI LNLGMLALFF IYGYLSGSR LGLLVTLVCF FFNHGETRV MWTPLRESF 120  
 SYPFLVLQML LVTHILRATK LVRGSLIAFC ISNVFMLEW QPAQFVLLTQ IASLFAVYVV 180  
 25 GYIDICKLRK IYIHIMISLA LCFVLMFGNS MLLTSSYASS LVIINGILAM KPHFLKINVS 240  
 ELSLWVIQGC FALPGTVILK YLTSKIFGIA DDAHIGNLLT SKFPSYKDFD TLLYTCAAEF 300  
 DPMKETPLR YTKTLLFPV LUVFVAIVRK IISDMWGLA KQQTIVRKHQ FDHGLVYHA 360  
 LQLLAYTALG ILIMRLKPL TPHMCVMASL ICSRQLFGWL FCKVHPGATV FAILAAMSIQ 420  
 GSANLQTQWN IVGBFSNLPQ EELIEWIKYS TKPDAVFAGA MPTMASVKLS ALRPIVNHPP 480  
 30 YEDAGLRART KIVYSMSRK AAEVKRELI KLKVNYYILE ESWCVRRSKP GCSMPEIMDV 540  
 EDPANAGKTP LCNLLVKDSK PHFTTVFQNS VYKVLVVKE

Seq ID NO: 267 DNA sequence

Nucleic Acid Accession #: U26744.1

Coding sequence: 59..1600

35 1 11 21 31 41 51  
 | | | | |  
 CTTCAAAGAA TATAGATGGT TTTGAAAAGT TCATGCTGTC CCTTCATTGA ATTTTAGAAT 60  
 GATTGAAGAT AGTGGGAAAA GAGGAAATAC CATGGCAGAA AGAAGACAGC TGTTTGCGA 120  
 40 GATGAGGGCT CAAGATCTGG ATCGCATCOG ACTCTCCACC TACAGAACAG CATGCAAGCT 180  
 TAGGTTTGT CAGAAAGAAAT GCAATTTGCA CTGTTGGGAC ATATGGAATG TCATAGAAGC 240  
 ATTGCGGGAA AATGCTCTGA ACAACCTGGA CCCAAACACT GAACCTCAAG TGTCGCCCTT 300  
 AGAGGCTGTG CTCTCCACTA TTTTATACCA GCTCAACAAA CGGATGCCAA CCACCTACCA 360  
 AATCCATGTG GAGCAGTCCA TCAGCCTCCT CCTTAACCTC CTGCTTGCAG CGTTTGATCC 420  
 45 GGAAGGCCAT GTTAAATTTT CAGTATTGTC TGTCAAAATG GCITTAGCCA CATGTGTGG 480  
 AGGGAAGATC ATGGACAAT TAAGATATAT TTTCTCAATG ATTTCTGACT CCAGTGGGGT 540  
 GATGGTTTAT GGAGCATATG ACCAATTCCT TCGGGGAAGT CTCAAACTAC CCACGGGAAGT 600  
 TTTGGAGGAT CCTTCATTGG GTTACACAGA ACAGTCAGCC AGATCCTGTT TCTCCCAACA 660  
 50 GAAAAAAGTC ACCTTAAATG GTTCTTGGGA CAGCCTTATG TCAGATCCTC CCCCAGAGTG 720  
 TCTGGTCTGG TTGCTCTCTC TGCATCGACT AGCAAAATGTG GAAAATGTCT TCCATCGGT 780  
 TGAGTGTTC TACTGCCACA GTGAGAGTAT GATGGGATTG CGCTACCGAT GCCACAGTG 840  
 TCACAATTAC CAGCTCTGTC AGGACTGCTT CTGGAGGGGA CATGCGGGTG GTTCTCATAG 900  
 CAACCCAGCA CAATGAAAG AGTACAGCTC ATGGAATACA CCGTCTAAGA AGCTGACTAA 960  
 55 TGCATTAAAG AAGTCCCTGA GCTGTGCTTC CAGCGGTGAA CCTTGTGACC CCATGTTCCC 1020  
 AGATCAGCCT GAGAGGCCAC TCAACTGGGC TCACATGTTT GATACTTGCC CTCCCAGACC 1080  
 TGTAAACCAGC ATGAACGACA CCTGTCTCTC CCCTCTGTT CCCTCCTCAG GAAGTCTTTT 1140  
 TATTACCAGG AGCATGCTTG AGAGTTCAAA COGGCTTGAT GAAGAACACA GGCTAATTGC 1200  
 CAGGTATGCG GCAAGGCTGG CAGCAGAGTC CTCTCTGCT CAGCCACCTC AGCAGAGAAG 1260  
 60 TGCTCTGAC ATCTCTTCA CCATCGATGC GAATAAGCAG CAAGGCAGC TGATTGCTGA 1320  
 GCTAGAAAC AAGAACAGAG AAATCTTACA GGAGATCCAG AGACTTOSGC TAGAGCATGA 1380  
 ACAAGCTTCT CAGCCCAAGC CAGAGAAGGC ACAGCAAAAC CCCACCTGCG TGGCAGAACT 1440  
 CCGGCTCCTC AGACAGCGCA AAGATGAGCT GGAACAGAGA ATGTCTGCTC TCCAGGAGAG 1500  
 CGGAGAGAG CTAAATGGTCC AGTTGGAGGG TCTCATGAAG CTACTAAAGG AAGAAGAACT 1560  
 65 GAAGCAGGGA GTAAGTTATG TCCCTACTTG CAGGTCTTAA CTAACAGTGG AGGGGCCCTGC 1620  
 CGACCTGCGG TTTTCTCATT GCTTTTGCTC TAATGTATGT TCATGCTTCA GTTTGGAAAG 1680  
 AGAAAAAGT CATACTAATT TGCTTCTTTT TCAATGTAGT GCTTGAATTG AGATATATAA 1740  
 ATTTAGCATT TTTTATAACT ATCACTACTA TCCACATCAA AAGAAGAACT ATGACATCTT 1800  
 TTAGAAAGG GAACGAATTG TCATTATTTG GAAACATTTT AGATCCCCAG AGGTATAAGT 1860  
 70 TCAAAACCAG TCTTAGCTTT TCAAGTTGTT GATCAGACCC TTCTCTTAAC AGAGAGATAC 1920  
 CACAGTCACT AGAGATACCC TGAGGTTTCAT GTCATCCCAA AACCACAGC ACTCAGAAGC 1980  
 TAACCTCTAC ACCCTCAC ACTGTGAGTA TTCAGTTCGG TTTTATTTA CTGAAACCT 2040  
 GTGAAACCTC TTTTATAAAA AATCAGGCAA TTAATCCCT TTTTATCACA CAATTATTGA 2100  
 GCCTTGTTC CCATGGCTCA CCAAAATGTG CTCATTTTGT TGAGAGAAAG ACTGTACTCC 2160  
 75 ATAAGTACT ATTCACGTC CATCTTTTGT GCTCTTCCCC AAAGCAGAACT CCTTACTGTT 2220  
 GGTGTGAGAT AATCTCTTTT TAAAAAGTAA CTCTCAGCTT TTTCTTTCAG ACCAGAGCCT 2280  
 TTCGGCTCG GGAGACGAGA GGGTCATTAC ATACTTTTTT TTTTCTGAG AAATAGGGGC 2340  
 ATTGTGACTT TATAGCTTAA ACTGGAGCTG TCTGAACCTG TGGTCAGGCT CAAGAGCCAG 2400  
 80 CAGGGGAGC AGCAAACTC

Seq ID NO: 268 Protein sequence

Protein Accession #: AAC50426.1

1 11 21 31 41 51  
 | | | | |

5 MIEDSGKRGN TMAERRQLFA EMRAQDLDRl RLSTYRTACK LRPVQKKCNL HLVDIWNVIE 60  
 ALRENALNNL DPNTLNVSR LEAVLSTIFY QLNKRMPTTH QIHVEQSISL LNFLLAAPD 120  
 PEGHGKISVF AVKMALATLC GKKIMDKLRY IFSMISDSSG VMVYGRYDQF LREVLKLPTE 180  
 VLEGPSFGVT EQSARSCPSQ QKKVTLANGEL DTLMSPDPPO CLVNLPLLHR LANVENVFHP 240  
 VECSYCHSES MMGFYRRCQQ CHNYQLQDQC FWRGHAGGSH SNQHQMKKEYT SWKSPAKKLT 300  
 NALSKSLSCA SSREPLEPMF PDQPEKPLNL AHIVDTWPPR PVTSMNDTLF SHSVPSSGSP 360  
 FITRSMLESS NRLDSEHRLI ARYAARLAAE SSSSQPPQQR SAPDISPTID ANKQQRQLIA 420  
 ELENKNREIL QEIRLRLLEH EQASQPTPEK AQONPTLLAE LRLLRQRKDE LEQRMSALQE 480  
 10 SRRELMVQLE GLMKLLKEEE LKQGVSVVPY CRS

Seq ID NO: 269 DNA sequence

Nucleic Acid Accession #: NM\_001276.1

Coding sequence: 127..1278

15 1 11 21 31 41 51  
 | | | | | |  
 AGTGGAGTGG GACAGGTATA TAAAGGAAGT ACAGGGCCCTG GGAAGAGGC CCTGTCTAGG 60  
 TAGCTGGCAC CAGGAGCCGT GGGCAAGGGA AGAGGCCACA CCTGCGCTG CTCTGCTGCA 120  
 20 GCCAGAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGTCT GCTCCAGTGC 180  
 TGCTCTGCAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240  
 GGGAGCTGCT TCCAGATGCT CCTTGACCGC TTCTCTGTA CCCACATCAT CTACAGCTTT 300  
 GCCAATATAA GCAACGATCA CATCGACACC TGGAGTGGGA ATGATGTGAC GCTCTACGGC 360  
 ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTGTCT TGTCGGAGGA 420  
 25 TGGAACTTTG GGTCTCAAGG ATTTTCCAAG ATAGCTCCA ACACCCAGAG TCGCCGAGCT 480  
 TTCAATCAAGT CAGTACCGGC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540  
 TGGCTCTACC CTGACCGGAG AGACAAACAG CATTTTACCA CCTAATCAA GGAATGAAG 600  
 GCCGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGTCTAG CGCAGCACTG 660  
 TCTGCGGGGA AGGTCAACAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG 720  
 30 GAITTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GCGTGGGAC CACAGGCCAT 780  
 CACAGTCCCC TGTTCGAGG TCAGGAGGAT GCAAGTCTGT ACAGATTGAC AACACTGAC 840  
 TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCTGCCA GTAAGCTGCT GATGGGCATC 900  
 CCCACCTTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGCTGTGG AGCCCCAATC 960  
 TCAGGACCGG GAATTCAGG CCGGTTACAC AAGGAGGCGG GGACCTCTG CTACTATGAG 1020  
 35 ATCTGTGACT TCCTCCGCGG AGCCACAGTC CATAGAACCC TCGGCCAGCA GGTCCCTCAT 1080  
 GCCACCAAGG GCAACCAAGT GGTAGGATAC GACGACCGG AAAGCGTCAA AAGCAAGGTG 1140  
 CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGCTAT GGGCCCTGGA CCTGGATGAC 1200  
 TTCCAGGGCT CCTTCTCGGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260  
 GCATCTGCTG CAACGTAGCC CTCTGTTCTG CACACAGCAC GGGGGCCAG GATGCCCGT 1320  
 40 CCCCCTCTGG TCCAGCTGG CCGGGAGCCT GATCACTGCT CCTGCTGAT CCCAGGCTGA 1380  
 GCCTCACTCT CCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA 1440  
 GCCCTGCTGG GCAGAGAGGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA 1500  
 GACTCGGGAT TAGTACACAC TTGTTGATGA TTAATGGAAA TGTTTACAGA TCCCAAGCC 1560  
 TGGCAAGGGA ATTTCTTCAA CTCCCTGCCC CTATGACCAAG GACACCATTT 1620  
 45 TGGCAAGCTC TATCAACAA GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680  
 TACCCCTTGC AAAGCCAGCT TGAAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT 1740  
 ACTTCCCTTT CCTAATTCCT CAGCTGCTCA ATAAAGTACA AGAGTTTAAC AGTGTGTTGG 1800  
 CGCTTTGCTT TGGTCTATCT TTGAGCGGCC ACTAGACCCA CTGACTCAC CTCCTCCATC 1860  
 50 TCTTCTGGGT TCCTTCTCTT GAGCCTTGGG ACCCTTGAGC TTGCAGAGAT GAAGGCGCGC 1920  
 ATGTT

Seq ID NO: 270 Protein sequence

Protein Accession #: NP\_001267.1

55 1 11 21 31 41 51  
 | | | | | |  
 MGVKASQTGF VVLVLQCCS AYKLVCYYS WSQYREGDGS CFPDALDRFL CTHIYSPAN 60  
 ISNDHIDTWE WNDVTLYGML NTLKNRNPNL KTLISVGGWN FGSQRFSKIA ENTQSRRTPI 120  
 KSVPPFLRTH GFDGLDLAWL YPGRDKQHF TTLIKEMKAE FIKEAQPGKK QLLLSAALSA 180  
 60 GKVTIDSSYD IAKISQHLDF ISIMTYDFHG AWRGTTGHS PLFRQEDAS PDRFSNTDYA 240  
 VGYMLRLGAP ASKLVNGIPT FGRSPTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC 300  
 DFLRGATVHR TLGQVVPYAT KGNQWVGYYD QESVKSRYQY LKDRQLAGAM VHALDLDDFQ 360  
 GSFCGQDLRF PLTNAIKDAL AAT

Seq ID NO: 271 DNA sequence

Nucleic Acid Accession #: NM\_006474.1

Coding sequence: 181..669

70 1 11 21 31 41 51  
 | | | | | |  
 GCTGCCTAGG GTCGTGAAAG CTGGGGCACC CTCCTCTCTC GGGGCTCCTG CTCCCACTCC 60  
 TCGGGCCCCC CCACCGTCGC GCTCTCCAG GCTGGGCTG TGGCGCGGT GCTTTAATT 120  
 TTCCCCAGAC TCAGAATCTT GCTGCTGGC CCCAGGAGA GCAACAATC AACGGGAACG 180  
 ATGTGGAAGG TGTCAGCTCT GCTCTTGGT TTGGGAAGCG CTGCGCTCTG GGTCTGCGCA 240  
 75 GAAGGAGCCA GCACAGGCCA GCCAGAAGT GACACTGAGA CTACAGGTTT GGAAGGCGGC 300  
 GTTGCCATGC CAGGTGCGCA AGATGATGTG GTGACTCCAG GAACCAAGCA AGACCGCTAT 360  
 AAGTCTGGCT TGCAACTCT GGTGGCAACA AGTGTCAACA GTGTAAACAG CATTCGCATC 420  
 GAGGATCTGC CAATTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA 480  
 GCCTCAAAAG TGGCCACAG TCACTCCAG GAGAAAGTGG ATGGAGACAC ACAGACAACA 540  
 GTTGAGAAGG ATGTTTGTG AACAGTGACC CTGTTGGAA TCATAGTTGG GGTCTTACTA 600  
 80 GCCATCGGTT TCATTGGTGG AATCATGTT GTGTTATGCG GAAAAATGTC GGGGAAGTAC 660  
 TCGCCCTAAA GAGCTGAAG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT 720  
 TCTGACTCT GTGGCCCTGT CCTGAGCTC GTGGGAGAAA GATGACCTG GGAACATTG 780  
 CGGGCCCATC CAGATTCAC GGTGACTTTC CGTTTGCCAA ATTAACGAG GAAAGACCTT 840

TCACCAGATT TGGTCTTAA ACTTT

Seq ID NO: 272 Protein sequence  
Protein Accession #: NP\_006465.1

5  
1 11 21 31 41 51  
| | | | |  
MWKVSALLFV LGSASLWVLA EGASTGQPED DTBITGLEGG VAMPGAEDDV VTPGTSEDRY 60  
KSLGLTLVAT SVNSVTGIRI EDLPT9ESTV HAQEQSPSAT ASNVATSHST EKVGDGTQTT 120  
10 VEKDLSTVT LVGIIVGVLL AIGFIGGIIV VVMKMSGRY SP

Seq ID NO: 273 DNA sequence  
Nucleic Acid Accession #: CAT cluster

15 1 11 21 31 41 51  
| | | | |  
GCGGCGCCCA GCTTGCAAG CCGAAGTCTG GCCGCGCTCT TCGACTCGCT GCGCCACGTC 60  
CCCGGGGGTG CGAGCCCGGC GGGGGGTGAG GTGGCTGGGC CGGCGGCCGG GCTAGGAGGT 120  
GCGGGCAGTG GGGGCGGGGG AGGGGACGTG GCAGGCCCGG CGGGGGCCAC GCGGATCCCA 180  
20 GGGGCCAGGA AGGTCCCGCT GCGGGCAAGC AATCTGCCTC GTCTCTTCTT CACGAGACCG 240  
TCCCGGGCAG GCGGCGGGGG GTGTGGCCCG TCGGGGCGGG ACGTGAGCTT GGGCGACCTG 300  
GAGAAGGGCG CGGAGGCGGT GAGATTCTTT GAGCTGCTGG GGCCCGACTA CGGCGCCGGC 360  
ACGAGGGCGG CAGTCTTGCT TGCCTCCCGG CCTCTCGACG TGTTCCTCCG CGGAGCCTCC 420  
GTAATGCGGG GACCCCGGGA GCTGGAGCCC GGCTCTTTTG AGCCGCCGCC GGCAGTGGTG 480  
25 GGAACCTTAC TGTACCCCGA GCGCTGGAGC GTCCCGGGCT GCTCCCGGAC CAAAAGAGC 540  
CCCTTGACTG CCCTCCCGGG CGGGTTGACC TTGAACGAGC CCTTGAGCCC CCTGTACCCC 600  
GCCGCTGCGA ATTTCTCCCG GCGGGGAGGA CGGGCCGGGC CATTGCGCTT CTTTCGCCCC 660  
CTTCTTCCA GACTGCGCTT TGC

Seq ID NO: 274 DNA sequence  
Nucleic Acid Accession #: Eos sequence

35 1 11 21 31 41 51  
| | | | |  
CAAAGAGGCC GGGCTCCAGC TCCGGGGGTC CCGCAGTAC GGAGGCTCCG GCGGGGAACA 60  
CGTCGAGAGG CTGCGCGGCA AGCAAGACTG CGGCTCCGTT GCGCGGCGCG TAGTCGGGCC 120  
CCAGCAGCTC AAAGAAGTCC ACGGCTCCGG CGGCTTCTTC CAGGTGCGCC AAGCTCAGT 180  
CGGGCCCCGA CGGGCCACAC CCGCGCGGCG CTGCCCGGGA CGGCTCGGTG AAGAAGGAGC 240  
40 GAGGCAGATT GCGTCCCGCG AGCGGGACCT TCCTGGCCCC TGGGATCGCC GTGGCCCCCG 300  
CGGGCGCTGC CAGTCCCGCT CCGCGCCGCC CAGTGCCGCG ACCTCCTAGC CGGCGCGCGC 360  
GCGCAGCCAC CTCACCCCCC GCCGCTCCGG CACCCCGGGG GAGTGCGCG AGCGAGTCGA 420  
AGAGCGGGCG CAGACTTCGG CTTTGCAAGC TGGCGGCCGC

Seq ID NO: 275 DNA sequence  
Nucleic Acid Accession #: NM\_001118.1  
Coding sequence: 74..1651

50 1 11 21 31 41 51  
| | | | |  
AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGTG 60  
GCCAAGAAAT GTCATGGCTG GTGTCTGTCA CGTTTCCTGT GCTGCTCACT GCGGGGCGTG 120  
TCCGTGGGGC CGGGGAGAGC TCCGCAAGAG ACGCGCAGCC TGCAAGTCCG CGGCCAGAG 180  
ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGTG GGCCAAGAG 240  
55 TGTCTAGGCT GGTGTGGTGC ACGTTTCCCT GGCTGCTCTC CTCTGCTGTC CTATGGCCCC 300  
TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCTCTG AGAAGATCCA 360  
GAGGGCCAAAT GAGCTGATGG GCTTCAATGA TTCTCTTCCA GGCTGTCTGT GGATGTGGGA 420  
CAACATCAAG TGTGTGAAGC CCGCCCATGT GGGTGAGATG GTCTGTGTCA GCTGCCCTGA 480  
GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCAATT GAGAGTCTGA 540  
60 TTTTGGTGAC AGTAATCTCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600  
GGAGGATGGC TGTTCGGAAC CCTTCCCTCA TTACTTTGAT GCCTGTGGGT TTGATGAATA 660  
TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACAAGGT 720  
TGGCTACAGC ACATCCCTCG TCACCTTCAC CACTGCCATG GTCATCTTTT GTGCTTCCG 780  
GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTGTG TCAATGCTGAG 840  
GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900  
65 CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTC TTCCACTACT GTGTGTGTG 960  
CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACTTT 1020  
CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGTGGGGGGA CCCCACATGT 1080  
GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT 1140  
70 GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGTT 1200  
TAATCTTGTG CTTTATTATG GCATTATOGT CATCTTGTG CAGAAACTTC AGTCTCCAGA 1260  
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CCCACTATTG GGAATCCACT ACACAGTATT TGCCCTTCCG CCAGAGAATG TCAGCAAAAG 1380  
GGAAAGACTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCTTTGTGG TGGCTGTTCT 1440  
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GGTGAATGGG GGCAACCCAGC TCTCCATCCT GAGCAAGAGC AGCTOCCAAA TCCGATGTC 1620  
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Seq ID NO: 276 Protein sequence  
Protein Accession #: NP\_001109.1

80 1 11 21 31 41 51  
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VVHVSLAALL LFLMAPAMHS DCIFKKEQAM CLKRIQRANE LMGFNDSSPG CPGMMDNITC 120  
 WKPAHVGMV LVSCPELPRI FNPQVNETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW 180  
 SEPPPHYFDA CGFDEYESET GDQDYIYLSV KALYTVGYST SLVLITAMV ILCRFRKLHC 240  
 TRNFHMLNP VSFMLRAISV FIKDWILYAE QDSNHCPIST VECRAVMVFP HYCVVSNYFW 300  
 LFIEGLYLFT LLVETFFPER RYFYWYIIG WGTPTVCVTV WATLRLYFDD TGCHDMNDST 360  
 ALWWVIRGFP VGSIMVNFVL FIGIIVILVQ KLQSPDMGN ESSIYLRAR STLLLIPLFG 420  
 IHYTVFAPSP ENVSKRERLV FELGLGSFQG FVVAVLYCPL NGEVQAEIKR KWRWSKVMRY 480  
 FAVDFKRRHP SLASSGVNGG TQLSILSKSS SQIRMSGLPA DNLAT

Seq ID NO: 277 DNA sequence  
 Nucleic Acid Accession #: NM\_004000.1  
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 CCAACTGTGC CCAGGACCGG CAGGAACGAG GAAAATTCAC CCCTGAGAAT ATTGACCCCT 180  
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Seq ID NO: 278 Protein sequence  
 Protein Accession #: NP\_003991.1

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 NSIILPLRNH NFDGLDVSWI YPDQKENTHF TVLIHELAE FQKDFTKSTK ERLLLTAGVS 180  
 AGRQMDINSY QVSKLAKDLF FINLLSDFDH GSWKEPLITG HNSPLSKGWQ DRGPSYINV 240  
 EYAVGWYHKK GMPSEKVMVG IPTYGHSPFL ASAETTUGAV ASGPAAAGPI TESSGFLAYY 300  
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Seq ID NO: 279 DNA sequence  
 Nucleic Acid Accession #: NM\_015166.1  
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 GCAAGACCCC CCAGCTATG CCCCAGACGC GAAGCCGAGC GACCTGCAGC TGTOGAAGAG 240  
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 CTTGGTGACC TGGGGGTTTT GCTGTACCT GGGGAACGTG TTCCCGGCTG AGATGGAITA 360  
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Seq ID NO: 280 Protein sequence  
 Protein Accession #: NP\_055981.1

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 CLLVTSGPSL YLGNVFPDEM DYLRCAAGSC IPSAIVSFTV SRRNANVIFN FQILPVSTFA 120  
 VTTTCLIFWG CKLVILNPSAI NINFNILILL LLELLMAATV IIAARSSSED CKKKKGSMSD 180  
 SANILDEVFP PARVLKSYSV VEVIAGISAV LGGIILALNVD DSVSGPHLSV TFPFIIIVACF 240  
 PSAIASHVAA ECPSCKLIVFV LIAISSLTSP LLFTASGYLS FSIIMRIVEMP KDYPPIAIKPS 300  
 YDVLILLILL VLLQLAGLNT GTAIQCVRFK VSARIQGASW DTQNGPQERL AGEVARSPK 360  
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Seq ID NO: 281 DNA sequence  
 Nucleic Acid Accession #: NM\_004518.1  
 Coding sequence: 43..2577

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 GCCCCCAAGC GCGGCAGCAT CCTCAGCAAA CCTCGCGCGG GCGCGCGCGG CGCCGGGAG 240  
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 CGGCGCGCGG GCTGGGCGTT CATCTACAC GCCTAGCTGT TCCTCTGCTT TTTCTCTGTC 360  
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 GCCGACGGCT GCTGCTCGCG GTACCGTGGC TGGAGGGGGC GGCTCAAGTT TGCCCGGAAA 540  
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5 AAGAAGCTGG ACTTCTGGT GAATATCTAC ATGCAGCGGA TGGGCATCCC CCGACAGAG 1920  
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 20 CTGGAGGGGC CCATGTGGG TGAAGGATGG GGGCTCCTGG CAGTGACCTT TTACAAAAGT 2760  
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Seq ID NO: 282 Protein sequence  
Protein Accession #: NP\_004509.1

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IVRSSSTGQ KNFSAPPAAP PVQCPPSTSW PQSHPRQGH GTSFVGHDGS LVRIPPPPAH 720  
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Nucleic Acid Accession #: AF152496.1  
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 Coding sequence: 15..2765

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Seq ID NO: 287 DNA sequence  
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 Protein Accession #: AAD43756.1

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TGAGTGTGCG AGACCAACA CTGGACTCCC TGGGTGGGGG CCTGAGGGC CCGTCTTCT 1500
GCCCCACCCC CTGCAACCTG ACACGCTATG GAAAGAGAT CTCCATGGTC AGGATCCCCA 1560
ACAGGGGCTC AGCCGGTAC CTGGGAGGA AGTACAACCG CAACAGAGCC TACATAGCGG 1620
AGAACTCTCT GGTCTAGAT GTCTTCTTTG AGGCCCTGAC CTCTGAAGCC ATGGAGCAGC 1680
GAGCAGCTTA TGGCTGTGCA GCGCTGCTGG GAGACCTCGG GGGACAGATG GGCCTGTTCA 1740
TTGGGGCCAG CATCTCACG TTGCTGAGA TCCTGAGTCA CATCTATGAG GTGTCTGGG 1800
ATGAGCTGAA GGGGATATGG AGGCGTCCCA AGACCCCTCC GCGGACCTCC ACTGGGGGCA 1860
TCTCCACTTT GGGGCTTCCG GAGCTGAAGG AACAGAGTCC CTGCGGAGC CTGGGCGAG 1920
CGGAGGGTGG GGGGCTCAGC AGTCTGTCCC CCAATCACCA CCAACCCACG GGTCCCCCAG 1980
GAGGTCTCTT TGAAGATTTT GCTTGTAGG ACGTGTCTGT GACTGAAAGG ACCCAGGAGT 2040
CTGGGACCCC TCTGCGGATC CCGAGCACAT TCTCTGCTC CTGGGAGAGG CCGGGGGGCG 2100
GTGCTCACTG GAGGGGCCAG GACTCAGTTC CTGCTCTCAT CTTCCCTGCG CTTGATGTCA 2160
GCTGCTTGGC ACAAAGTCC TTCTTGTCCA CACCCCTTAT CCCCAGGCTG GTGCCCGGG 2220
AGGGCTGAGG ACCAGGCCAT GGGCCCTCAC GGAGAGGAAG GGAAGGAAGG AGAGGGAGGG 2280
GAGGATAGA GCCCATCCCA GCGGGGGAGG GGGAGCCCTC TGTACATTTG TAAATATTTA 2340
GGGAAAGCCG GGTGGGGGGA GGGGATACAG ATGTAGAAAG TGGGTAGGGC TACAGGGGTG 2400
GGTGATTTAG GACAGGCCAG GGTCCAGCC CCAATGTGAG CAGGATAGGG AGAGCCCGAG 2460
GACTCAGGAG TGCTGGGCTG GTCTTACTTC CTGCCCCCTC CCAGGCCAGC CTCCTCTCTT 2520
GGCAGGGGGA GATCTGGGCT CAGCAGGCTC GGGCCAGCTC CCACTTCCCC CTGCACAGC 2580
CCACCCCTTA GAGTCCCTTC TATAGGGAGG GGGCAGGAGA CCTTCCAGAC TTGCGCTGAG 2640
CTTGAAGGTT GGAAGGGAG CCTTCTCAGT CTTCTCTCCC TCCAGTCTGA TTTTATAAAG 2700
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Seq ID NO: 290 Protein sequence  
Protein Accession #: NP\_061144.1

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1 11 21 31 41 51
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GPHGLRRTLW ALALLTSLAA FLYQAAGLAR GYLTRPHLVA MDPAPAPFAV GPPAVTLCNI 120
NRRFHSALSD ADIFHLANIT GLPPKDRDGH RAAGLRYPBP DMVDILNRTG HQLADMLKSC 180
NFGGHHCSAS NFSVVYTRYG KCYTFNADPR SSLPSRAGGM GSGLEIMLDI QQEYLPPIWR 240
ETNETSFPEAG IRVQIHSQEE PPYIHLQGFV VSPGFQTFVS CQEQLRTYLP QFWGNCRAS 300
ELREPELQYV SAYSVSACRL RCEKEAVLQR CHCRMVHMPG NETICPNFIY IECADHTLDS 360
LGGGPEGPCF CPTPCNLTRY GKEISMVRIP NRGSAARYLAR KYNRNETYIR ENFLVLDVFP 420
EALTSEAMEQ RAAYGLSALL GDLGGQMLFP IGASILTLLB ILDYIYBVSW DRLKRVWRRP 480
KTPLRITSTGG ISTLGLQELK EQSPCPSLGR AEGGGVSSLL PNHRHPGPP GGLFEDFAC
  
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Seq ID NO: 291 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 62..895

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CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACACAG 180
AQAAGCAGCG TCTGGCAAT ACAGGCTCAC CTAAGCAGAA GCTAAGGCGG TGTGTGAATT 240
TGAAGCGCGC CATCTGSCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGAATTCA 300
TGCTCTGTCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATTG TGAAGCCAGG 360
GCCCACTGT GGAATTGGAA AAACCTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
TGAAAGATCG GATGCTATT GCTACAACCC ACACGCAAGG GAGTGTGGTG GGTCTTTTAC 480
AGATCCAAAG CAAATTTTAA AATCTCCAGG CTTCCCAAAAT GAGTACGAAAG ATAAACCAAT 540
CTGCTACTGG CACATTAGAC TCAAGTATGG TCAGGCTATT CACCTGAGTT TTTTAGATT 600
TGACCTTGAA GATGACCCAG GTTGTCTGGC TGATTATGTT GAAATATATG ACAGTTACGA 660
TGATGTCCAT GGTCTTGTGG GAAGATACTG TGGAGATGAG CTTCAGATG ACATCATCAG 720
TACAGGAATAT CATATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT 780
CCAAATCAAA TATGTGCAAA TGGATCTCTG ATCCAAATCC AGTCAAGGAA AAAATACAA 840
TACTACTTCT ACTGGAATA AAAACTTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAA 900
AAAAAAGGA TGATCAAAAC ACACAGTGTT TATGTTGGAA TCTTTTGGAA CTCCTTTGAT 960
  
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CTCACTGTGA TTATTAACAT TTATTTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020  
 TAGGGAAAT TGGAAATAT AGGAACTTT AAAAGAGAAA ATGAAACCTC TCATAATCCC 1080  
 ACTGCATAGA AATAACAAGC GTTAACATT TCATATTTT TCTTTTCAGT CATTTTCTTA 1140  
 TTTGTGGTAT GTGATATAT GTACCTATAT GTATTTGCAT TTGAAATTTT GGAATCCTGC 1200  
 TCTATGTACA GTTTGTGATT ATACTTTTAA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260  
 TCATTGATTA TTTACAAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320  
 TGTTTTATGC ATTATTTAAG CTTGTCTCTA TTGTTGGAAT TTCAGGTCAT TTTCTATAAT 1380  
 ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAAAA AA

Seq ID NO: 292 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
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 MIILYLFL LLWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60  
 EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCQFGRGTGI IDYGIRLNRS 120  
 ERNDAYCYNP HAKECCGVFT DPKQIFKSPG PFNEYEDNQI CYWHIRLKYG QRIHLSPLDF 180  
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240  
 QIKYVAMDPV SKSSQGRKNTS TTSTGNKNFL AGRFSLH

Seq ID NO: 293 DNA sequence  
 Nucleic Acid Accession #: NM\_007115.1  
 Coding sequence: 69..902

1 11 21 31 41 51  
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 GGGGATTCAA GGATGGAATT TTTCTAACT CCATATGGCT TGAACGAGCA GCCGGTGTGT 180  
 ACCACAGAGA AGCAGCGTCT GGCATAATACA AGCTCACCTA CGCAGAAGCT AAGGCGGTGT 240  
 GTGAATTGGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG 300  
 GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360  
 AGCCAGGGCC CACTGATGTA TTGGAAAAA CTGGCATTAT TGATATGGA ATCCGTCTCA 420  
 ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAGAGAG TGTGGTGGCG 480  
 TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAATGAG TACGAAGATA 540  
 ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTCAC CTGAGTTTIT 600  
 TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660  
 GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720  
 TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780  
 GAGGTTTCCA ATCAAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840  
 ATACAAGTAC TACTTCTACT GGAATAAATA ACTTTTATAG TGGAAAGATT AGCCACTTAT 900  
 AAAAAAAAAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAAATCTT TGGAACTCCT 960  
 TTGATCTCAC TGTATTATAT AACATTATTT TATTATTTT CTAAATGTGA AAGAAATACA 1020  
 TAATTTAGGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAATGAA ACCTCTCATA 1080  
 ATCCCACTGC ATAGAAATAA CAAGCGTIAA CATTTTCATA TTTTTCCT TCAGTCATT 1140  
 TTGTAATTTG GTATATGTA TATATGTACC TATATGTATT TGCAATTGAA ATTTTGAAT 1200  
 CCTGCTCTAT GTACAGTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTC 1260  
 TGAATCTGAT GATTATCTTA CAATAACATG ATTTTAAACA GCTGTAAAT ATTCTATGAT 1320  
 ATGAATGTTT TATGATTTAT TTAAGCCTGT CTCTATTGTT GGAATTTCAG GTCATTTTCA 1380  
 TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

Seq ID NO: 294 Protein sequence  
 Protein Accession #: NP\_009046.1

1 11 21 31 41 51  
 | | | | |  
 MIILYLFL LLWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60  
 EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCQFGRGTGI IDYGIRLNRS 120  
 ERNDAYCYNP HAKECCGVFT DPKRIFKSPG PFNEYEDNQI CYWHIRLKYG QRIHLSPLDF 180  
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240  
 QIKYVAMDPV SKSSQGRKNTS TTSTGNKNFL AGRFSLH

Seq ID NO: 295 DNA sequence  
 Nucleic Acid Accession #: NM\_001218.2  
 Coding sequence: 116..1180

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 CGCGCGCAGC CTGCACGCGG CGGCCGTGCT CCTGCTGGTG ATCTTAAAGG AACAGCCTTC 180  
 CAGCCCGGCC CCAGTGAACG GTTCCAAGTG GACTTATTTT GGTCTGTATG GGGAGAAATAG 240  
 CTGGTCCAAG AAGTACCCGT CGTGTGGGGG CCTGCTGCAG TCCCCATAG ACCTGCACAG 300  
 TGACATCTCT CAGTATGACG CCAGCCTCAC GCCCCTCGAG TTCCAAGGCT ACAATCTGTC 360  
 TGCCACCAAG CAGTTTCTCC TGACCAACAA TGGCCATTCA GTGAAGCTGA ACCTGCCCTC 420  
 GGACATGCAC ATCCAGGGCC TCCAGTCTG CTACAGTGCC ACGCAGCTGC ACCTGCCTG 480  
 GGGGAACCCG AATGACCCGC ACGGCTCTGA GCACACGCTC AGCGGACAGC ACTTGCCTG 540  
 CGAGCTGCAC ATTTGTCATT ATAACTCAGA CCTTATCTT GACGCCAGCA CTGCCAGCAA 600  
 CAAGTCAGAA GGCTCGCTG TCCTGGCTGT TCTCATTTAG ATGGGCTCCT TCAATCCGTC 660  
 CTATGACAAG ATCTTCAGTC ACCITCAACA TGTAAGATAC AAGGCCAGG AAGCATTCGT 720  
 CCGGGGATTC AACATTGAAG AGCTGCTTCC GGAGAGGACC GCTGAATATT ACCGCTACCG 780  
 GGGGTCCCTG ACCACACCCC CTTCGAACCC CACTGTGCTC TGGACAGTTT TCGAAACCC 840  
 CGTGCAAAAT TCCAGGAGC AGCTGCTGCG TTTGGAGACA GCCCTGTACT GCACACAT 900

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GGACGACCTC TCCCCAGAG AAATGATCAA CAACTTCCGG CAGGTCCAGA AGTTCCGATGA 960
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GGGCATCATC CTCTCACTGG CCCTGGCTGG CATTCCTGGC ATCTGTATTG TGGTGGTGGT 1080
GTCCATTGCG CTTTTCAGAA GGAAGAGTAT CAAAAAAGGT GATAACAAGG GAGTCATTTA 1140
CAAGCCAGCC ACCAAGATGG AGACTGAGGC CCACGCTTGA GGTCCCGGGA GCTCCCGGGC 1200
ACATCCAGGA AGGACCTTGC TTTGGACCTT ACACACTTGG GCTCTCTGGA CACTTGGGAC 1260
ACCTCAAGGT GTTCTCTGTA GCTCAATCTG CAAACATGCC AGGCTCAGG GATCCTCTGC 1320
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TGCACTCTCA GACCAAGCAG CAGGAATTCA AAGCTGCTTG CTGTAAGTGT GTGAGATTGT 1440
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CAACTTCTTT CCTCTGGAGA CGGGGCATCT CCTCTGATT TCCTTCTGCT ATGACAAAAC 1680
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CCTCTGGATC ACAGACACTG CACAGACCTT AGGGAATGGC AGGTTCAAGT TCCACTTCTT 1860
GGTGGGGATG AGAAGGGAGA GAGAGCTAGA GGGACAAAGA GAATGAGAAG ACATGGATGA 1920
TCTGGGAGAG TCTCACTTTG GAATCAGAAT TGGAATCACA TTCTGTTTAT CAAGCCATAA 1980
TGTAAGGACA GAATAATACA ATATTAAGTC CAAATCCAAC CTCTGTCAG TGGAGCAGTT 2040
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CTGTGCTCTG GAGGAGACAT GAGTTCGAG ATGACCCAAT CTGCTTTGA ATCTGGAGGA 2160
AATAGGCAGA AACAAAATGA CTGTAGAAT TATTCTCTGT AGGCCAAAT TCATTTCAGC 2220
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CTGAAGATGT CAAATCGTGG TTTAGATCAA ATATATTTCAG AGCTATAAAA GCAGGAGGTT 2340
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GACAGCATGA AATGCTCTCT TGAAGCATAG CTTTTTAAAT ATCTTTTCCC TTCTACTCCT 2640
CCCTCTGACT CTAAGAAATC TCTCTCTGG AATCGCTTGA ACCAGGAGG CGGAGGTTGC 2700
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Seq ID NO: 296 Protein sequence  
Protein Accession #: NP\_001209.1

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HWGNPNDFHG SEHTVSGQHP AAEHLIVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSPN 180
PSYDKIFSHL QHVKKYKQGEA FVEGPNIEL LPERTAEYR YRGLSTPPC NPTVLWTVFR 240
NPVQISQEL LALETALYCT HMDDPSPREM INNFRQVQKF DERLVYTSFS QVQVCTAAGL 300
SLGIILSLAL AGILGICIVV VVSIWLPFRK SIKKGONKGV IYKPKMET EABA
  
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Seq ID NO: 297 DNA sequence  
Nucleic Acid Accession #: NM\_006632.1  
Coding sequence: 377..1582

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GACAAGAAGA CCGCATCATC CTGCGCCAC CTGTAGCTGG CCATTGCAA CCGGAGGAG 180
CTTAACAAGC TGTCTGGCGA AGTCAACATC GCGCAGGCG GTGTCTGTC CAACATTCAG 240
GGCGTGTCTC TGCCCGAGAA GACCAAGAGC CACCAAGAG CCAAGGGTA AAAACATTCA 300
CTAGAGAGAG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCACAG CAAGGGAGAG 360
CAAGAACGCA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAG GTCCAAGTTT 420
ATGTTCTGCT CGCATATGAA TAGCCCTGCT CTACATTTC TGCAATTTCA CAACGATAGC 480
ACAAAATGTC ATCATGAACA TCAACATGGT AGCCATGGTC AACAGCACA GCGCTCAATC 540
CCAGCTCAAT GATTCTCTG AGGTGCTGCC TGTGACTCA TTTGTTGGCC TAAGTAAAGC 600
CCCAAGAGT CTCTCTGCAA AGTCTCAAT ACTTGGGGT CAGTTTGCAA TTTGGGAAA 660
GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTTACT 720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCATTAGT GAAACCTTG GGTGGCCCTT 780
TGCTCTCTAT ATCTTTGAGG GTGTGGCTG TGTCTGTGC CTCTCTGCT TGTGTTGAT 840
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CTCCTTGAAA CAACAGGTGC GGTCTTCTAA GCAGCCTCTT CCCATCAAG CTATGCTCAG 960
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TGGACTTCTA TCTGCCCTTC CTTTATTGTT TGCCCTGGTC ATAGGCAATG TGGAGGGCTA 1140
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AATTTTAGGA AGTCTCCCTT CTTGAGCACT CATTTGTCT CTGCTTACC TCAATTCGG 1260
CTATATCACA GCAACTGCTT TGCTGAGGCT CTCTTGGGGA TTAAGCACAT TGTGTCACT 1320
AGGGAATTTT ATCAATGCTC TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC 1380
ATCAAGAGGA TTTTGGAGCA TAGCACTGT CATTTGATCC ACTGTGAGG GATTCTTCT 1440
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GTTAGGACTA CTCTTCTACC TCATATTGAG AGAAGCAGAT GTCCAAGAA GGGTAAAGA 1560
GAGAAAACCT ACTCGTTTAT GAAGTTATCC CACCTTGGAT GGAAGAATCA TTAGGCACCG 1620
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Seq ID NO: 298 Protein sequence  
Protein Accession #: NP\_006623.1

1 11 21 31 41 51  
5 MQVDETLIPR KGPSLCSARY GIALVLHFCN FTTIAQNVIM NITMVMVNS TSPQSQNLDS 60  
SEVLVDSFG GLSKAPKSLP AKSSILGGQF AIWEKNGPPO ERSRLCSIAL SGMLLGCFPTA 120  
ILIGGFISET LGWPFVFIYF GGVGCVCCLL WFWVIYDDPF SYPWISTSEK EYIISSLKQO 180  
VGSSKQPLPI KAMLRSLPIW SICLGCFSHQ WLVTMVVYI PTYISSVYHV NIRDNGLLSA 240  
LPFIVAVWIG MVGGYLAFL LTKKPRITV RKIATILGSL PSSALIVSLP YLNSGYITAT 300  
10 ALLTLSCGLS TLQSGIYIN VLDIAPRYSS FLMGASRGFS SIAPVIVPTV SGFLLSQDPE 360  
FGWRNVFLL FAVNLLGLLF YLIFGEADVQ EWAKERKLTR L

Seq ID NO: 299 DNA sequence  
Nucleic Acid Accession #: NM\_003058.1  
Coding sequence: 145..1812

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20 TCGGGCCCTC CTGCCTGCAG GATCATGCCG ACCACGCTGG ACGATGTCTT GGAGCATGGA 180  
GGGGAGTTTC ACTTTTTCCT GAAGCAAATG TTTTCTCTCT TGGCTCTGCT CTGGCTTACC 240  
TTGCGGCCCA TCTACGTGGG CATCGTCTTC CTGGGCTTCA CCTCTGACCA CCGCTGCGCG 300  
AGCCCGCGAG TGGCCGAGCT GAGTCTGCGC TGGGCTGGA GTCTCTGAGA GGAAGTGAAC 360  
25 TACAGCGTGC CGGCCCCAGG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420  
GAGGTGGACT GGAACACAGG CACCTTTGAC TGGTGGGACC CCTTGGCCAG CCGGACACCC 480  
AACAGGAGCC GCTTCCCACT GGGCCCCCTG CGGACGCGCT GGGTGTACGA GACGCTTGGC 540  
TCGTCCATCG TCACCGAGTT TAACCTGGTA TGTGCCAATC CTTGGATGTT GGACCTATTC 600  
CAGTCATCAG TGAATGTAGG ATCTCTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC 660  
30 AGGTTTGGCC GTAAGCTCTG CCTCCTAACT ACAGTCTCTA TAAATGCTGC AGCTGGAGTT 720  
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GTCAGCAAGC CAGGCTGGTT AATAGGCTAC ATCTGTATTA CAGAATTGT TGGGCGGAGA 840  
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GCTGGGGTGG CTACGCACT TCCTCACTGG AGGTGGTTCG AGTTCACAGT TGCCTGCCCC 960  
35 AACTTCTCT TCTTGTCTTA TTAAGTGTGC ATACCTGAGT CTCCCGAGTG GCTGATCTCC 1020  
CAGAATAAGA ATGCTGAAGC CATGAGAATC ATTAAGCACA TCGCAAGAA AAAATGGAAA 1080  
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CCTCATTTCT TTGACTTGGT CAGAACTCCT CAGATAAGGA AACATACTAT GATATTGATG 1200  
TACAACTGGT TCACGAGCTC TGTGCTCTAC CAGGGCTCTA TCATGCACAT GGGCCTTGCA 1260  
40 GGTGACATA TCACTCTGGA TTTCTTCTAC TCTGCCCTGG TTGAATTTCC AGCTGCCTTC 1320  
ATGATCATCC ATGCTGATCG CGCATCGGA CGCCGTTACC CTGGGCTGCG ATCAAAATATG 1380  
GTTCAGGGGG CAGCCTGTCT GGCTCAGTT TTTATACCTG GTGATCTACA ATGGCTAAAA 1440  
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TTGCTTCCAG AACTAAAGG GAAAGCTTTG CCTGAGACCA TCGAGGAAGC CGAAATATATG 1740  
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Seq ID NO: 300 Protein sequence  
Protein Accession #: NP\_003049.1

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65 PCRDRWVYET PGSSIIVTEFN LVCANSWMLD LFQSSVNVGF FIGSMSIGYI ADRFGRKLCL 180  
LTTVLINAAA GVMAISPTY TWMLIFRLIQ GLVSKAGWLI GYLITTEFVG RRYRRTVGIF 240  
YQVAYTVGLL VLAGVAYALP HNRWLQFTVA LPNFFFLYY NCIPESPRWL ISQNKNAEAM 300  
RIIKHIAKIN GKSLPASLQR LRLEERTGKK LNPFFLLDVR TPQIRKHTMI LMYNFTSSV 360  
LYQGLIMEMG LAGDNILYLF FYSLVVEFPA AFMIILTIDR IGRYPWAAS NMVAGAACLA 420  
70 SVFIPGDLQW LKIIISCLGR MGIWAVEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480  
TPFLVYRLTN IWLELPLMVF GVLGLVAGGL VLLLPETKKG ALPETIEEAR NMQRPRKNKE 540  
KMIYLVQVQL DIPLN

Seq ID NO: 301 DNA sequence  
Nucleic Acid Accession #: NM\_012206.1  
Coding sequence: 52..1131

1 11 21 31 41 51  
80 GTTACCCAGC ATTGTGAGTG ACAGAGCCTG GATCTGAACG CTGATCCCAT AATGCATCCT 60  
CAAGTGTGCA TCTTAAGCCT CATCTACAT CTGGCAGATT CTGTAGCTGG TTCTGTAAAG 120  
GTGGTGGAG AGGCAGGTCC ATCTGTACAC CTACCGTGCC ACTACAGTGG AGCTGTACAC 180  
TCAATGTGCT GGAATAGAGG CTATGTCTCT CTATTCACAT GCAAAATAGG CATTTGTCTG 240  
ACCAATGGAA CCAACGTAC CTATCGGAAG GACACACGCT ATAAGCTATT GGGGACCTT 300  
TCAAGAAGGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGTCTGACAG TGGCGTATAT 360

5 TGTGCGGTG TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACOGT ATCATTGGAG 420  
 ATTGTGCCAC CCAAGGTCCAC GACTACTCCA ATTGTACAA CTGTTCACAC CGTCACTGACT 480  
 GTTGGAAACGA GCACCACTGT TCCAACGACA ACGACTGTTC CAACGACAAC TGTTCACACA 540  
 ACAATGAGCA TTCCAACGAC AACGACTGTT CCGACGACAA TGACTGTTC AACGACAACG 600  
 AGCGTTCCAA CGACAACGAG CATTCACAACA ACAACAAGTG TTCCAGTGAC AACCAACGGTC 660  
 TCTACCTTTG TTCTCCAAAT GCCTTTGGCC AGGCAGAACCT ATGAACCACT AGCCACTTCA 720  
 CCATCTTCAC CTCAGCCAGC AGAAACCCAC CCTACGACAC TGCAGGGAGC AATAAGGAGA 780  
 GAACCCACCA GCTCACCATT GTACTCTTAC ACAACAGATG GGAATGACAC CGTGACAGAG 840  
 TCTTCAGATG GCCTTTGGAA TAACAATCAA ACTCAACTGT TCCTAGAACA TAGTCTACTG 900  
 10 ACGGCCAATA CCACTAAAGG AATCTATGCT GGAGTCTGTA TTTCTGTCTT GGTGCTTCTT 960  
 GCTCTTTTGG GTGTCTCAT TGCCAAAAAG TATTTCTTCA AAAAGGAGGT TCAACAACCTA 1020  
 AGTGTTCAT TTAGCAGCCT TCAAAATAAA GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC 1080  
 CAAGCAGAAG ACAATATCTA CATTGAGAAT AGTCTTTATG CCAACGACTA AGACCCAGTG 1140  
 15 GTGCTCTTTG AGAGTTTACG CCCATGACTG CAGAAGACTG AACAGGTATC AGCAGATCAG 1200  
 ATGTCTTTTA GTGTCCAAGA CAATTTTCTT GTTTCAGTTT CATCTGGCAT TCCACATGT 1260  
 CAGTGATCT GGGTAGAGTA ACTCTCCAC TCCAACTGT GTATAGTCAA CCTCATCATT 1320  
 AATGTAGTCT TAATTTGTTT TGCTAAACT GGTCTCAATCC TTCTGATCAT TGCAGAGTTT 1380  
 TCTCTCAAC ATGAACACTT TAGAATTGTA TGTCTCTTT AGACCCATA AATCTGTAT

Seq ID NO: 302 Protein sequence  
 Protein Accession #: NP\_036338.1

25 1 11 21 31 41 51  
 MHPQVVLISL ILHLADSVAG SVKVGGEAGP SVTLPCHYSG AVTSMCNWRG SCSLFTCQNG 60  
 IVWNTNGTHV YRKDTRYKLL GDLRRDVSLS TIENTAVSDS GUYCCRVHR GWFNMDKITV 120  
 SLEIVPPTKT TPIVITTVPT VITVITVPTT PTTTIVPTT VPTTMSIPTT TIVPTMTVS 180  
 TTTSPPTTTS IPTTSPVPT TTVSTFVPPM PLPRQNHFPV ATSPSSPQPA ETHPTTLQGA 240  
 30 IRRPTSSPL YSYTTDNDT VTESDGLWN NNQTLQFLFH SLTANTTKG IYAGVCISVL 300  
 VLLALLGVII AKKYFFKKEV QQLSVSPSSL QIKALQNAVE KEVQAEENIY IENSLYATD

Seq ID NO: 303 DNA sequence  
 Nucleic Acid Accession #: NM\_001044.1  
 Coding sequence: 129..1991

35 1 11 21 31 41 51  
 ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGGTGTC 60  
 40 AAAGCCGAGG CCGGGGCGGC CAGACCAAGA GGAAGAAGC ACAGAAATCC TCAACTCCCA 120  
 GTGTGCCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCCGTG GTGGCCCGGG 180  
 CTAAGGAGCC CAATGCCGTG GCGCCGAGG AGGTGAGACT CATCTTGTTC AAGGAGCAGA 240  
 ACGGAGTGCA GCTCACCAGC TCCACCTCCA CCAACCCGGG GCAGAGCCCC GTGGAGGCCC 300  
 AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTCTCCT GTCCGTGATT GGCTTTGCTG 360  
 45 TGGACCTGGC CAACTCTGTC CGGTTCCTCT ACCTGTGCTA CAAAAATGGT GCGGGTGCCT 420  
 TCCTGGTCCC CTACCTGCTC TTCATGGTCA TTGCTGGGAT GGCATTTTC TACATGGAGC 480  
 TGGCCCTGGC CAGATTCAAC AGGGAAGGGG CCGCTGGTGT CTGGAAGATC TGCCCCATAC 540  
 TGAAAGGTGT GGGCTTCAAG GTCATCTCCA TCTCACTGTA TGTGCGGTTC TTCTACAAGC 600  
 TCATCATGCG CTGGGCGCTG CACTATCTCT TCTCCTCTT CACCAAGGAG CTCCCTGGA 660  
 50 TCCACTGCAA CAACTCTGCG AACAGCCCA ACTGCTCGGA TGCCCATCCT GGTGACTCCA 720  
 GTGGAGACAG CTCGGGCTTC AACGACACTT TTGGGACCAC ACCTGCTGCC GAGTACTTTG 780  
 AACGTGGGGT GCTGCACTTC CACCAGAGCC ATGGCATGGA CGACCTGGGG CCTCGCGGCT 840  
 GGCAGCTCAC AGCCTGCTG GTGCTGGTCA TCGTGTGCT CTACTTCAGC CTCTGGAAGG 900  
 CGGTGAAGAC CTCAGGGAAG GTGGTATGGA TCACAGCCAC CATGCCATAC GTGGTCTCTA 960  
 55 CTGCGCTGCT CTGCGTGGG GTCACTCTCC CTGAGGCCAT AGACGGCATC AGAGCATACC 1020  
 TGAGCGTTGA CTCTACCGG CTCTGCGAGG CGTCTGTTTG GATTGACGGG GCCACCCAGG 1080  
 TGTGCTTCTC CTGCGGCGTG GGGTTOGGGG TGCTGATGCG CTCTCCAGC TACAACAAGT 1140  
 TCACCAACAA CTGCTACAGG GACGCGATTG TCACCACTCC CATCACTCC CTGACGAGCT 1200  
 TCTCTCGCGG CTTCGTGCTC TTCTCTCTCC TGGGGTACAT GGCACAGAAG CACAGTGTGC 1260  
 60 CCATCGGGGA CGTGGCCAAG GACGGGCCAG GGCTGATCTT CATCATCTAC CCGGAAGCCA 1320  
 TCGCCAGCTC CCTCTGTGCC TCAGCCTGGG CCGTGGTCTT CTTCATCATG CTGCTCACCC 1380  
 TGGGTATGGA CAGCGCCATG GGTGGTATGG AGTCAGTGAT CACCGGGCTC ATCGATGAGT 1440  
 TCCAGTCTCT GCACAGACAC CGTGAGCTCT TCAAGCTCTT CATGCTCTG GCGACCTTCC 1500  
 TCTCTGCTCT GTTCTGCTC ACCAACGCTG GCATCTACGT CTTCAGCTC CTGGACCAAT 1560  
 65 TTGAGCGCGG CAGCTCCATC CTCTTTGGAG TGCTCATGGA AGCCATCGGA GTGGCCTGGT 1620  
 TCTATGGTGT TGGGCACTTC AGCGACGACA TCCAGCAGAT GACCGGGCAG CGGCCAGCC 1680  
 TGTACTGGCG GCTGTCTGCG AAGCTGGTCA GCGCCTGCTT TCTCTGTTTC GTGGTCTGCG 1740  
 TCAGCATGTT GACCTTCAGA CCCCCCACT ACAGGAGCTA CATCTTCCCC GACTGGGCCA 1800  
 ACGCGCTGGG CTGGGTCTTC GCCACATCCT CCAATGGCCAT GGTGCCCATC TATGGGCTCT 1860  
 70 ACAAGTCTCT CAGCCTGCCT GGTCTCTTC GAGAGAACT GGCTAGGCC ATTGCACCCG 1920  
 AGAAGGACCG TGAGCTGGTG GACAGAGGGG AGGTGOGCCA GTTCAAGCTC CGCCACTGGC 1980  
 TCAAGTGTGA GAGGGAGCAG AGACGAGAGC CCCAGGAAGT CATCTGCAA TGGGAGAGAC 2040  
 ACCAACAAC CAAGGAAATC TAAGTTTCCA GAGAAAGGAG GGCAACTTCT ACTCTTCAAC 2100  
 CTCTACTGAA AACACAAACA ACAAGCAGA AGACTCTCTT CTCTGAGCT TTTACACTT 2160  
 75 TCCGTGCGCG GAGCGCACTC GCGGTGTCTT TGTGTGCTG TAATAAGGAC GTAGATCTGT 2220  
 GCAGCGAGGT CCAACCCGTT GTTGTCTCTG CAGGGCAGAA AAACGTCTAA CTTCATGCTG 2280  
 TCTGTGTGAG GCTCCCTTCC TCCCTGCTCC CTGCTCCCGG CTCTGAGGCT GCGCCAGGGG 2340  
 CACTGTGTTT TCAGGCGGGG ATCAGATCC TTGTAGAGCG ACCTGCTGAG AATCCCGGTG 2400  
 CTCACAGTAG CTTCCTAGAC CATTTACTTT GCCCATATTA AAAAGCCAAG TGTCTGTCTT 2460  
 80 GGTTTAGCTG TGCAGAGGTG GAAATGGAGG AAACCAACAA TTCATGCAAA GTCCCTTCCC 2520  
 GATGCGTGGC TCCAGCAGCA GGCCTGAAAT TGAGGTTTCA GTTGACACAT TGCACACACA 2580  
 GTCGTCTCAG AGCTCATGGA GGATGGGGT OCTGGTATGT CTCACAGGA AATTCTGTTT 2640  
 ATGTTCTTGC AGCAGAGAGA AATAAACTC CTTGAAACCA GCTCAGGCTA CTGCCACTCA 2700  
 GGCAGCCTGT GGGTCTTGT GGTGTAGGGA ACGGCGCTGAG AGGAGCGTGT CCTATCCCCG 2760  
 GACGATGCA GGGCCCCAC AGGAGCGTGT CCTATCCCCG GACGATGCA GGGCCCCAC 2820

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10  
15  
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AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCAG 2880
AACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCAG GACGCATGCA GGGCCCCCAC 2940
TGGAGCGTGT ACTACCCAG GACGCATGCA GGGCCCCCAC AGGAGCGTGT CCTATCCCTG 3000
GACCGGACGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC CCCAGGACGC ATGCAGGGCC 3060
CCCACAGGAG CGTGTACTAC CCCAGGATGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC 3120
CCCAGGACGC ATGCAGGGCC CCCATGCAGG CAGCCTGCAG ACCAACACTC TGCCTGGCCT 3180
TGAGCGGTGA CCTCCAGGAA GGGACCCAC TGGAAATTTA TTCTCTCAG GTGCGTGCCA 3240
CATCAATAAC AACAGTTTTT ATGTTTGCGA ATGGCTTTT AAAATCATAT TTACCTGTGA 3300
ATCAAAACAA ATTCAAGAAT GCAGTATCCG CGAGCCTGCT TGTGATATT GCAGTTTTTG 3360
TTTACAAGAA TAATTAGCAA TACTGAGTGA AGGATGTTGG CCAAAAGCTG CTTTCCATGG 3420
CACACTGCCC TCTGCCACTG ACAGGAAAGT GGATGCCATA GTTTGAATTC ATGCTCAAG 3480
TGGTGGGCC TGCCTACGTG CTGCCGAGG GCAGGGGCCG TGCAGGGCCA GTCATGGCTG 3540
TCCCCTGCAA GTGACGTGG GCTCCAGGGA CTGGAGTGA ATGCTCGGTG GGAGCGTCA 3600
GCCTGTGAAC TGCCAGGACG CTGCAGTTAG CACAGAGGAT GGCCTCCCA TTGCCTTCTG 3660
GGGAGGGGCA CAGAGGACGG CTTCCCATC GCCTTCTGGC GCTGCACTC AGCACAGAGA 3720
GGGCTTCCC CATTCCTTC TGGGAGGGA CACAGAGGAC AGTTTCCCA TGCCTTCTG 3780
TTGTGTTTGA ACAGCACAGA GAGCGGCTTC CCCATCGCCT TCTGGGAGG GGCCTCGTGT 3840
AGCAACCCAG GTGTGTCCG TGTCTGTGA CCAATCTCTA TTCAGCATCG TGTGGTCCC 3900
TAAGCAAT AAAAGACATC CACAATGGAA AAAAAAAG GAATTC

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Seq ID NO: 304 Protein sequence  
Protein Accession #: NP\_001035.1

25  
30  
35

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1 11 21 31 41 51
| | | | |
MSKSKSVGL MSSVVAPEKE PNAVGPKEVE LILVKEQNGV QLTSSSTLINF RQSFVEAQRD 60
ETWGGKIDPL LSVIGFAVDL ANVWRFPYLC YKNGGGAFLV PYLLFMVIAG MPLFYMELAL 120
GQFNREGAAG VWKICPILKG VGPTVILISL YVGFYFNVII ANALHYLFSS FTTELPHIHC 180
NNSWNSPNCS DAHPGDSGGD SSGLNDTFGT TPAAEYFERG VLHLHQSHGI DDLGPPRNQL 240
TACLVLVIVL LYFSLWKGVK TSGKVVWITA TMPYVVLTLAL LLRGVTLPGA IDGIRAYLSV 300
DFYRLCEASV WDAATQVCF SLGVGFVULI AFSSYNKFTN NCYRDAIVTT SINSLTSPSS 360
PFVVSFLGY MAQKHSVPIG DVAKDGPGLI PIYPERAIAT LPLSSAWAVV PFIMLLTLGI 420
DSAMGGMESV ITGLIDEPQL LHRHRELFTL FIVLATPILLS LFCVTNGGIY VFTLLDHPAA 480
GTSILFGLVI EAIGVAPFYG VQGFSDDIQQ MTGQRPSLYW RLCWKLVSFC FLLEVVVVSI 540
VTFRPPHYGA YIFPDWANAL GWVIATSSMA MVPIYAAKPE CSLPGSFREK LAYALAPEKD 600
RELVDREGEV QFTLRHRLKV

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Seq ID NO: 305 DNA sequence  
Nucleic Acid Accession #: NM\_001216.1  
Coding sequence: 43..1422

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1 11 21 31 41 51
| | | | |
GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 60
AGCCCTCGGC TCCTCTGTGT GATCCCGGCC CCTGCTCAG GCCTCACTGT GCAACTGCTG 120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCACAGAGT TGCCTCCGAT GCAGAGGAT 180
TCCCCTTGG GAGGAGGCTC TTCTGGGGA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240
AGTGAAGAGG ATTACCCAG AGAGGAGGAT CCACCCGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGAGAGGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
TCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCTG GAGATCCTCA AGAACCCAG 420
ATAATGCCC ACAGGGACRA AGAAGGGGAT GACACAGATC ATTGGCGCTA TGGAGGCGAC 480
CGCCCTGCG CCCTGGTGTG CCCAGCCTGC GCGGGCGCTC TCCAGTCCCC GGTGGATATC 540
CGCCCTAGC CGCCCTGCTT CTGCGCGGCC CTGCGCCCCC TGGAACTCCT GGCCTTCCAG 600
CTCCCGCGC TCCAGAACT GCGCCTGCGC AACATGGCC ACAGTGTGCA ACTGACCCGT 660
CCTCTGGGC TAGAGATGCG TCTGGGTCCC GCGGGGAGT ACOGGCTCTC GCAGCTGCAT 720
CTGCACTGGG GGGCTGCAGG TGTCTCGGGC TCGGAGCACA CTGTGGAAGG CCACGTTTC 780
CTGCGCAGA TCAAGTGTG TCACCTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCTTTC 840
GGGCGCGCG GAGGCTGCGC GGTGTGCGC GCCTTTCTGG AGGAGGGGCC GGAAGAAAAC 900
AGTGCTATG AGCAGTTGCT GTCTCGCTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
CAGGTCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCG CTACTTCCAA 1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGAGC TGTGTTTAA 1080
CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCT GTGGGACCT 1140
GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCGAG CTTTGAATGG GCGAGTGATT 1200
GAGGCTCTCT TCCTGCTGG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
AATCTCTGCC TGGCTGCTGG TGACATCTTA GCGCTGTTT TTGGCTCTCT TTTTCTGTC 1320
ACCAGGCTG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
GTGAGTACC CCCAGCAGA GGTAGCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
TGTGAGAGC CAGCCAGAG CATCTGAGG GAGAGCGGTA ACTGCTCTGT CTGCTCATT 1500
ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT

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Seq ID NO: 306 Protein sequence  
Protein Accession #: NP\_001207.1

75  
80

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1 11 21 31 41 51
| | | | |
MAPLCPSPWL PLLIPAPAPG LTVQLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60
GEEDLPSEED SPREDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTEAPG 120
DPQSPQMANH RDKEGDDQSH WRYGGDPFVP RVSPACAGRF QSPVDIRPOL AAFCPALRPL 180
ELLGFPQLPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
VEGRFPFAEI HVVBLSTAPA RVDEALGRPG GLAVLAAPLE EGPEENSAYE QLSRLLEEIA 300
EGSETEQVPG LDISALLPSD PSRYFYEGSS LTPPCAQGV IWTVFNTQVM LSAQLHLTSL 360
DTLMGPGDSR LQLNFRATQP LNRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
QLLFAVTSVA FLVQMRQRH RGTGKGVSYR PAEVAETGA

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Seq ID NO: 307 DNA sequence  
Nucleic Acid Accession #: NM\_003039.1  
Coding sequence: 76..1581

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5      1      11      21      31      41      51
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      CTTCTCTCTC CATTCACTGC ACGCGTIACT TTGGCTAAAA GGAGGTGAGC GGCACCTCTGC   60
      CCTTCCAGAG CAAGCATGGA GCAACAGGAT CAGAGCATGA AGGAAGGGAG GCTGACGCTT   120
      GTGCTTGCCC TGGCAACCCCT GATAGCTGCC TTTGGGTGCT CCTTCCAGTA TGGGTACAAC   180
10     GTGGCTGCTG TCAACTCCCC AGCACTGCTC ATGCAACAAT TTTACAATGA GACTTACTAT   240
      GGTAGGACCG GTGAATTCAT GGAAGACTTC CCCTTGACGT TGCTGTGGTC TGTAACCGTG   300
      TCCATGTTTC CATTTGGAGG GTTTATCGGA TCCCTCCTGG TCGGCCCTT GGTGAATAAA   360
      TTGGCAGAA AAGGGGCCCT GCTGTTCAAC AACATATTTT CTATCGTGCC TGCGATCTTA   420
      ATGGGATGCA GCAGAGTGGC CACATCATTT GAGCTTATCA TTATTTCAG ACTTTTGGTG   480
15     GGAATATCTG CAGGTGTATC TTCCAACGTG GTCCCATGT ACTTAGGGA GCTGGCCCTT   540
      AAAAACTGCG GGGGGCTCTC CGGGGTGGTG CCCGAGCTCT TCATCACTGT TGGCATCCTT   600
      GTGGCCCAAG TCITTTGGTCT TCGGAATCTC CTTCGAAAG TAGATGGCTG GCGATCTCTG   660
      CTGGGGCTGA CCGGGGTCCC CGGGGGCTG CAGCTCCTTC TGCTGCCCTT CTTCGCCGAG   720
      AGCCCCAGGT ACCTGCTGAT TCAGAAAGAA GACGAAGCGG CCGCAAGAA AGCCCTACAG   780
20     AGCTGCGCG GCTGGGACTC TGTGGACAGG GAGGTGGCGG AGATCGGCA GGAGGATGAG   840
      GCAGAGAGG CGCGGGCTT CATCTCGGTG CTGAAGCTGT TCCGATGCG CTGCTGCGC   900
      TGGCAGCTGC TGTCCATCAT GTCTCTCATG GGCGGCCAGC AGCTGTGCGG CGTCAACGCT   960
      ATCTACTACT ACGCGGACCA GATCTACCTG AGCGCGGCGG TGCGGAGGA GCAOGTGCAG   1020
      TAGCTGAGCG CGCGCACCGG GCGCGTGAAC GTGCTCATGA CCTTCTGCGC CGTGTGTGTC   1080
25     GTGAGCTCC TGGGTGGAG GCTGCTGCTG CTGCTGGGCT TCTCATCTG CCTCATAGCC   1140
      TGCTGGGTGC TCACTGCAGC TCTGGCACTG CAGGACACAG TGTCTGGAT GCCATACATC   1200
      AGCATCGTCT GTGTCACTC CTACGTCTCA GGACATGCCC TCGGGGCCAG TCCCATACCC   1260
      GCGCTGCTCA TCACTGAGAT CTCTCTGCGG TCCTCTGCGC CATCTGCTT CATGGTGGG   1320
      GGCAGTGTGC ACTGGCTCTC CAACTTCACC GTGGGCTTGA TCTTCCGCTT CATCCAGGAG   1380
30     GCGCTCGGCC CGTACAGCTT CATGTCTTTC GCGGTGATCT GCCTCTCAC CACCATCTAC   1440
      ATCTCTCTGA TTGTCCCGGA GACCAAGGCC AAGACGTTCA TAGAGATCAA CCAGATTTTC   1500
      ACCAAGATGA ATAAGGTGTC TGAAGTGTAC CCGGAAAAGG AGGAACTGAA AGAGCTTCCA   1560
      CCTGTCACTT CGGAACAGTG ACTCTGGAGA GGAAGCCAGT GGAGCTGGTC TGCCAGGGGC   1620
      TTCCCACTTT GGCCTATTTT TCTGACTTCT AGCTGTCTGT GAATATCCAG AAATAAAACA   1680
35     ACTCTGATGT GGAATGCACT CCTCATCTCC AGCCTCCCCA CCCCAGTGGG AACTGTGCAA   1740
      AGGCGTGCCT TGCTGTCTCT GAAGCTGGGC TGTCTCTCTC CATGTTGGCC TGTCAACAGA   1800
      CCGAGTCAA TTAACAGCT GGTCTCTCAC TTTGCTGGTT CAGCCTTCGT GTGGCTCCTG   1860
      GTAACTGTGC TCACCTTGA TGGGTCAACC TTTGTGTGGC TCTGGTAAAC ATAACAACAA   1920
      CAGTTACTAT AGTGTGAGA TGAAGGAAT CAATTTTTC CAGAGAAACT AACTCGGTGG   1980
40     CCCCACAGCG TCTTCGGGG CCATGGGCAT TGTGTTAGAG CCAATTCAT CCTCTTACCA   2040
      GATCTTTTTC CAGAAATACC TGTCTAGGAA GGTGTGATGT CAGAAACAT GACATCCAGA   2100
      AAGCTGAGGA ACAGGTTCCT GTGGAGACAC TGAGTCAGAA TTCTTCATCC AAATTATTTT   2160
      GTTAGTGAAA AATGGAATTG CTTCTGTGTA GTCAATAAAA TGAACCTGAT CACTTTTC
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Seq ID NO: 308 Protein sequence  
Protein Accession #: NP\_003030.1

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50     1      11      21      31      41      51
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      MEQDDQSMKE GRLTLVLALA TLIAAPGSSP QYGVNVAAVN SPALLMQQFY NBTYYGRIGE   60
      FMEDPPLTLI WSVTVSMFPF GSGFISLLVG PLVNKFGKRG ALLFNNIFS I VPAILMGCSR   120
      VATSFELIII SRLLVGICAG VSSNVVPMYL GELAPKILRG ALGVVPQLFI TVGILVAQIF   180
      GLRNLANVD GWPILLGLTG VPAALQLLLL PFPPESPRYL LIQKDEBAAA KQALQTLRGW   240
55     DSVDRBVAEI ROEDEAEKAA GFISVLKLF MRSLRWQLLS IIVLMGGQQL SGVNAIYYFA   300
      DQIYLSAGVP EEHVQYVTAG TGAANVMVTF CAVFVVELLG RRLILLGLFS ICLIACCVLT   360
      AALALQDTSV WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRP AFMVGSSVHW   420
      LSNFTVGLIF PFIQEGGLPY SFIVFAVICL LTTIYIPLIV PETKARTPIE INQIFKMNK   480
      VSEVYPEKEE LKELPPVTSE Q
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Seq ID NO: 309 DNA sequence  
Nucleic Acid Accession #: NM\_001252.1  
Coding sequence: 138..719

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65     1      11      21      31      41      51
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      GTTTCCTTCT TTCTTCTCG GCAGGCTGCC GGGCCGCCAT CGCCCTCTCT GCGCTAGCGG   120
      AGGTGATCGC CGGGGAGATG CCGGAGGAGG GTTCGGGCTG CTGGGTGCGG GCGAGGCCCT   180
70     ATGGGTGCGT CCTGCGGGCT GCTTTGGTCC CATTTGTCGC GGGCTTGGTG ATCTGCCTCG   240
      TGGTGTGATC CCAGGCTTTC GCACAGGCTC AGCAGCAGCT GCGCTGAGAG TCACCTGGGT   300
      GGGAGCTAGC TGAGCTGCAG CTGAATCACA CAGGACCTCA GCGAGACCCC AGGCTATACT   360
      GGCAGGGGGG CCGAGCAGCT GCGCGTCTCT TCCTGCATGG ACCAGAGCTG GACAAGGGGC   420
      AGCTACGTAT CCATCGTGAT GGCATCTACA TGGTACACAT CCAGGTGAGC CTGGCCATCT   480
75     GCTCTCTCCAC GAOGGCTTCC AGGCACACC CCACCACTCT GCGCGTGGGA ATCTGCTCTC   540
      CCGCTCCCG TAGCATCAGC CTGCTGCTC TCAGCTTCCA CCAAGGTTGT ACCATTGCCT   600
      CCGAGCGCTG GAGCGCCCTG GCGGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC   660
      TTTTGCTTTC CCGAAACACT GATGAGACCT TCTTTGAGT GCACTGGGTG GCGCCCTGAC   720
      CACTGCTGCT GATTAGGGTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAA   780
80     AGTGTACACA CAGGGGCCAC CCGGGGTGG GGTGGGAGTG TGGTGGGGGG TAGTGGTGGC   840
      AGGACAAGAG AAGGCATTGA GCTTTTCTT TCATTTTCTT ATTAATAA
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Seq ID NO: 310 Protein sequence  
Protein Accession #: NP\_001243.1



1 11 21 31 41 51  
 MPEEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVABL 60  
 5 QLNHTGPQDD PRLYWGQGP LGRSFLHGPE LDKGQLRIHR DGIYMHQIV TLAISSSTTA 120  
 SRHHPTTLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLLPSRN 180  
 TDETFPGVQW VRP

Seq ID NO: 311 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..3978

1 11 21 31 41 51  
 15 ATGTGGGGTG AAGGACCTTA CCTTATCTCA GATCTGGACC AGCGAGGCGG CGCGAGATCC 60  
 TTTGCAGAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGGGACC CTGTGCAAGG 120  
 TTAGCACCCA ACCCGGTGGA TGATGCGGGG CTACTCTCCT TCGCCACATT TTCTGGCTC 180  
 ACGCCGGTGA TGGTGAAAGG CTACCGGCAA AGGCTGACCG TAGACACCTT GCCCCCATTTG 240  
 TCGACATATG ACTCATCTGA CACCAATGCC AAAGATTTC GAGTCTTTTG GGATGAAGAG 300  
 GTAGCAAGGG TGGGTCTTGA GAAGGCTCTT CTGAGCCACG TGGTGTGGAA ATTCAGAGG 360  
 20 ACACCGGTGT TGATGGACAT CGTGGCCAAC ATCCTGTGCA TCATCATGGC AGCCATAGGG 420  
 CGACAGTTTC TCATTACCCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG 480  
 GTTGGCATTG GACTGTGCAT AGCCCTTTT GCCACCGAGT TTACCAAGT CTTCTTTTGG 540  
 GGCCTTGCTT GGGCATCAA CTACCGCAGC GCCATCGGT TGAAGGTGGC GCTCTCCACC 600  
 25 TTGGTTTTTG AAAACCTAGT GTCTTCAAG ACATTGACCC ACATCTCTGT TGGGAGGTTG 660  
 CTCAATATAC TGTCAGATGA TAGCTATTCT TTGTTGAAG CTGCCCTTGT TTGTCTTTG 720  
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 GCCAAGCTCA ATTCACTTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTTCA 900  
 30 ACAATGAATG AGTTTCTGAC CTGCATCAGG CTGATCAAAA TGTATGCCTG GGAGAAATCT 960  
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 AGGCATTTAT GCAAGAAACA GAGGTCAAG GCATACAGTG AGAGGAGTCC ACCAGCCAG 1440  
 GGAGCCACTG GCCCAGAGGA GCAAGTGAC AGCCTCAAT CGGTCTGCA CAGCATAAGC 1500  
 40 TTGTGTGTGA GAAAGTTATG TCGTTATCCC GAAGCCGAGC TCCTGGCTTG GAGGTGGCCA 1560  
 GCAGTGTGTT TTGGGAGAAAT CATCAGAGGA TACAGGCTTC ATGGATTTC TGCTAAAGAC 1620  
 AAGGATGAAT CTAGAAGGCT TCTTACTTGG CCCCAAGAG TGGATAGGAC TCAAGGGCA 1680  
 GCCAATACC TGGGGAAGAT CTTGGGAATA TGTGGGAATG TGGGAAGTGG AAAGAGCTCC 1740  
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 45 ACTTTGGCCT ACCTTTTACA GCAGGCATGG ATCTTTTCAT GAAATGTGAG AGAAAAATA 1860  
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 60 CCAATGAGTT TCTTTGACAC GACTCCCACT GGCAGGCTAA TGAACCGTTT TTCCAAGGAT 2760  
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 70 CTTGTTCTCG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCGG GATTGTGGA 3360  
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 75 TTGGATCCCT TTGAGAGTCA CACGATGAG ATGCTCTGGC AGGTTCTGGA GAGAATTC 3600  
 ATGAGAGACA CAATAATGAA ACTCCAGAA AAATTACAGG CAGAAGTCAC AGAAAATGGA 3660  
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Seq ID NO: 312 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 5 MVGEGPYLIS DLDQRRRRS PAERYDPSLK TMIPVRPCAR LAPNFVDDAG LLSPATPSWL 60  
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 TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALP ATEFTKVFFW 180  
 ALAWAINYRT AIRLRVALST LVFENLVSPK TLTHISVGEV LNILSSDSYS LPEAALFCPL 240  
 PATIPILMVF CAYHAFPIIG PTALIGISVY VIFIPVQMF AKLNSAFRRS AILVTDKRVQ 300  
 TMNEFLTICIR LIKMYAWEKS FTNTIQDIRR RERKLEKAG PVQSGNSALA PIVSTIAIVL 360  
 10 TLSCHILLRR KLTAPVAFSV IAMFNVMKFS IAILPFSIKA MAEANVSLRR MKKILIDKSP 420  
 PSYITQPEDP DTVLLLANAT LTWEHEASRK STPKKLQNK RHLCKQRSE AYSERSPPAK 480  
 GATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSAKD 540  
 KDESRRLLTW PQEVDRTQRA AKYLGIKILGI CGNVGSGKSS LLAALLGQMQ LQKGVVAVNG 600  
 TLAYVSQQA W IPHGNVRENI LPGEKYDHQR YQHTVRVCG L QKDLNLFPYG DLTEIGERGL 660  
 15 NLSSGQQRRI SLARAVYSR QLYLLDDPLS AVDAHVGKHV FEBCIKKTLR GKTVVVLVTHQ 720  
 LQFLESCDEP ILLEGEICE KGTHELMES RGRYAKLIHN LRGLQPKDPE HLYNAAMVEA 780  
 FKESPAEREE DAGIIGYLLS LFTVFLFLM IGSAAPSNW LGLWLDKGSR MTCGPQGNRT 840  
 MCEVGAVLAD IQGHVYQWVY TASMVFMLVF GVTKGPFVTK TILMASSSLH DTVFDKILKS 900  
 PMSFEDTTP T GRIMNRFSD MDELVDRLPF HAENFLQQFF MIVPILVILA AVFPAVLV 960  
 20 ASLAVGFFIL LRIFHRGVE LKKVENVSRS FWFTHITSSM QGLGIIHAYG KKESCITYTS 1020  
 SKGLSLSYII QLSGLLQVCV RTGTETQAKF TSVELLREYI STCVPECTHP LKVGTCPKDW 1080  
 PSCGBEITFRD YQMYRDNTP LVLDLSNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140  
 SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLFVGTVRYN LDPFESHTDE MLWQLERTF 1200  
 MRDTIMKLPE KLOAEVTENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMDSKTDTL 1260  
 25 VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENKGVIE FDKPEVLAEK PDSAFAMLLA 1320  
 AEVRL

Seq ID NO: 313 DNA sequence  
 Nucleic Acid Accession #: Z31560  
 Coding sequence: 1-966

1 11 21 31 41 51  
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 AGCCCGGAGC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGTCCCG CGGCGAGCG 180  
 CGCAAGATGG CCCAGGAGAA CCCCAAGATG CACAACCTGG AGATCAGCAA GCGCTGGGC 240  
 CGCGAGTGG AACTTTTGTG GGAGACGGAG AAGCGGCGT TCATCGACGA GGCTAAGCG 300  
 CTGCGAGCGC TGCACATGAA GGAGCACCGG GATTATAAAT ACCGGCCCCG GCGGAAAAC 360  
 40 AAGACGCTCA TGAAGAAGGA TAAATACAG CTGCCCGGCG GGCTGCTGGC CCGCGCGGC 420  
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 ATGGACAGTT ACGGCGACAT GAACGGCTGG AGCAACGGCA GCTACAGCAT GATGCAGGAC 540  
 CAGCTGGGCT ACCCGCAGCA CCGCGGCTCT AATGCGCAG GCGCAGCGCA GATGCAGGCC 600  
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 45 ATGAACGGCT CGCCCACTA CAGCATGTCC TACTCGCAGC AGGGACCCCC TGGCATGGCT 720  
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 TCTTCTCTCC ACTCCAGGGC GCGCTGCCAG GCGGGGACC TCGGGACAT GATCAGCATG 840  
 TATCTCCCCG GCGCGAGGT GCGCGAACCC GCGCGCCCCA GCAGACTTCA CATGTCCCAG 900  
 CACTACAGA CGGCGCGCGT GCGCGCAAG GCGCATTACG GCACACTGCC CCTCTCAC 960  
 50 ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAGAAAAA ACGAGGGAAA 1020  
 TGGGAGGGGT GCAAAAGAGG AGAGTAAGAA ACAGCATGGA GAAACCCGG TACGCTCAAA 1080  
 AAAAA

Seq ID NO: 314 Protein sequence  
 Protein Accession #: CAA83435

1 11 21 31 41 51  
 55 HSARMYNMME TELKPPGPQQ TSGGGGNGST AAAAGGNQKN SPDRVKRPMN AFMVWSRGQR 60  
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 60 KTLMKDKYT LPGGLLAPGG NSMAGSVGVG AGLGAGVNR MDSTAHMNGW SNGSYSMQD 180  
 QLGYPQHPGL NAHGAAMQMP MERYDVSAIQ YNSMTSSQTY MNGSPTYSMS YSQGTPGMA 240  
 LSGMSGVVK SASSSPFVVT SSSHSRAPCQ AGDLRDMISM YLPGAIEVPEP AAPSRLEMSQ 300  
 HYQSGFVPGT AINGTLPLSH M

Seq ID NO: 315 DNA sequence  
 Nucleic Acid Accession #: U91618  
 Coding sequence: 29..541

1 11 21 31 41 51  
 70 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAATCC AGCTTGTATG 60  
 CATGTACTCT CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTCAAGAG AGGAAATGAA 120  
 AGCATTAGAA CGAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180  
 75 TCCTCTTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240  
 AGCTGAGGAA ACAGGAGAGT TTCAATGAAG GGAGCTTGTG GCAAGAAGGA AACTTCTTAC 300  
 TGCTTTAGAT GCGCTTAGCT TGAAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360  
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420  
 TGACAAAAAT GGAAGAGGAG AAGTCATAAA GAGAAAAATT CCTATATTC TGAACCGGCA 480  
 80 GCTGTATGAG AATAAACCCA GAAGACCTTA CATACTCAA AGAGATTCTT ACTATTACTG 540  
 AGAGAAATAA TCATTTATTT ACATGTGATT GTGATTATC ATCCCTTAAT TAAATATCAA 600  
 ATTATATTG TGTGAAAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT 660  
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TTTTTCATA TAAATCTAAA 720  
 TCTTCAAAAA AAAAAAAAAA AATGGGGGCC GCAATT

Seq ID NO: 316 Protein sequence  
Protein Accession #: AAB50564

5 1 11 21 31 41 51  
MMAGMKIQLV CMILLAPSSW SLCSDESEEM KALEADPLTN MHTSKISKAH VPSWKMTLLN 60  
VCSLVNMLNS PAETGEVHE EELVARRKLP TALDGFSLA MLTIYQLHKE CHSRAPQHWB 120  
LIQEDILDTG NDNKGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSEYY

10 Seq ID NO: 317 DNA sequence  
Nucleic Acid Accession #: NM\_006536.2  
Coding sequence: 109..2940

15 1 11 21 31 41 51  
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AGCATTGCAG GTCTTATTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180  
GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240  
20 ATTGCAATTA ATCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAACAT TAAGSAAATG 300  
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ATAAAGATT TAATACCTGC CACTGGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420  
TCATATGAAA AGGCAAAAGT CATACTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480  
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25 TTCTACTGA ATGATACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCAT 600  
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ATAAATGGGC AAAATCAAA TAAAGTGACA AGGTGTTTCT CTGACATCAC AGGCATTTT 720  
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30 AGTTTATCTT CTGTGGTTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCACAA 900  
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35 GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTTGAA 1140  
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40 AAACCTGAATG AAGAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAAGCG AGATGATAAG 1380  
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45 AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680  
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50 TATGCCAATG TGAACAGGGG ATTTTATCCC ATTTCTAATG CCACGTGCAC TGCCACAGTT 2040  
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CCAGGGAGTC ATGCTATGTA TGTACCAAGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280  
55 GCTCCAGGAA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340  
AGCTCAGGAG GCTCTTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACACC TGATGTGTT 2400  
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CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820  
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65 CATACTTTAA CAGAGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATA 2940  
ATAAATATCC AAGTGTCTT CCTCTTAGA TATAAGACC ATGGCCTTCG ACTACAAAA 3000  
CATACTAACA AAGTCAATT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTACA 3060  
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70 GCAGAGGGAA GGGTAAAGTC GACCCAGTGT CAAGGAAAGT TTGTTTATT GAGGTGGAAA 3240  
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TCATTAGTT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGCACTAC AGGTGCTTG 3360  
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75 TTCTACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540  
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TACCTAGGAA A

Seq ID NO: 318 Protein sequence  
Protein Accession #: NP\_006527.1

1 11 21 31 41 51  
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 GDDPYTLQYR GCGKEKYIH FTFNPLNDN LTAGYGSRRG VVHEWAHLR WGVFDEYNND 180  
 KPPYINGQNK IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKBGCTFIY NSTQMATASI 240  
 5 MFMSLSLSVV EFCNASTHQN EAPNLQNMCM SLRSANDVIT DSADFHSFP MNGTELPPPP 300  
 TFSLVQAGDK VVCLVLDVSS KMAEADRLQ IQQAARFYLQ QIVEIRTFVG IASFDSKGEI 360  
 RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSLGKKG EVVEKLGKA YGSVMILVTS 420  
 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLL GGLKFFVPDI SNSNSMIDAF 480  
 SRISSGTGD I FQHQIQLST GENVKPHQL KNTVTVDNTV GNDTMFLVTM QASGPPEIIL 540  
 FDPDGRKYIT NNFITNLTFR TASLWIPGTA KPGHWYITLN NTHSLQALK VVTTSRASNS 600  
 10 AVFPATVEAF VERDSLHFPF VMIIYANVQ GFYPILNATV TATVEPETGD PVTLRLLDDG 660  
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 15 LILKGLTAM GLIGIILII VVTHHTLSRK KRADKENGNT KLL

Seq ID NO: 319 DNA sequence  
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 Coding sequence: 82..3600

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 25 CTCTCTCATG CCCAACAGC CTGCTCCGT GGGGCTGCT ATCCACCTGT TGGGGACCTG 180  
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 TGGTGGCACT CCCAGATGA TGTGAACCTT GTCTCTCTGC AGCTGGAOCT GGACAGGAGA 420  
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 35 ATCAAACT TGAGAGTCAA TTTCACAGG CTGGCCCTGT TGCCCAAG GGGCTACAC 780  
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 40 CAAAGGTGCG ACTGCAATGG GCACTCAGAG ACATGTCACT TTGACCCCGC TGTGTTTGGC 1080  
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 45 CCAGTGACCG GGCAGTGTGT GTGCAAGGAG CATGTGCAGG GAGAGCGCTG TGACCTATGC 1320  
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 50 CAACCAAGTC ACAGGGCAGT GCGCTGTGCG GAAGGCTTTG GTGGCTGAT GTGCAGCGCT 1620  
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 Protein Accession #: NP\_000219.1

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 HYPRNRPPGA SIQETCISCE CDPDQAVPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL 420  
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Protein Accession #: NP\_001935.1

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DKDGEGLSTQ CECNIKVKDV NDNFPMFRDS QYSARIBENI LSSELLRFQV TDLDEEYTDN 300
WLAVYFPTSG NEGNWFEIQT DPRINNEGILK VVKALDYEQL QSVKLSIAVK NKAEPHQSVI 360
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Protein Accession #: NP\_077741.1

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 TGAAGCCTGG AGGAGGTACT TCTGGTGCC TCCTTGGGGG ACTGCTTGA AAAGTGAAGT 360  
 CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420  
 AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCAACATC CCTCTGGCA 480  
 50 TAAAGCTCCA AGTGAATACG CCCTGGTGG GTGCAAGTCT GTTGAAGGCTG CTTGTGAAGC 540  
 TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600  
 TTGGTGACTG CACCCATTC CCTGGAAGCC TGCAAAATTC TCTGCTTGAT GGACTTGGCC 660  
 CCTCCCTCCG TCAAGGTCTT CTGGACAGCC TCACAGGGAT CTTGAATAAA GCTCTGCTG 720  
 AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA 780  
 CCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTGTG ATCAAGGTCT 840  
 55 AAGCCTTCCA GGAAGGGGCT GGCTCTGCT GAGCTGCTC CCAGTGCTCA CAGATGGCTG 900  
 GCCCATGTGC TGAAGATGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCTCTCTCT 960  
 TCCACCAAGG CGTGTGTAA ATCCATGTG CCTCACCTAA TAAATGGCT CTTCTCTGCT 1020  
 AAAAAAAAA AAAAAAAAA AAAAAAAAA

60 Seq ID NO: 330 Protein sequence  
 Protein Accession #: NP\_057667.1

65 1 11 21 31 41 51  
 MFQTGGLIVP YGLLAQTMQA FGGLFVPLDQ TLPLAVNPAL FLSPTGLAGS LTNALSNGLL 60  
 SGGLLGILEN LPLLDLKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120  
 VQSPDGHRLY VTPLGIKLG VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC 180  
 THSPGLQTS LLDGLGPLPI QGLDLSLTGI LNKVLPVLVQ GNVCPVNEV LRGLDITLVH 240  
 DIVNMLIHGL QFVIKV

75 Seq ID NO: 331 DNA sequence  
 Nucleic Acid Accession #: NM\_004363.1  
 Coding sequence: 115..2223

80 1 11 21 31 41 51  
 CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60  
 TCCTGGAACT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120  
 TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCTGGC AGAGGCTCCT GCTCAGACC 180  
 TCACCTCTAA CCTTCTGGA CCOCGCCACC ACTGCCAAGC TCACTATTGA ATCCAGCCG 240  
 TTCATGTTC CAGAGGGGAA GGAGGTGCTT CTACTGTGCC ACAATCTGCC CCAGCATCTT 300  
 TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAT TATAGGATAT 360  
 GTAATAGGAA CTCACCAAGC TACCCAGGG CCGCATACA GTGGTGGAGA GATAATATAC 420  
 CCCAATGCAT CCTGTCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCTTA 480

CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCG 540  
 GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600  
 GTGGGCTTCA CCTGTGAACC TGAGACTCAG GCGCAACT ACCTGTGGTG GGTAAACAAT 660  
 CAGAGCCTCC CGGTCACTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720  
 5 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAAT 780  
 GCCAGGCGCA GTGATTCAGT CATCTGTAAT GTCTCTATG GCCCGGATGC CCCCACCAAT 840  
 TCCCTCTTAA ACACATCTTA CAGATCAGGG GAAATCTGA ACCTCTCCTG CCAAGCAGCC 900  
 TCTAACCCAC CTGCACAGTA CTCTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960  
 10 GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020  
 AACTCAGACA CTGGCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080  
 CCAAAACCCCT TCATCACCAG CAACAACCTC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140  
 TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200  
 CTCCCGTCA GTCCAGGCT GCAGCTGTCC AATGACAACA GGACCTCAC TCTACTCAGT 1260  
 15 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAAGCAATT AAGTGTGAC 1320  
 CACAGCGACC CAGTCATCCT GAATGTCCTC TATGGCCAG AGACCCAC CATTTCCCCC 1380  
 TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCGTCCATGC AGCCTCTAAC 1440  
 CCACTGCAC AGTATTCTTG GCTGATTGAT GGGAAACATCC AGCAACACAC ACAAGAGCTC 1500  
 TTTATCTCCA ACATCACTGA GAAGAACAGC GGAATCTATA CCGTCCAGGC CAATAACTCA 1560  
 20 GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCAGAG TCTCTGGGGA GCTGCCCAAG 1620  
 CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680  
 TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740  
 GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCATCTATT CAATGTACA 1800  
 AGAAATGAGC CAAGAGCCTA TGTATGTGGA ATCCAGAATC CAGTGAATGC AAACCGCAGT 1860  
 25 GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAG 1920  
 TCGTCTTACC TTTGGGAGC GAACTCAAC CTCTCTGCC ACTCGGCTC TAACCCATCC 1980  
 CCGCAGTATT CTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTATC 2040  
 GCCAAATCA CGCCAAATAA TAACGGGACC TATGCTGTG TGTCTCTAA CTGGCTACT 2100  
 GGCAGCAATA ATTCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGGT 2160  
 30 CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTGGGGT TGCTCTGATA 2220  
 TAGCAGCCCT GTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTGTGTTT GCTTCTCTC 2280  
 TAAAGCATTT GCAACAGCTA CAGTCTAAA TTGCTTCTT ACCAAGGATA TTACAGAAA 2340  
 AGACTCTGAC CAGAGATCGA GACCATCTTA GCCAACATCG TGAACCCCA TCTCTACTAA 2400  
 AAATCAAAA ATGAGCTGGG CTGGTGGCG OGCACTCTTA GTCCAGTTA CTGGGAGGC 2460  
 35 TGAGGCAGGA GAATCGCTTG AACCGGGAG GTGGAGATTG CAGTGAAGCC AGATCGCAC 2520  
 ACTGCATCC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAAG 2580  
 TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCATG CACTGTCTGA GAATTTCCAA 2640  
 AACTTTAATG AACTAATCTA CAGCTTCATG AAATGTCCA CCAAGATCAA GCAGAGAAAA 2700  
 TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCTTTA AATGTCTTGT 2760  
 40 TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTACAG CAATTTGATA 2820  
 AAATATACT TGTGAACAA AAATGAGAC ATTACATTT TCTCCCTATG TGGTCTCTCC 2880  
 AGACTTGGGA AACTATTCAT GAATATTTAT ATTGTATGTT AATATAGTTA TTGCACAAGT 2940  
 TCAATAAAAA TCTGCTCTT GTATAACAGA AAAA

Seq ID NO: 332 Protein sequence  
 Protein Accession #: NP\_004354.1

1 11 21 31 41 51  
 MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVRNLPO 60  
 50 HLFYGSWYKQ ERVDGNRII GYVIGTQAT PGPAYSGREI IYPNASLLIQ NIIQNDTFY 120  
 TLHVKSLLV NBEATGQPRV YPELPKPSIS SNNSKPVEDK DAVAFTECEP TQDATYLVWV 180  
 NNQSLFVSPR LQLSNGNRTL TLFNVTRNDT ASYKCEQNP VSARRSDSVI LNVLYGPDAP 240  
 TISPLNTSYR SGNLNLSCA AASNPPAQYS WFNVTFOQS TQELFIPNIT VNNSGYSYTO 300  
 55 AHNSTGLNR TTVTTITVYA EPPKPPITSN NSNPVEDEDA VALTCEPEIQ NITYLVWVWN 360  
 QSLFVSPRLQ LENDNRLTL LSVTRNDVGF YEOIQNELS VDHSDFVILN VLYGPDPTI 420  
 SPSYTYRPG VNLSLSCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTOQAN 480  
 NSAGHSRTT VKTITVSAEL KPSPISNSNS KPVEDKDAVA FTCEPEAQNT TYLVWVNGQS 540  
 LPVSPRLQLS NGNRTLTLEN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPIISP 600  
 60 PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQHTQVL FIAKITPMNN GTYACFVSNL 660  
 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

Seq ID NO: 333 DNA sequence  
 Nucleic Acid Accession #: NM\_006952.1  
 Coding sequence: 11..793

1 11 21 31 41 51  
 AATCCGACA ATGGCGAAG ACAACTCAAC TGTTCGTGTC TTCCAGGGCC TGCTGATTTT 60  
 70 TGGAAATGTG ATTATTGGTT GTTGGCGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTGT 120  
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACACAGATG ACATCTATGG 180  
 GCGTGCCTGG ATCGGCATAT TTGTGGCAT CTGCCTCTTC TGCCGTCTCTG TTCTAGGCAT 240  
 TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT 300  
 AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360  
 75 ACCCAACCTC TTCTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAAACAA 420  
 TGATGACCAAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480  
 CAATTGCTGT GCGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCGGGAC 540  
 TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600  
 AGAACCTCTC AACCTGGAGG CTGTGAACT AGGCGTGCTT GGTTTTATC ACAATCAGGG 660  
 80 CTGCTATGAA CTGATCTCTG GTCCAAATGAA CCGACAACCC TGGGGGGTTG CTTGGTTGG 720  
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 AATTGAATAT TAAGAA

Seq ID NO: 334 Protein sequence  
 Protein Accession #: NP\_008883.1

1 11 21 31 41 51  
 5 MAKDNSTVRC FQGLLIIFGNV IIGCCGIALT AECIPFVSDQ HSLVPLEAT DNDDIYGAAW 60  
 IGIFVGLICLF CLSVLIGIVGI MKSSRKILLA YFILMFIVYA PEVASCITAA TQRDFPTPNL 120  
 FLKQMLERYQ NNSPPNDDQ WKNGVTKTW DRLMLQDNCC GVNGPSDNQK YTSAPRTENN 180  
 DADYPWPQRQ CVMNNLKEPL NLEACKLGVP GFYHNGCYE LISGPMNRHA WGVAVFGFAI 240  
 LCWTFWVLLG TPFYWSRIEY

10 Seq ID NO: 335 DNA sequence  
 Nucleic Acid Accession #: NM\_002638.1  
 Coding sequence: 120..473

1 11 21 31 41 51  
 15 CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CGCCCTGGA GCCAGGCCAA 60  
 GCTGCAGCC ATAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120  
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGAGC CTGGTTCTAG 180  
 AGCGAGCTGT CACGGGAGTT CCTGTTAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240  
 20 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAAGTAA AGGTCAAGAT AAAGTCAAAG 300  
 CGCAAGAGCC AGTCAAAGGT CCACTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360  
 TCCGTTGCCG CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCAGGAA 420  
 TCAAGAAAGTG CTGTGAAGGC TCTTGGCGGA TGGCCTGTTT CGTTCGCCAG TGAAGGGAGC 480  
 CGGTCTCTGC TGCACTCTGC CCGTCCCGAG AGCTACAGGC CCATCTGCTT CCTAAGTCCC 540  
 25 TGGTGGCCTT CCGCTTCCCA CACTGTCCAT TCTTCTCTCC ATTCAAGATG CCCACGGCTG 600  
 GAGCTGCCCT TCTCATCCAC TTTCATAATA

Seq ID NO: 336 Protein sequence  
 Protein Accession #: NP\_002629.1

1 11 21 31 41 51  
 30 MRASSFLIVV VFLIAGTLVL EAAVTGVPEVK GQDTVKGRVP FNGQDPVKQ VSVKGQDKVK 60  
 35 AQEFVKGFSV TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCEGSCG MACFVFPQ

Seq ID NO: 337 DNA sequence  
 Nucleic Acid Accession #: NM\_001793.2  
 Coding sequence: 71..2560

40 1 11 21 31 41 51  
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGCCCGTGGC GGCAGCTGCT TCACCCCTCT 60  
 CTCTGCAGCG ATGGGGCTCC CTGGTGGACC TCTCGCGTCT CTCTCCTTC TCCAGGTTTG 120  
 45 CTGGCTGCGA TGCGCGGCGT CCGAGCCGCT CGGGCGGCTC TTCAGGGAGG CTGAAGTGAC 180  
 CTTGAGGCGG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTATGGG 240  
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGGCGAA 300  
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360  
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420  
 50 TGAAATATGGC AAGGTCCTT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480  
 AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACAGCCCCC CTGAGGGTGT 540  
 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600  
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660  
 CCGCATGAC ATCTCCATCA TGTGACCGA CCAGATGAC CACAAGCCCA AGTTTACCCA 720  
 55 GGACACCTTC CGAGGAGTG TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAGGT 780  
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAT GGGGTGGTTG CTTACTCCAT 840  
 CCATAGCCAA GAACCAAGG ACCCAACGGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900  
 CACCATCAGC GTCACTCTCA GTGGCCTGGA CGGGGAAAAA GTCCCTGAGT ACACACTGAC 960  
 CATCCAGGCC ACAGACATGG ATGGGAGCGG CTCCACCACC ACGGCAGTGG CAGTAGTGA 1020  
 60 GATCCTTGAT GCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080  
 GCGTGAAGAT GCAATGGGCC ATGAGGTGCA GAGGCTGACG GTCAGTGATC TGGACGCCCC 1140  
 CACTCACCA GGTGGCGTGG CCACCTACCT TATCATGGGC GGTGAAGACG GGGACCATTT 1200  
 TACCATCACC ACCCACTCTG AGAGCAACCA GGGCATCCTG ACAACCCAGG AGGGTTTGGA 1260  
 TTTTGAGGCC AAAAACCCAG ACACCCCTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320  
 65 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380  
 ACCTGTGTTT GTCCCACTCT CCAAGTCTGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440  
 GCGTGTGTTT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGTACCG 1500  
 CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560  
 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACCAACTCT ATGAAGTCAT 1620  
 70 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCCTGGC ACGGGAACCC TTCTGCTAAC 1680  
 ACTGATTGAT GTCAATGACC ATGGCCCACT CCGTGAAGCC CGTCAGATCA CCATCTGCAA 1740  
 CCAAGCCCT GTGGCCAGGG TGCTGAACAT CAAGGACAAG GACCTGTCTC CCCACCTC 1800  
 CCCTTTCCAG GCGGAGCTCA CAGATGACTC AGACATCTAC TGAAGCGCAG AGGTCAACGA 1860  
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920  
 75 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980  
 GTGCGCACTG CATGGCCATG TCGAAACCTG CCGTGGACCC TGGAAAGGAG GTTTCATCCT 2040  
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGTGCTGCT TTTTGTGGT 2100  
 GAGAAGAGAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGGTGACAA 2160  
 CGTCTTCTAC TATGTGGGAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220  
 GCTCCACCGA GGTCTGGAGG CCGGGCCGGA GGTGTTCTCT CGCAATGACG TGGCACCAAC 2280  
 80 CATCATCCCG ACACCATATG ACGTCTCTG GCCAGCCAAC CCAGATGAAA TCGCAACTT 2340  
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCGCCCT ACGACACCT 2400  
 CTTGGTGTTC GACTATGAGG CGAGCGCGCG TCCCTGAGCT CCTCACCTC 2460  
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGGCTTCAA 2520  
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGAAGACTAG GCGGCTGCC TGCAGGGCTG 2580

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GGGACCAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640  
GACTTCGGAG CTGTGCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700  
ACGTAGAGT GGTGCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760  
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCCTCAG AGGCCAAGTT TCCAGAAGCC 2820  
TCTTACCTGC CGTAAATGC TCAACCTGT GTCTGGGCC TGGCCCTGCT GTGACTGACC 2880  
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940  
TTTTTTAAT GCTATCTCA AACGTTAGA GAAAGTCTT CAAAAGTGCA GCCCAGAGCT 3000  
GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTTCAGAC CCCAATGCC CTCCATTCCGA 3060  
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGGC CCTTATTTT TATTTTCCCT 3120  
GTGCGTTCG TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180  
TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 338 Protein sequence  
Protein Accession #: NP\_001784.2

1 11 21 31 41 51  
MGLPRGPLAS LLLQLVCNLQ CAASEPCRAV FREAETVLEA GGAEQEPGQA LGKVFMCPCG 60  
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120  
KGFFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLILN KPLDREBIAX 180  
YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTP RGSVLEGVLP GTSVMQVTAT 240  
DEDDAIITYN GUVAYSIEHQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
TMDGDGSGTT TAVAVVEILD ANDNAPMFDK QRYEAHVPEV AVGHEVQRLT VTDLDAPNSP 360  
AWRATYLMG GDDGDHFTIT THPESNOGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ ESIPTGEFVC VYTAEDPDKE NQKISYRILR 480  
DPAGWLMAMP DSGQVTAUGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540  
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNNEGD 600  
TVVLSLKKFL LVLLLVLRKK RKIKEPLLLP EDDTRDNVFI YGEEGGGED QDYDITQLHR 660  
GAVLALLFL LVLLLVLRKK RKIKEPLLLP EDDTRDNVFI YGEEGGGED QDYDITQLHR 720  
30 GLEARPEVVL RNDVAPTII TPMYRBRPAN PDEIGNPIIE NLKAANTDPT APPYDTLLVF 780  
DYEAGSDDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 339 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..672

1 11 21 31 41 51  
ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GCGCGCGGCC CCGGGGCGGG 60  
CGGGGCTCCC CCTACCGGCC AGACCCCGGG AGAGGCGCGC GGAGGCTCGG AAGGTTCCAG 120  
AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180  
CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGAGCG CAACCTGACT 240  
GCGAGACAAC GAGATCCAGA GGACTCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG 300  
TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAAATG 360  
ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CAGGTTTTTT CATGGTTGCG 420  
AAGCAGTGCT CGCTGTGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480  
CTCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAGTGTGT GTAAAATTCC CTACTGCAAT 540  
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAGAAT ATGCTGGGAG CATGGGTGAG 600  
AGCTGTGGTG GCGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGCGCTC 660  
50 AGCCTGTCTT GA

Seq ID NO: 340 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
MRLQRPRQAP AGRRRAPRGG RGSFYRPDPG RGARRLRFRQ KGEGAPRAD PPWAPLGTTA 60  
LLALLLVVAL PRVWDANLT ARQRPEDSQ RTDEGDNRVW CHVCRENTF ECQNPRCKW 120  
TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEKRF LLEPPMPFFY LKCKKIRYCN 180  
60 LBGPPINSSV FKEYAGSMGE SCGLWLAIL LLLASTAAGL SLS

Seq ID NO: 341 DNA sequence  
Nucleic Acid Accession #: XM\_035292.2  
Coding sequence: 53..1576

1 11 21 31 41 51  
GCTGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60  
TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCGGCGCGCC GAGGAGAAGG AAGAGGCGCG 120  
GGAGAAGATG CTGGCGCGCA AGAGCGCGGA CGCTCGCGCG CCGGAGGCGG AGGGCGAGGG 180  
CGTGACCCCTG CAGCGGAACA TCAAGCTGCT CAACGGCGTG GCCATCATG TGGGGACCAT 240  
TATCGGCTCG GCATCTCTG TGAAGCCAC GGGCGTGCTC AAGGAGGCGG GCTCGCGCGG 300  
GCTGCGCTCG GCGGTGTGGG CCGGTGCGG CGTCTTCTCC ATCGTGGCGG CGCTCTGCTA 360  
CGCGAGCTC GGCACACCA TCTCCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420  
CTACGCTCG CTGCGCGCTT TCCTCAAGCT CTGATCGAG CTGCTCATCA TCGCGCCTTC 480  
ATCGCAGTAT ATCGTGGCCC TGGTCTTGG CACCTAAGCT CTCAGCGGC TCTTCCCGAC 540  
CTGCGCGGTG CCGGAGGAGG CAGCCAGGCT CGTGGCTGCG CTCTGGTGG TGCTGCTCAC 600  
GGCGGTGAAC TGCTACAGCG TGAAGGCGCG CACCGGGTCC CAGGATGCCT TTGCGCGCGG 660  
CAAGCTCTCG GCGCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720  
70 TGTGTCCAAT CTAGATCCCA ACTTCTCAT TGAAGGCACC AAACCTGGATG TGGGGAAACAT 780  
TGTGCTGGCA TTATACAGCG GCCTCTTGG CTATGAGGGA TGAATTACT TGAATTGGT 840  
CAGAGAGGAA ATGATCAACC CCTACAGAAA CCGTCCCGTG GCCATCATCA TCTCCCTGCC 900  
CATCGTAGCG CTGGTGTAGG TGTGACCAA CCGTGGCTAC TTCAACACC TGTCACCGA 960  
80 GCAGATGCTG TGTGCCGAGG CCGTGGCGGT GCACTTCGGG AACTATCAC TGGGCGTCAT 1020

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GTCCTGGATC ATCCCGGTCT TCGTGGGCTT GTCCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTACATACC TCAGAGCTCT TCTTGGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCAACCC CGTGCCGTCC CTGCTGTTC CCGTGTGTGAT 1200
GAGCTGCTCT TACGCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TGGTGGCCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTCTCA TCCTGGCCCTG 1380
CCTCTTCCCTG ATCGCCGTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGTGGT 1560
CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

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Seq ID NO: 342 Protein sequence  
Protein Accession #: XP\_035292.2

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1 11 21 31 41 51
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
GTIIGSGIVF TPTGVLEKAG SPGLALVWVA ACGVFSIVGA LCVABLGTTI SKSGGDYAYM 120
LEVYGSPLPAP LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPPEEA AKLVACLCLVL 180
LLTAVNCYSV RAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSPBGTKLNV 240
GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
STEQMLSSSA VAVDFGNYHL GVMWNIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
SILSMIHPQL LTFVPSLVFT CVMTLLYAPS KDIPSVINFP SFENWLCLVAL AIIGMINLRH 420
RKPFLERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GPTIILSGLP VYFFGVWWRN 480
KPKWLLQGIIF STTVLQQLM QVVPQET

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Seq ID NO: 343 DNA sequence  
Nucleic Acid Accession #: NM\_005268.1  
Coding sequence: 168..989

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1 11 21 31 41 51
TAAAGAGCAA AAGAAATGCG GGCCGCGCTG ACAOGGCTT CCCCAGAAAC CTTCCCCGCT 60
TCTGGATATG AAATTCAGAC TGCTTGCTGA GTCTTATGCG CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGAOCGCTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGTCTCTGGT CTTTCATCTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTGCGCAGCC CGGCTGCTCC AACGCTCTGT 360
TGTATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCTGTGTGA 420
CATGCCCTCT ACTGCTCGTG GTCATGCACG TGGCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GCGAGCGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAAGTGCC 660
ACGCAGATCT ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAAAC 720
TTTTCACCTT CTTTCATGGT GCCACAGCTG CCATCTGCAT CCGCTCAAC CTGCTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCCTGG AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCACCCC CAOGGTACCA CCTCTTCTCG CAAACAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCC TCTCTTACCA GACCCGCCCC 960
GAGACCATGT GAAGAAACC ATCTGTGTAG GGGCTGCTG GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGAGGCTC TGGGAGCCAG TTCTAGTACC 1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCATCTGGCC AGTTCGCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

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55  
Seq ID NO: 344 Protein sequence  
Protein Accession #: NP\_005259.1

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65

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1 11 21 31 41 51
MNWSIFEGLL SGVNYSTAF GRWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QKRHRREAHG ENSGRLYLNP 120
KKRGRGLWWT YVCSLVFKAS VDLAFLYVPH SFYPKYILPP VVKCHADPCP NIVDCFIKSP 180
SEKNIFTLEM VATAAICILL NLVELIYLVK KRCHECLAAR KQAAMCTGHH PHGTTSSCKQ 240
DDLLSGDLIF LGSDSHPPILL PDRPRDHVKK TIL

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Seq ID NO: 345 DNA sequence  
Nucleic Acid Accession #: NM\_002391.1  
Coding sequence: 26..457

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1 11 21 31 41 51
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCAOCGAGGC TTCTCTCTCC TCACCTCCT 60
CGCCCTGCTG GCGCTCACTT CCGCGGTGCG CAAAAGAGAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGGCGCT AGTGGGCTGC GGGGCGCTGC ACCCCAGCA GCAAGGATTG 180
CGCGGTGGGT TTCCGCGAGG GCACCTGCGG GGCCAGAAC CAGCGCATCC GGTGCAAGGT 240
GCCTTGCAAC TGGAGAAGG AGTTTGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
TGGTGTGAT GGGGACACG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGGCC TGACCCCCA AGACCAAGC 420
AAAGGCCAAA GCAAGAGAA GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
GCCCTGTGTT TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
CACCAGTGCC TTCTGTCTGC TGGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
ACTCCCAGC CCCACCCCTA AGTGCCCAA GTGGGGAGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAGCAAT GTGAGTCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
ATTACTAAGA AACACATCAA ATAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780

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TAATAT

Seq ID NO: 346 Protein sequence  
Protein Accession #: NP\_002382.1

5  
10  
1 11 21 31 41 51  
| | | | |  
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEN AWGPCTPSSK DGVGFREGT 60  
CGAQTQRIRC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120  
RVTKPCTPKT KAKAKAKKKK GKD

Seq ID NO: 347 DNA sequence  
Nucleic Acid Accession #: NM\_006783.1  
Coding sequence: 1..786

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20  
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30  
1 11 21 31 41 51  
| | | | |  
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC 60  
GGGAAGGTGT GGATCAGAGT CATCTTTATT TCCGAGTCA TGATCCTAGT GGTGGCTGCC 120  
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180  
AAAAATGTGT GCTATGACCA CTTTTCCTCG GTGTCCACCA TCCGGCTGTG GGGCTCCAG 240  
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300  
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360  
ATTAAGAAAG ACAAGGTTTC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420  
TTTTTCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCTT TTACRAATGGG 480  
TACCACCTGC CCTGGGTGTT GAAATGTGGG ATGACCCCTT GCCCAACCTT TGTGACTGTC 540  
TTTATTTCTA GGCACACAGA GAAGACCGTG TTTACCATT TTTATGATTTC TGCCTCTGTG 600  
ATTTGCATGC TGCTTAAAGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTITAGG 660  
AGATCAAGAA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720  
CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGSTTTCCCA 780  
AGCTAA

Seq ID NO: 348 Protein sequence  
Protein Accession #: NP\_006774.1

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40  
1 11 21 31 41 51  
| | | | |  
MDWGTLLHTPI GGVNKHSTSI GKVVITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60  
KNVCYDHPFP VSHRLWALQ LIFVSTPALL VAMHVAYYRH ETRKFRRGE KRNDFKDIED 120  
IKKKKVRIEG SLWWTYSSSI FFRIFEAAR MVVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180  
FISRPTKTV FTIFMISASV ICMILLNVAEL CYLLLVKCFR RSKRAQTQKN HPNHALKESK 240  
QNEWELISD SQNAITGFP S

Seq ID NO: 349 DNA sequence  
Nucleic Acid Accession #: NM\_002571.1  
Coding sequence: 99..587

50  
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1 11 21 31 41 51  
| | | | |  
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCCTCTGC 60  
TCACCTCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120  
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCCTCT CATGGCCATG GOGACCAACA 180  
ACATCTCTCT CATGCGGACA CTGAAGGCCCT CTCTGAGGGT CCACATCACC TCACCTGTTC 240  
CCACCCCGGA GGACCAACCTG GAGATCGTTC TGACAGATG GGAGAAACAC AGCTGTGTTC 300  
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360  
TGGCGAAGCA GGCCACGCTG CTGGATCTG ACTACGACAA TTTCTGTITT CTCTGCCTAC 420  
AGGACACACC CACCCCTATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTGTGTTC 480  
AGGACATGTA GATCTGCAG GGAATTCATCA GGGCTTTTCA GCCCTGCCCC AGGCACCTAT 540  
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCGGTGCCG TTTCTAGCTC ACCTCCGCTT 600  
CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCC 660  
TTTCAAGAA TAACCAAGC TCAGAAGAGC ATGAAGTGGT CATCTGTGTC GCCATCCCTT 720  
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780  
GCAAGAGTTA TTAATAAACC CTTGGAGCAT G

Seq ID NO: 350 Protein sequence  
Protein Accession #: NP\_002562.1

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1 11 21 31 41 51  
| | | | |  
MDIPQTKQDL ELPLAGTWE SMAMATNNIS LMATLKAPLR VHITSLPPT EDNLEIVLHR 60  
WENNSCVENK VLGERKTGNFK KFKINYTVAN EATLLDIDYD NFLFLCLQDT TPIQSMMDQ 120  
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMBEPC RF

Seq ID NO: 351 DNA sequence  
Nucleic Acid Accession #: NM\_006500.1  
Coding sequence: 27..1967

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1 11 21 31 41 51  
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ACTTGGTCT CGCCCTCCGG CCAAGCATGG GGCTTCCAG GCTGGTCTGC GCCTTCTTGC 60  
TCGCGGCTG CTGCTGCTGT CCGGCTGCTG CCGGAGAGGT GAGCAGCCTG 120  
CGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180  
AGTCCCAAG CAACCTCAGC CATGTGACT GTTTTCTGT CCACAAGAG AAGCGGAGCG 240  
TCATCTTCCG TGTCCGCCAG GCCCAGGCC AGAGGGAACC TGGGAGTAC GAGCAGCGGC 300

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TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCTGACTCA AGTCACCCC CAAGACGAGC 360  
GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG 420  
TCTACAAAGC TCCGGAGGAG CCAAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480  
GTAAGGAGCC TGAGGAGGTG GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCTCAAG 540  
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAAT 600  
CGTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGSCACAGC 660  
TGGTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAATACCCG CTGCCCAGTG 720  
GGAACCATAT GAAGGAGTCC AGGGAAGTCA CGTCCCTGT TTTCTACCCG ACAGAAAAAG 780  
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840  
GTTTGGCTGA TGGCAACCTT CCAACACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900  
GGGAGGCGAG GGAAGAGACA ACCAACGACA ACGGGGTCTT GGTGCTGGAG CCTGCCCGGA 960  
AGGAACACAG TGGGGCTAT GAATGTGAGG CCTGGAACTT GGACACCATG ATATCGCTGC 1020  
TGAGTGAACC ACAGGAACATA CTGGTGAAT ATGTGTCTGA CGTCCGAGTG AGTCCGCGAG 1080  
CCCTTGAGAG ACAGGAAGGC AGCAGCCTCA CCTGACCTG TGAGGAGAG AGTAGCCAGG 1140  
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAGG GGGCCTGTGC 1200  
TTCACTTGCA TGACCTGAAA CGGGAGGCAG GAGGCGGCTA TGGTCTGCTG GCGTCTGTGC 1260  
CCAGCATACC CGGCTGAAAC CGCACACAGC TGGTCAAGCT GGCCATTTTT GGCCCCCTT 1320  
GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAGAGAAA TATGGTGTG AATCTGTCTT 1380  
GTGAAGCGTC AGGGCACCCC CGGCCACCA TCTCTGGAA CGTCAACGCG ACGCAAGTG 1440  
AACAAAGACA AGATCCACAG CGAGTCTGA GCACCTGAA TGTCTCTG ACCCGGAGC 1500  
TGTGGAGAG AGGTGTGAA TGCAAGGCTT CCAACGACCT GGGCAAAAC ACCAGCATCC 1560  
TCTTCTGGA GCTGGTCAAT TTAACCAACC TCACACCAGA CTCACACACA ACCACTGGCC 1620  
TCAGCACTTC CACTGCCAGT CCTCATACCA GAGCCAACAG CACCTCCACA GAGAGAAAGC 1680  
TGCCGAGGCC GAGAGACCGG GGGGTGGTCA TCGTGGCTGT GATTGTGTGC ATCTGTGTCC 1740  
TGGCGGTGCT GGGCGCTGTC CTCTATTTC TCTATAAGAA GGGCAAGCTG CGGTGAGGC 1800  
GCTCAGGAGA GCAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAACTT GTAGTTGAAG 1860  
TTAAGTCAAG TAAGCTCCCA GAAGAGATGG GCCTCTGCA GGGCAGCAGC GGTGACAAAG 1920  
GGGCTCCGGG AGACCGAGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT 1980  
CAGCTCCCTT CCCTGCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG 2040  
CCTCCAAAGG GACTAGAGAG AAGCCTCCTG CTCGCCCTAC CTGCAACCC CTTTTCAGAG 2100  
GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTT TCAGGGACCA 2160  
GTCCACCACC ATCTCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCCAGTCTC 2220  
CCGAGCGGGT AGGAGAGTTT CTTCGAGAAC GTGTTTTTC TTTACACACA TTATGGCTGT 2280  
AAATACCTGG CTCTGCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTTCTGCCC 2340  
CAAAGAGTC AGGACAGGAC CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC 2400  
GCTGTCTCAT GTTGAAGTGC GCTGTTTACA CCGCTCCGG AGAGCACCCC AGCGGCATCC 2460  
AGAAGCAGCT GCAGTGTTC TCCCACCACC CTCTGCTCG CCTCTTCAA GTCTCTGTG 2520  
ACATTTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCTAT CCTTAAAGA TACGTGCCGG 2580  
GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCGGA GGGGGGGGA 2640  
TCACAAAGTC AGGACAGGAC CATCCTGGCT AACACGGTGA AACCTGTCT CTAATAAAA 2700  
TACAAAAAAA AATTAGCTAG GCGTAGTGT TGGCACCTAT AGTCCAGCT ACTCGGAAGG 2760  
CTGAAGCAGG AGAATGATAT GAATCCAGGA GGTGGAGCTT GCAGTGAGCC GAGACCGTGC 2820  
CAGTCACTC CAGCTCGGC AACACAGCGA GACTCCGCT CGAGGAAAAA AAAAGAAAAG 2880  
ACGCGTACCT GCGGTGAGGA AGCTGGGCGC TGTTTTCGAG TTCAGGTGAA TTAGCCTCAA 2940  
TCCCGTGTGT CACTGTCTCC CATAGCCCTC TTGATGGATC ACGTAAACT GAAAGGCGAGC 3000  
GGGAGCAGA CAAAGATGAG GTCTACACTG TCCTTCATGG GGATTAAGC TATGGTTATA 3060  
TTAGACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAGG CCCAAATGAG 3120  
AGAATGTAC TTAGGGATG AAAACGGGGC CTGGCTAGAG CTTGGGTGT GTGTGTCTGT 3180  
CTGTGTGAT GCATACATAT GTGTGATAT ATGGTTTTGT CAGGTGTGTA AATTGCAAA 3240  
TTGTTTCTT TATATATGTA TGTATATATA TATATGAAA TATATATATA TATGAAAAAT 3300  
AAAGCTTAT TGTCCAGAA AATCATACAT TGCTTTTTTA TTCTACATG GTACCAAGG 3360  
AACCCTGGGG CCTGTGAAA TACAACCAA AGGCACCAA AACCGTTCC AGTTGGCAGC 3420  
AGAGATCAGG GGTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG 3480  
CTACCTACT TTTAGCAGC AAAACGTCCC GTATGAAGCA GCACGAAGG CCTGGCAGGC 3540  
TGTAGCAGG AGCTATGTC CTTCCTATCG TTTCCTTCCA CTT

Seq ID NO: 352 Protein sequence  
Protein Accession #: NP\_006491.1

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1 11 21 31 41 51  
GLPRLVCAFL LAACCCCPRV AGVPGEABQP APELVEVEVG STALLKGLS QSQGNLSHVD 60  
WFSVHKEKRT LIFRVROGG QSEPGYEYQR LSLQDRGATL ALTQVTPQDE RIFLCQGRKP 120  
RSQYRIQLR VYKAPEEPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIPQ VIWYKNGRPL 180  
KEBRNRVHIQ SSQTVESSGL YTLQSLKQA LVKEDKDAQF YCELNYRLPS GNHMKESREV 240  
TVPVFPYTEK VMLEVEPVGM LKEGDRVEIR CLADGNPPPH FSISKQNPST REAEETIND 300  
NGVLVLEPAR KEHSGRYECQ AMNLDIMSL LSEPQELLVN YVSDVRVSPA APERQEGSSL 360  
TLTCEABSSQ DLBFQWLREE TDQVLERGFV LQLHDLKREA GGGYRCVASV PSIPGLNRTQ 420  
LVKLAIFGPP WMAFKERKVV VKENMVLNLS CEASGHPRT ISMNVNGTAS EQDQDPQRLV 480  
STLNVLVTFE LLETGVECTA SNDLGRNTSI LFLELVNLIT LTPDSNTTGT LSTSTASPH 540  
RANSTSTERK LPPEPESRGVV IVAVIVCILV LAVLGAVLYF LYKKGKLPGR RSGRQEITLP 600  
PSRKTELVEE VKSDKLPPEM GLLQGSSGDK RAPGDQGEKY IDLRH

Seq ID NO: 353 DNA sequence  
Nucleic Acid Accession #: NM\_003183.3  
Coding sequence: 165..2639

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1 11 21 31 41 51  
TCGAGCCTGG CGGTAGAATC TTCCCACTAG GCGGCGCGGG AGGAAAAAGA GGATTGAGGG 60  
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GSAAGGCTGC CCAGAGAGGT GGAGTCGGTA GCGGGCGCGG GAACATGAGG CAGTCTCTCC 180  
TATTCTGAC CAGCGTGGT CCTTTCGTGC TGGCGCGCGG ACCTCGGAT GACCGGGCT 240  
TCGCCCCCA CCAGAGACTC GAGAAGCTTG ATTCCTTGCT CTCAGACTAC GATATTCTCT 300



CTTTATCTAA TATCCAGCAG CATTCCGGTAA GAAAAAGAGA TCTACAGACT TCAACACATG 360  
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 GTACTGCAACG TTTTTCACAA AATTTCAAGG TCGTGGTGGT GGATGGTAAA AACGAAAGCG 480  
 AGTACACTGC AAAATGGCAG GACTTCTTCA CTGGACACGT GGTGGGTGAG CCGTACTCTA 540  
 5 GGGTCTAGC CCACATAAGA GATGATGATG TTATAATCAG AATCAACACA GATGGGGCCG 600  
 AATATAACAT AGAGCCACTT TGGAGATTG TTAATGATAC CAAAGACAAA AGAATGTTAG 660  
 TTTATAAATG TGAAGATATC AAGAATGTTT CACGTTTGCA GTCTCCAAAA GTGTGTGGTT 720  
 ATTTAAAAAT GGATAATGAA GAGTTGTCTCC CAAAAGGGTT AGTAGACAGA GAACCACTCG 780  
 AAGAGCTTGT TCATCGAGTG AAAAGAAGAG CTGACCCAGA TCCCATGAAG AACACGTGTA 840  
 10 AATTATTGGT GGTAGCAGAT CATCGCTTCT ACAGATACAT GGGCAGAGGG GAAGAGAGTA 900  
 CAACTACAAA TTACTTAATA GAGCTAATITG ACAGAGTTGA TGACATCTAT CGGAACACTT 960  
 CATGGGATAA TGCAGTTTTT AAAGGCTATG GAATACAGAT AGAGCAGATT CGCATTCTCA 1020  
 AGTCTCCACA AGAGGTAAAA CCTGGTGAAA AGCACTACAA CATGGCAAAA AGTTACCCAA 1080  
 15 ATGAAGAAAA GGATGCTTGG GATGTGAAGA TGTGCTAGA GCAATTTAGC TTTGATATAG 1140  
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 CAAAGGCTTA TTATAGCCCA GTTGGGAAGA AAAATATCTA TTTGAATAGT GGTGTGACGA 1320  
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 AATTGGGACA TAATTTTGA GCAGAACATG ATCCGATGG TCTAGCAGAA TGTGCCCGA 1440  
 20 ATGAGGACCA GGGAGGAAA TATGTATGT ATCCCATAGC TGTGAGTGGC GATCACGAGA 1500  
 ACAATAAGAT GTTTTCAAA TGCAGTAAAC AATCAATCTA TAAGACCAAT GAAAGTAAAG 1560  
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 25 GCACGTTGAA GGAAGSTGTC CAGTGCAGTG ACAGGAACAG TCCTTGTCTGT AAAAAGTGTG 1740  
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 30 ACCTTTCTGG CCGCTGTGTG CCCTATGTG ATGCTGAACA AAAGAAGTTA TTTTGTAGGA 2040  
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 35 CTCTGTTTCA CCCCAGTAAC GTCCGAATGC TGAGCAGCAT GGATTTCTGCA TCGGTTCCGA 2340  
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 CCAGCACAGA CTCCCATATG GACGAGGATG GGTTTGAGAA GGACCCCTTC CCAATAGCA 2520  
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 40 CTGCCTCCTT TAACTGCAAG CGTCAGAATC GTGTTAACAG CAAAGAAACA GAGTGCTAAT 2640  
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 45 TTGACCTGTG GTGCAGAAAG AGAAAAATACA GCTGGATTGG GTTATGAATA TTTACGTTTT 2940  
 TGTAAATTA TCTTTTATAT TGATAACAGC ACTGACTAGG GAAATGATCA GTTTTTTTTT 3000  
 ATACACTGTA ATGAACCGCT GAATATGAAG CATTGTGCAT TATTTGTGA GAAAGTGGGA 3060  
 ATAGTTTTTT TTTTTTTTT TTTTTTTTGC CTTCAACTAA AAACAAAGGA GATAAATTTA 3120  
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 50 CAGGGAATAT ATATATCTAA ATTTAGAAAT CATTGGGTTT AATATGGGCT TTCATAATTC 3240  
 TAAGACTAAT GCTCAGAAC TAAACACTAC CTTACAGTGA GGGCTATACA TGGTAGCCAG 3300  
 TTGAATTTAT GGAATCTACC AACTGTTTAG GGCCCTGATT TGCTGGGCAG TTTTCTCTGA 3360  
 TTTTATAAGT ATCTTCATGT ATCCCTGTGA CTGATAGGGA TACATGCTCT AGAAAAATTC 3420  
 55 CTATTGGCTG GGAAGTGTGG CTCATGCCCTG TAATCCAGC ACTTGGAGAG CTGAGGTTG 3480  
 CGCCACTACA CTCCAGCGTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 354 Protein sequence  
 Protein Accession #: NP\_003174.2

60 1 11 21 31 41 51  
 MRQSLLEFLTS VVPFVLAPRP PDDPGFGPHQ RLEKLDLSLS DYDILSLSN QHVSVRKRD 60  
 QSTHVELL TFSALKRHF LYLTSSTERF SQNFVUVVD GKNEBYTAK WQDFPTGHV 120  
 GEPDSRVLAH IRDDVLIIRI NTDGAENIE FLWRPVNDTK DKRMLVYKSE DIKNVSRQLS 180  
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Protein Accession #: NP\_068604.1

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 CNTQAEALLAA GCQRESIVVM ESSPQITEET QIDTTLRRSQ MSPQGLRVRL RPEERHFEL 120  
 EVFEPLESFV DLYILMDFSN SMSDDLNLK KMGQNLARVL SGLTSDYTIG FGKPFVDKVS 180  
 PQTDMRPEKL KEPMFNSDPP FPFKNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL 240  
 QTAVCTRDIG WRFPDTHLLV FSTESAPHYE ADGANVLAGI MSRNDERCHL DTTGTYTYQR 300  
 TDYPSVPTL VRLLAKNHII PIPAVTNYSY SYTEKLHTYF FVSSLGLVQE DSNINIVELLE 360  
 EAFNRIRSNL DTRALDSPRG LRTEVTSKMP QKRTGSPHII RRGEVGIYQV QLRALHVDG 420

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THVQQLPEDQ KGNHLKPSF SDGLKMDAGI ICDVCTCELO KEVRSARCSF NGDFVCGQCV 480  
CSEGWSSGQC NCSTGSLSDI QPCLREGEDK PCSGRGEOQC GHCVCYGEGR YEGQFCBYDN 540  
FQCPRTSGLF CNDRGRCMSG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCEGR 600  
CHCHQQSLYT DTICEINYSI IHPGLCEDLR SCVQCAWGT GEKKGRTECE CNPKVKMVE 660  
LKRAEEVVVR CSFRDEDDDC TYSYTMEDGD APGPNSTVLV HKKKDCPPGS FWWLIPLLLL 720  
LLPLALLLLL LCKVYCACCK ACLALLPCCN RGHMVGFKED HYMLRENMA SDHLDTFMLR 780  
SGNLKGRDVV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840  
AQLRQVEEEN LNEVYRQISG VHKLQQTFR QPNAGKQKD HTIVDTVLMA PRSAKPALLK 900  
LTERQVEQRA FHDLVVAPGY YTLTADQDAR GMVEFQEGVE LVDVVRVPLFI RPEDDDEKQL 960  
LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020  
KSQVSYRTQD GTAQGNRDYI FVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080  
VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLAGP QNPNAKAAGS 1140  
RKIHFNWLPF SGKPMGYRVK YWIGDSESE AHLDSKVPS VELTNLYPYC DYEMKVCAYG 1200  
AQEGEPYSSL VSCRTHQEVF SEPRLAFNV VSVTVQLSW AEPATNGEI TAYEVCYGLV 1260  
NDDNRPIGEM KKVLDVNPKN RMLLIENLRE SQPYRYTVKA RENGAGWPER EAINLATOP 1320  
KRPMSIPIF DIPIDVDAQS EDYDSFLMYS DDVLRSPSGS QRPVSDDTE HLNVGRMDFA 1380  
FPGSTNSLHR MTTSAAYG THLSPHVPHR VLSTSSLTTR DYNLSLRSEH SHSTTLPRDY 1440  
SLTTSVSHD SRLTAGVPDT PTRLVPSALG PTLRLVSWQE PRCEPPLQGY SVEYQLLNGG 1500  
ELHRLNPNP AQTSTVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES QVHPQSLCP 1560  
LPGSAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEN AQGGGPATAF 1620  
RVDGDSPEER LTVPLGSENV PYKFKVQART TEGFPEREG IITIESQDGG PFPQLGSRAG 1680  
LFQHPLQSEY SSTTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEP VSRTLTSTGT 1740  
LSTHMDQQEF QT

Seq ID NO: 361 DNA sequence  
Nucleic Acid Accession #: NM\_013332.1  
Coding sequence: 1..63

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1 11 21 31 41 51  
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GCACGAGGGC GCTTTGTCT CCGGTGAGTT TGTGGCGGG AAGCTTCGCG GCTGGTGCTT 60  
AGTAACCGAC TTTCCTCCGG ACTCCTGCAC GACCTGCTCC TACAGCCGGC GATCCACTCC 120  
CGGCTGTTC CCGGAGGGT CCAGAGGCC TCCAGAGGA GAAGGCAGCT CTGTTCTCT 180  
GCAGAGGAGT AGGGTCCTTT CAGCCATGAA GCATGTGTTG AACCTCTACC TGTAGGTGT 240  
GGTACTGACC CTACTCTCCA TCTTCGTTAG AGTGTAGGAG TCCCTAGAAG GCTTACTAGA 300  
GAGCCCATCG CCGGGACCT CCGGACCA CAGAACCAA CTAGCCAA CAGAGCCAC 360  
CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATCTGGCC 420  
ATATTTTGA ACACCTGACCT AGACATGTCC AGATGGGAGT OCCATTCTTA GCAGACAAGC 480  
TAGACACCGT TGTAAACAGA GAACATATTAC TAGGCCTTGA AGAACCTGTC TAACTGGATG 540  
CTCATTCGCT GGCAAGGCC TGTTAGGCC GGTTCGGTG GCTCATGCTC GTAATCCTAG 600  
CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTGAG GAGTTCGAGA CCAGCCTCGC 660  
CAACATGGCG AAACCCCATC TCTACTAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720  
GGCCTGTAAT CCCAGTTCCT TGGGAGGCTG AGGCGGAGAG ATTGCTTGA CCGGGGAGC 780  
GAGGTTCGAG TGAACCGAGA TGGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840  
CATCTCAAAA AAAAAAAGAA AAAAAAAGC CTGTTAATG CACAGTGTG AGTGGATTGC 900  
TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCCGGG GTCTGGTGTG TGCTGTGCTT 960  
TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG 1020  
TGATATTTTC AACCTACTT CCTAAACATC TGTCTGGGT TCCTTTAGTC TTGAATGTCT 1080  
TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140  
CAGTTGAAGA GTTGTGTG GTGGGCTGTT GGGAGTGGAG ATGAGTGTGT CAGTGCCCAT 1200  
TTCTCATTTT ACATTTTAAA GTCTGTCTC CAACATAGTG TGTATTGTG TGAAGGGGGT 1260  
GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATGTGG CCACCATGTG GCTTAAATGA 1320  
TTTTTTCTAA CTAATARAAGT GGAATATATA TTTCAAAAAA AAAAAAAAAA AA

Seq ID NO: 362 Protein sequence  
Protein Accession #: NP\_037464.1

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1 11 21 31 41 51  
| | | | |  
MKHVLNLYLL GVVLTLLSIF VRVMSLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60  
RSM

Seq ID NO: 363 DNA sequence  
Nucleic Acid Accession #: NM\_023915.1  
Coding sequence: 250..1326

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GGCAAGAGGG TTTCGTTTTC ATGCTTTACC AGAAAAATCCA CTTCCTGACC GACCTTAGTT 60  
TCAAGCTTAA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120  
GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAC CAGGAATAAC CTATGCTGAA 180  
CCACGCGCTC AATCGTCCCC AAGTGTTCCT TGACACGCAT CTTTGCTTAC AGTGATCAC 240  
AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAAGCA GCTGCACGGC 300  
CAAGAGAGTC ACATATTCAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360  
AATGAATTTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTGT GGCAGCATC 420  
TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAC CAGCTTCATA 480  
TTCTATCTCA AAAACATAGT GGTTCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540  
ATAGTCCATG ATGACGAGT TGGACCTTGG TACTTCAAGT TTATCTCTG CAGATACACT 600  
TCAGTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCAAT 660  
GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC 720  
ACGAAGGTTT TATCTGTTTG TGTGTTGGTG ATCATGGCTG TTTTGTCTTT GCCAACATC 780  
ATCCTGACAA ATGCTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAGT 840  
CCTTTGGGGG TCAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900  
GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960

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AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAAACATA ACCAGAGCAT CAGGGTGTGT 1020
GTGGCTGTGT TTTTACCTGT CTTTCTACCA TATCACTTGT GCAGAAATCC TTTTACTTTT 1080
AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAAA TCCTATATTA CTGCAAGAA 1140
ATTACACTTT TCTGTCTGCG GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG 1200
TGTAGGTGAT TTTCAAGAA GCTGTTCAAA AAATCAAATA TCAGAACCGAG GAGTGAAAGC 1260
ATCAGATCAC TGCAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTCACTGAT 1320
GTGTAGGCGT TTTATTGTTT GTTGGAAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT 1380
TTCATTATCC TTAATAAAAA AA

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Seq ID NO: 364 Protein sequence  
Protein Accession #: NP\_076404

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MGFNLTLAKL PNNELHQGES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
GLAVWIFPHI RNKTSFIFVL KNIVVADLIM TLTFFPRIVH DAGFGPWYFK FILCRYTSVL 120
FYANMYTSIV FLGLISIDRY LKVVVKPFQDS RMYSTPTKV LSVCVWVIMA VLSLPNIILT 180
NGQPTEDNIH DCSKLSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYLAIS RYIHKSSRQF 240
ISQSSRKRIH NQSRVWVAV FFTCFLPYHL CRIPPTFSLH DRLDESQAK ILYYCKEITL 300
FLSACNVCLD PIIYFFMCRS PSRRLPKKSN IRTRESIRS LQSVRRSEVR IYYDYTDV

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Seq ID NO: 365 DNA sequence  
Nucleic Acid Accession #: NM\_005365.1  
Coding sequence: 1..948

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ATGTCCTCTG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60
GAGGACTTGG GCTGTATGGG TGCACAGGAA CCCACAGGCG AGGAGGAGGA GACTACCTCC 120
TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCAGAGT 180
CCTCAGGAGG GCGCTTCTCT CTCATTTCCT GTCTACTACA CTTTATGGAG CCAATTCGAT 240
GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGTTCGACCC AGCTCAGCTG 300
GAGTTCATGT TCCAAGAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCTGCTCT 360
CACAAATATC GAGTCAAGGA CCGGTTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAGCCT CCGAGTTTAT GCAGGTGATC 480
TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACTGCT 540
CTTGGCCTCT CGTGCATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCGGCCCTC 600
CTGATCATTG TCCTGGGTGT GATCCTAACC AAAGACAAC GCGCCCTGTA AGAGGTTATC 660
TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAG AGCATGTGT CTACGGGGAG 720
CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAAC ACCTGGAGTA CCGGCAGGTG 780
CCCGGAGATG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
AGCTATAGA AGGTCAATAA TTATTGGTTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900
CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

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Seq ID NO: 366 Protein sequence  
Protein Accession #: NP\_005356.1

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MSLEQRSPHC KPDEDLEAQQ EDLGLMGAQE PTGEEBETTS SSDSKREEVS AAGSSSPQPS 60
PQGGASSSIS VYITLWSQFD EGSSSQEEEE PSSSVDPAQL EPMFQEALKL KVAELVHFL 120
HKYRVRKEPV KAEMLESVIK NYKRYFFVIP GKASEFMQVI FGTDVKEVDP AGHSYILVTA 180
LGLSCDSMLG DGHSMFKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMPYGE 240
PRKLLTDQWV QENYLEYRQV PGSDPAHYEF LMGSKAHAET SYEKVINYL 300
PSLYEEVLGE EQEGV

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Seq ID NO: 367 DNA sequence  
Nucleic Acid Accession #: NM\_014400  
Coding sequence: 86..1126

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GGTTACTCAT CTTGGGCTCA GGTAAAGAGG CCCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
GAGCCCAAGG GAGCAGGACG GAGCCATGGA CCCCGCCAGG AAAGCAGGTG CCCAGGCCAT 120
GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
GTGCTACAGC TGGGTGCGA AAGCAGATGA CGGATGCTCC CGAACAGA TGAAGACAGT 240
GAAGTGCGCG CCGGGCGTGG ACGTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCCA 300
CGACAAATTC AATGCTGGCA TGCGGGGTTG CGGTTGCGGA CTCCCGGCA AGAATGACCG 360
CGGCTCGGAT CTTACGGGCG TCTGGCGTTC CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
CTGCAACGCC AAGCTCAACC TCACTGCGG GCGCTGCGAC CCGGCAGGTA ATGAGAGTGC 480
ATACCCGCCC AACCGCGTGG AGTGCTACAG CTGTGTGGCG CTGAGCGCGG AGGCGTGCCA 540
GGGTACATCG CCGCGGCTCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGCGTG 600
CTTGACCGGC AAGCTCAACT TGAAGGACAG TAATGTGACT GTGTCTTTCG CTGTCCGGGG 660
CTGTGTCCAG GATGAATTTT GCACTCGGGA TGGAGTAACA GGCCCAAGGT TCACGCTCAG 720
TGGCTCTGTF TGGCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
CCCTCGAATC CACCCCTTGG TCCGGCTGCC CCTCCAGAG CCCACGACTG TGGCTCAAC 840
CACATCTGTC ACCACTTCTA CTTGGGCCCC AGTGAGACCC ACATCCACCA CCAAAACCAT 900
GCCAGCGCCA ACCAGTCAAG CTCGAGACA GGGAGTAGAA CAGAGGCTCT CCGGGATGA 960
GGAGCCGAGG TTAGCTGGAG GGGCGGCTGG CCACAGGAC CGCAGCAATT CAGGGCAGTA 1020
TCCTGCAAAA GGGGGGCCCC AGCAGGCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
ATTGGCAGCC CTCTGTGTGG CGTGGCTGCG TGGTGTCTTA CTGTGAGCTT CTCACCTGG 1140
AAATTCCCTT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTATC ACTTCTGTT 1200
CCACCACTGT GACTGGGCTG GCCCAGCCCC TGTTTTTCCA ACATTCCCCA GTATCCCCAG 1260
CTTCTGCTGC GCTGTTTTCG GGCCTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320

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5  
 GGGTGTCTA GCTTTTGGAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380  
 TCCTCTTGAG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440  
 AGGATGTCAA GCTTCTACT CACTTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500  
 GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCTT ACTCCCCGCA TCTTTGGGGA 1560  
 ATCGGTTCCC CATATGTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620  
 CTTATGTCTG TGTGTGATCA GTTCTGCGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680  
 TTGTATAGTG AAAAAAAA

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 Seq ID NO: 368 Protein sequence  
 Protein Accession #: NP\_055215

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 1 11 21 31 41 51  
 MDPAKAGAQ AMIWTAGWLL LLLLRGGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGV DV 60  
 CTEAVGAVET IHGQPSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQCAQ DRCAKLNLT 120  
 SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVLT 180  
 AANVTVSLPV RGCVDQDEFCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPLVR 240  
 LPPPEPTTVA STTSVTSTTS AFVRFSTTK PMPAPTSTQP RQGVHEASR DEEPRLTGGA 300  
 AGHQDRSNSG QYPKGGPQQ PHNKGCVAPT AGLAALLLAV AAGVLL

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 Seq ID NO: 369 DNA sequence  
 Nucleic Acid Accession #: NM\_005329.1  
 Coding sequence: 1..1662

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 CACTACCTGT CCTTCGGCCT GTACGGCGCC ATCCTGGGCC TGCACCTGCT CATTACAGGC 180  
 CTPTTTGCCCT TCCTGGAGCA CCGGCGCATG CGACGTGCGG GCCAGGCCCT GAAGTGCGCC 240  
 TCCCGCGGCG GGGGCTCGGT GGCACCTGTC ATTGCCGCAT ACCAGGAGGA CCTGACTAC 300  
 TTGCGCAAGT GCGTGGCTC GGCACGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360  
 GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTCCA CGAGGTGCTG 420  
 GCGGGCAGCG AGCAGGCGCG CTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480  
 GGTGAGACGG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TGGGGATGT GGTGCGGGCC 540  
 AGCACCTTCT CGTGACATCAT GCAGAAGTGG GGAGGCAAGC GCGAGGTGAT GTACACGGCC 600  
 TTCAAGGCCCT TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660  
 GATCCAGCCT GCACCATCGA GATGCTTGA GTCTGAGG AGGATCCCCA AGTAGGGGGA 720  
 GTGCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCTCT CCTGAGCAGC 780  
 GTGGGGTACT GTGGGCTCTT CAACGTGGAG CGGGCCTGCC AGTCTACTT TGGCTGTGTG 840  
 CAGTGATTA GTGGGCGCTT GGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900  
 GACTGGTACC ATCAGAAGTT CTTAGGCGAG AAGTGCAGCT TCGGGGATGA CCGGACCTC 960  
 ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020  
 ACAGAGACCC CCACTAAGTA CCTCGGTGG CTCAACCAGC AACCCGCTG GAGCAAGTCT 1080  
 TACTTCCGG AGTGGCTCTA CAACTCTCTG TGGTTCCATA AGCACCACCT CTGGATGACC 1140  
 TACGAGTCAG TGGTCACGGG TTCTTCTCCC TTCTTCTCTA TTGCCACGGT TATACAGCTT 1200  
 TTCTACCGGG GCGCATCTG GAACATTCTC CTCTTCTGTC TGACGGTGCA GCTGGTGGGC 1260  
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 CTCTACTCCC TCTCTATAT GTCCAGCCTT CTGCGGGCCA AGATCTTTGC CATTGTCTAC 1380  
 ATCAACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTTATTGGC 1440  
 CTCATTCTCT TGTCCATCTG GGTGGCAGTT CTCTGGAGG GGCTGGCTA CACAGCTTAT 1500  
 TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCTCTG TCTCTGGGGC TATACTGTAT 1560  
 GGCTGCTACT GGTGGCGCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG 1620  
 AAGAAGCCGG AGCAGTACAG CTGGGCTTTT GCTGAGGTGT GA

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 Seq ID NO: 370 Protein sequence  
 Protein Accession #: NP\_005320.1

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 VVDGNRQEDA YMLDIFHEVL GGTQAGFPV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180  
 STFSICIMQKN GGRKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240  
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGFLGMY RNSLLQQFLE 300  
 DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLWR LNQQTRWSKS 360  
 YFREWLKYNL WFKHKLHMT YESVVTGFFP FFLIATVIQL PYRGRINIL LFLITVQLVG 420  
 IIKATYACFL RGNAMIFMS LYSLLYMSL LPAKIFALAT INKSGWGTSG RKTIVNFIG 480  
 LIPVSIWVAV LLEGLAYTAY QDLFSETEL AFLVSGAILY QCYWVALLML YLAIIARRCG 540  
 KKPEQYSLAF AEV

75  
 Seq ID NO: 371 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 148-7095

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 1 11 21 31 41 51  
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 CGGCGAGGGG CCGCAGACCG TCTGGAATG CGAATCCTAA AGCGTTTCTT CGCTTGCAAT 180  
 CAGCTCCTCT GTGTTGCGCG CCGGATTTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTGTGTGAAG AGATTGGCTG GTCCATATCA GGAGCACTGA ATCAAAAAA TTGGGGAAAG 300  
 AAATATCCAA CATGTAAATG CCAAAAAA TCTCTATCA ATATTGATGA AGATCTTACA 360  
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTGAGGTTT GGGATAAAAC ATCATTGGAA 420



	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTGAGCGGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTATCTGTA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCACCTT	600
5	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGAATTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
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	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
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	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCAATGA	AGCAGTTTGT	1080
	AGTTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTCAC	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAGACTTGT	1260
15	GGTGCTATTC	TCATAAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCCAGAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTCTAC	1500
20	AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACCAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAGC	ATATTCTCTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGACTGACGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
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	GCAACTCTCT	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAGAACCAAG	AGACAAATAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
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	TTGTTTACTG	CCCAAAATAA	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACTCTTA	4020
	TGGCTGAAGA	GCAAAATGTT	CTATCTAATG	AGGAAAAACT	TATAATTCAG	GACTTTATCT	4080

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25 Seq ID NO: 378 Protein sequence:  
 Protein Accession #: EOS sequence

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 SYTGKEEIEH AVCSSEPENV QADPENYTSI LVTWERPRVV YDTMLKFAV LYQQLDGEDQ 240  
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 PELIGTEEII KEZEEEGKDIE BGAVINPGRD SATNQIRKKE PQISTTTHYN RIGTKYNEAK 360  
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 IPIKHPFKHV ADLHASSGFT EEFETLKEFY QEVQSCVDL GITADSSNHP DNKHKNNRYIN 780  
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55 Seq ID NO: 379 DNA sequence  
 Nucleic Acid Accession #: EOS sequence  
 Coding sequence: 148-4632

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Seq ID NO: 380 Protein sequence:  
 Protein Accession #: EOS sequence

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	LDSHIHAYVN	ALLIPGPAKG	TKLEKQFQGL	TLSPRLCRG	TSAHCNLPL	PGLTDPPTSA	1200
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	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TPCALTTLMH	QLEKENSVDV	YQVAKMINLM	1440
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	GATAAGGTGC	CCTTGATATC	TTCTCTGCCA	GTGGCTGGGG	GTGATTGTCT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGGTAGTG	AATCTGGTGT	TCTTTATAAA	AGCCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
70	AGCAGTGATG	CCATGATGCA	TGCAGTTTCT	TCAGGGCTCT	AACCTTCTTA	TGCTTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTCCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
	GATTCTGTGG	GTGTAACCTA	TGAGGGTTCC	TTAATTAGAG	GCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	GGTAAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
75	GGGCTGACAG	CCCTTAACAT	TTCTTCAACT	GTTCCTGTAG	CTGAATTTAC	ATATACAACA	3240
	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
	ACTGAACCTG	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAGG	CACAGTCACT	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAAGGCGAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
80	GATCATGAGA	TTAGTCAAGT	TCCAGAAAT	AACCTTTTCC	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	TTGCTGACAC	TTGCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTTCTAG	TGAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAG	TGAAGTATTG	CTACAACCTT	CCTTTGAGGC	TTCTGATGTT	3720
	GACACTCTTG	TTAAACACTG	TCTTCCAGCT	GTGCCCAGTG	ATCCAATATT	GGTTGAAACC	3780



	CCCAAAGTTG	ATAAAATTAG	TTCTACAAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAAAACA	TGCTGCACCT	TACATCTGTA	CCAGTTTITG	ATGTGTGCGC	TACTTCTCAT	3900
	ATGCACCTCT	CTTCACTTCA	AGGTTTGACC	ATTTCTCTATG	CAAGTGAGAA	ATATGAACCA	3960
5	GTITTTGTTAA	AAAGTGAAAG	TTCCCAACCA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAACT	CAGGCCCATC	CCCCAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTATCT	AATTGATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAACT	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCCAACAG	TTGCTTCTGA	TACATTGTTA	TCTACTGATC	ATTCTGTTCC	TATAGGAAAT	4260
10	GGGCATGTTG	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCGTGAAC	CTCAACAAAG	4320
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25	TTAGAGSACA	GATCATCCCT	TAGAGTTATA	TCCACACCTC	CAACACCTAT	CTTTCCAATT	5220
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	TCAAATATAC	AGCAGAGTGA	CTATCTGCA	GCCCTAAAGC	AATGCACAG	GGAAAGAAAT	6300
	CGAACTTCTT	CTATCATCCC	TGTGGAAGA	TCAAGGGTTG	GCATTTTCAT	CCTGAGTGGA	6360
45	GAAGGCACAG	ACTACATCAA	TGCTCTCTAT	ATCATGGGCT	ATTACACAG	CAATGAATTC	6420
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	GTTTACTGGC	CAATAAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGST	CACCTTATG	6600
	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAATAACTTA	TAATTCAGGA	CTTTATCTTA	6660
50	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTCAAGTGTC	TAAATGGCCA	6720
	AATCCAGATG	AGCCCATTTT	TAAAACTTTT	GAACCTATTA	GTGTTATATA	AGAAGAAGCT	6780
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60	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACATAA	ATGATTGAAT	TTTACAGTAT	7320
	TCTTAAGAAAT	GGAATTTGTTG	TATTTTCTTC	TGTATTGATT	TTAAACAGAA	ATTTCAATTT	7380
	ATAGAGGTTA	GGAATTTCAA	ACTACAGAAA	ATGTTTGTIT	TTAGTGTCAA	ATTTTATAGT	7440
	GTATTGTAG	CAATTATCAG	GTTTGCTAGA	AATATAACTT	TTAATACAGT	AGCCTGTAAA	7500
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65	AATAATCTGT	TACTTATTGT	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	7620
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	TAGTTTAATG	ACGATGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTCTGTA	CATTGTATTG	7740
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Seq ID NO: 382 Protein sequence  
Protein Accession #: NP\_002842.1

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	FKASKITFW	GKCMSSDGS	EHSLGQKFP	LEMQIYCFDA	DRFSSFBFAV	KRGKRLRLS	180
80	ILFEVGTEN	LDPKAILDGV	ESVSRFGKQA	ALDPPILLAL	LPNSTDKYI	YNGSLTSPPC	240
	TDVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGVYMLMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEFENVOA	DPENYTSLLV	TWERPRVVDY	TMIEKPAVLY	QQLDGEDQTK	360
	HEPLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPFE	420
	LIGTEHIIKE	EEBEGKIDIEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTHYNRI	GTRYNEAKTN	480

	RSPTRGSEFS	GKGDVFNSTL	NSTSQPVTKL	ATEKDLSLTS	QTVTELPFHT	VEGTSASLND	540
	GSKTVLRSFH	MNLSGTAESL	NTVSIETEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITTYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSGTDI	660
5	TAQPDVGGSR	ESFLQNTYTE	IRVDESEKIT	KSPSAGPVMS	QGPSVTDLDM	PHYSTFAYFP	720
	TEVTPHAFPT	SSRQQLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSSEVPFL	VTPLLLDNQI	780
	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAFL	PFSSASFSSSE	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPLHSL	PVAGDILLLE	PSLAQYSDVL	STTHAASETL	EPGSESGVLY	900
	KTLMPSQVEP	PSSDAMMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVVYQG	960
10	SLFSGPSHIP	IPKSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
	PVSVAEFTYT	TSVFGDDNKA	LKSKSEIYGN	ETELQIPSPN	EMVYPSESTV	MPNMYDNVVK	1080
	LNASLQETS	SISSTKGMFP	GLAHTTTKV	FDHEISQVPE	NMFSVQPTH	VSQASGDTSL	1140
	KPVLSEANSE	ASSDPASSEM	LSPSTQLLPY	ETSASFSTEV	LLQPSFQASD	VDTLTKTVLP	1200
	AVPSDFILVE	TPKVDKISS	MLHLIVNSA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
15	TISYASEKYE	PVLLKSESSH	QVPSLYSND	ELFQTANLEI	NQAHPPKGRH	VPATPVLSD	1320
	EPLNTLINK	IHSDEILTST	KSSVTGKVPF	GIPTVASDTF	VSTDHVSPIG	NGHVAITAVS	1380
	PHRDGSVTST	KLLFPKSKATS	ELSHSAKSDA	GLVGGGEDGD	TDGDDDDDD	RDSGLSIIHK	1440
	CMSCSSYRES	QKVMNDSYT	HENSLMDQNN	PISYSLSENS	EDNRVTSVS	SDSQTGMDRS	1500
	PGKSPSANG	SQKNDGKKEE	NDIQTGSALL	PLSPESKAWA	VLTSDEESGS	GGGTSDSLNE	1560
20	NETSTDPSFA	LTNKTGADGI	LAAGDSEITP	GFPQSTSSV	TSENESEPHV	SEAEASNSSH	1620
	ESRIGLAEGL	ESEKKAIVPL	VIVSALTFC	LVLVLGILIY	WRCKFQTAHF	YLEDSTSPRV	1680
	ISTPPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGFTEEP	ETLKEFYQEV	QSCVDLGIT	1740
	ADSSNHPDNK	HKRYINIVA	YDHSRVKLAQ	LAEKDGLTD	YINANYVDGY	NRPKAYIAAQ	1800
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25	LAYTTNKPFI	LRNTKIKKGS	QKGRPSGRVV	TQYHYTQFED	MGVPEYSLPV	LTFVRKAAYA	1920
	KRHAVGPPVV	HCSAGVGRTO	TYIVLDSMLQ	QIQHEGTVNI	FGFLKHRSQ	RNYLVQTEEQ	1980
	YVPIDHDLVE	AILSKETEVL	DSHILHAYNA	LLIPGPAGKT	KLEKQFQLLS	QSNIIQSDYS	2040
	AALKQCNREK	MRTSSIIIPVE	RSRVGISSLS	GBGTDYINAS	YIMGYYSQNE	FIITQHPLH	2100
	TIKDFWRMWN	DHNAQLVVM	PDGQNAEED	FVYWPKNDEP	INCESPKVTL	MAEEHKCLSN	2160
30	EEKLIQDPFI	LEATQDDYVL	EVRFHQCPKW	PNPDSPISKT	PELLISVKEE	AANRDGPMIV	2220
	HDEHGGVITAG	TFCALTTLMH	QLEKENSDVD	YQVAKMINLM	RPGVFADIEQ	YQFLYKVLIS	2280
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Seq ID NO: 383 DNA sequence

Nucleic Acid Accession #: NM\_005688.1

Coding sequence: 126...4439

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	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTC	GGGTATAGAA	180
	GTGTGAGGCA	GGAACACAG	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTOG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAC	AGCAGCCGCA	GCCGAGGGCC	300
45	TCTCTCTTGA	TGCTTCCATG	CATTCTCAGC	TCAGAACTCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCAATGGCTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
	ACCCAGTGGG	CAATGCTGGG	CTTTTCTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAA	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
50	AAGTTGGGGC	AGACGCTGCT	TCCTTGGGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCCAGC	660
	TCATCTCTTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCACT	GGACCCAGCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACTCT	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCTCT	CTCTGACGG	AAATCGTGG	GTCTTGTGCT	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGGCGGG	GGCCATCCTA	ACCATGGCAT	900
55	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGTCTCAA	CGATGGGCGG	AGAAATGTTT	AGGCAGCAGC	CGTTGGCAGC	CTGTCTGGCTG	1020
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	GCTTCTCTGG	ATCAGCTGTT	TTTATCCTCT	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
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	ACAGAGGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGGCG	ACTGAGCATC	1740
70	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCCCTCTGGA	CAGTGACGAG	CGGCCACGTC	1800
	CCGAGAGGGA	AGAAGGCAAG	CACATCCACC	TGGGCCACCT	GCGCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCTCT	AATGCTACTC	2040
	TGAGAGACAA	CATCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAA	TCTGTGCTGA	2100
	ACAGCTGTCT	CCTGAGGCTT	GACCTGGCCA	TTCTTCCGAC	CAGCGACCTG	ACGAGGATTT	2160
75	GAGAGCGAGG	AGCCCACTTG	AGCGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCGCGGGCCT	2220
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	TGGGCAACCA	CATCTTCAAT	AGTGTATACC	GGAAACATCT	CAAGTCCAA	ACAGTTCTGT	2340
	TGTTTACCCA	CAGTTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
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80	CCATTTTTAA	TAACCTGTTG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
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	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
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 Protein Accession #: NP\_005679.1

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5	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCCGGTG	1560
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15	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAAG	AGTTGGGCTC	CTGGGAAGTC	2220
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	TATGCTCAGG	TCACCTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTGTCTTAT	3840
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	TTACCTCCAT	CCATCCTTCC	AACATATATT	TATTTAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
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Protein Accession #: NP\_005553.1

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	PEGCTQCFCY	GHSASCRSSA	EYSVKITST	FRQDVVDGWA	VQRNGSPAKL	QWSQRHQDVF	240
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75 Seq ID NO: 392 Protein sequence  
 Protein Accession #: AAD16433.1

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	TGCCCTGTGT	TATCTCTGCC	TTTGATGTGG	ATGAAAAAAA	GGGAAAAACA	ATATTTCACT	3300
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Seq ID NO: 394 Protein sequence  
Protein Accession #: NP\_006171.1

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	SKIIPLANLQ	IPNCGLPAN	LAAPNLVBE	GKSITLSCSV	AGDPVPMYMW	DVGNLVSKRM	240
80	NETSHTOGSL	RITNISDDSD	GKQISCVARN	LVGEDQDSVN	LTVHPAPTIT	FLESPTSDDH	300
	WCIPFTVKGN	PKPALQWFFN	GAILNESKYI	CTKHIVTNHT	EYHGCLQLDN	PTHMNNNGDYT	360
	LIARNEYRGD	EKQISAPFMG	WPGIDDGANP	NYPDVITYEDY	GTAANDIGDT	TNRSEIPIST	420
	DVTDKTRGRH	LSVYAVVVIA	SVVGFCLLVN	LFLLKLARHS	KFGMKGPASV	ISNDDDSASP	480
	LHHISNGSNT	SSSSEGGPDA	VIIGMTKIPV	IENPQYPGIT	NSQLKPDFTV	QHKKRHNIVL	540
	KRELGEAGFG	KVFLABCYNL	CPEQDKILVA	VKTLLKSDASN	ARKDPHREAS	LLTNLQHEHI	600



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 PPESIMYRIF TTESDVWSLG VVLWEIPTYG KQPHYQLSNV EVIECITQGR VLQRPRTCPQ 780  
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Seq ID NO: 396 Protein sequence  
 Protein Accession #: AAL67965.1

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Seq ID NO: 397 DNA sequence

Nucleic Acid Accession #: AB052906

Coding sequence: 74..814

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TTCTGGCTAG	CTAAACAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAATCAA	1140
GTACTTCTTT	GAATGATGAT	CTCTTTCTTG	CAAAATGATAT	TGTCACTAAA	ATAATCAOCT	1200
TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGTCTTGAAA	GAGAATTTTT	AAATTAATTTA	1260
ATAAGAAAAA	ATTATATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTC	TGTACTGATA	1320
TTTAAATAAA	GAGTTCTATT	TCCCAAAAAA	AAAAAATAAA	AA		

Seq ID NO: 398 Protein sequence

Protein Accession #: BAB61048.1

50  
55

1	11	21	31	41	51	
MAAAATKIL	LCLPLLLLLS	GWSRAGRADP	HSLCYDITVI	PKFRPGRWRC	AVQGVQDEKT	60
FLHYDCGNKT	VTPVSPGLKK	LNVTTAWKAQ	NPVLREVVDI	LTEQLRDIQL	ENYTPKEPLT	120
LQARMSCEBQ	ABGHSSGSWQ	PSFDGQIFLL	FDSEKRMWTT	VHPGARKNKE	KWENDKVVM	180
SFHYFSMGDC	IGWLEDFLMG	MDSTLEPSAG	APLAMSSGTT	QLRATATTLI	LCCLLIILPC	240
PILPGI						

Seq ID NO: 399 DNA sequence

Nucleic Acid Accession #: NM\_001898.1

Coding sequence: 57..482

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65  
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1	11	21	31	41	51	
GGCTCTCACC	CTCCTCTCCT	GCAGCTCCAG	CTTGTGCTC	TGCTCTGAG	GAGACCATGG	60
CCAGTATCT	GAGTACCTGC	CTGCTCCTGC	TGGCCACCT	AGCTGTGGCC	CTGGCCTGGA	120
GCCCCAAGGA	GGAGGATAGG	ATAATCCGGG	GTGGCATCTA	TAACGCAGAC	CTCAATGATG	180
AGTGGGTACA	GCGTGCCCTT	CACCTCGCCA	TCAGCGAGTA	TAACAGGCC	ACCAAAAGATG	240
ACTACTACAG	ACGTCCGCTG	CGGGTACTAA	GAGCCAGGCA	ACAGACCGTT	GGGGGGGTGA	300
ATTACTTCTT	OGAOTAGAG	GTGGGCGGCA	CCATATGTAC	CAAGTCCAG	CCCAACTTGG	360
ACACCTGTGC	CTTCCATGAA	CAGCCAGAAC	TGCAGAGAA	ACAGTTGTGC	TCITTCGAGA	420
TCACGAAGT	TCCTGGGGAG	AACAGAAGGT	CCCTGGTGAA	ATCCAGGTGT	CAAGAATCCT	480
AGGGATCTGT	GCCAGGCCAT	TCGCACCAAC	CACCAACCC	TCCACCCCC	TGTAGTGCTC	540
CCACCCCTGG	ACTGGTGGCC	CCCAACCTGC	GGGAGGCTC	CCCATGTGCC	TGCGCCAAGA	600
GACAGACAGA	GAAGGCTGCA	GGAGTCTTTT	GTTCCTCAGC	AGGGCGCTCT	GCCCTCCTCT	660
CTTCTCTCTT	GCTTCTAATA	GCCTGGTATC	ATGGTACACA	CCCCCCCACC	TCTTGCATTT	720
AAACAGTAGC	ATGCC					

Seq ID NO: 400 Protein sequence

Protein Accession #: NP\_001899.1

80

1	11	21	31	41	51	
MAQYLSTLL	LIATLAVALA	WSPKEEDRII	PGGIYNADLN	DEWVORALHF	AISEYNKATK	60
DDYYRRPLRV	LRARQQTGG	VNYFFDVEVG	RTICTKSQPN	LDTCAFHEQP	ELQKKQLCSF	120

EIYEVFWENR RSLVKSRCQS S

Seq ID NO: 401 DNA sequence

Nucleic Acid Accession #: NM\_003976.2

Coding sequence: 299..961

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1	11	21	31	41	51	
CTCTGAGCTT	CTCTGAGCCT	TGTTTGCTCA	TCTGGAAAAA	GGGGATTAAA	CCATTACCT	60
CATGGAGTTG	TGAAGAATA	GCTGCAAAGC	ACCTAACACA	TAGTAAGGTT	CCCAGTGCAG	120
CTACTTCTGC	TGGGTTGAGT	CTAGCTGTGT	AGGCCOCTTG	TTCTCACCT	GGAGAACTG	180
GGGTGGCAGG	CGGTGCCCC	ACAAAAGATA	ACTCATCTCT	TAATTGCAA	GCTGCCTCAA	240
CAGGAGGGTG	GGGGAACAGC	TCAACAATGG	CTGATGGGGG	CTCCTGGTGT	TGATAGAGAT	300
GGAACTTGGT	CTTGGAGGCC	TCTCAACGCT	GTCCCACTGC	CCCTGGCCTA	GGCGGCAGCC	360
TGCCCTGTGG	CCCACCTGGG	CGCCTCTGGC	TCTGCTGAGC	AGGCTCGCAG	AGGCCTCCCT	420
GGGCTCCGGG	CCCCGCAGCC	CTGCCCCCGG	CGAAGGCCCC	CCGCTGTGTC	TGGCGTCCCC	480
CGCCGGCCAC	CTGCCGGGGG	GACGCAACGC	CCGCTGGTGC	AGTGAAGAG	CCCGCGGGCC	540
CGCCGCGCAG	CCTTCTGGGC	CGCGCCCCCG	GCCTCTGCA	CCCCCATCTG	CTCTTCCCCG	600
CGGGGGCCGC	GGGGGCGGG	CTGGGGGGCC	GGGCAGCCGC	GCTCGGGCAG	CGGGGGCGGG	660
GGGCTGCGCG	CTGCGCTCGC	AGCTGGTGGC	GGTGGCGGG	CTCGGCCTGG	GCCAOCGCTC	720
CGACGAGCTG	GTGCGTTTCC	GCTTCTGCAG	CGGCTCCTGC	CGCGCGCGGC	GCTCTCCACA	780
CGACCTCAGC	CTGGCCAGCC	TACTGGGGCG	CGGGGCCCTG	CGACCGCCCC	CGGGCTCCCG	840
GCCTGTGAGC	CAGCCTGTCT	GCGACCCAC	GCGTACGAA	GCGGTCTCTC	TCTTGGACGT	900
CAACGTCAGC	TGGAGAACCG	TGGACCGCCT	CTCGCCAC	GCTCGCGCTG	GCCTGGGCTG	960
AGGGCTCGCT	CCAGGGCTTT	GCAGACTGGA	CCCTTACCGG	TGGCTCTTCC	TGCTTGGGAC	1020
CCTCCCGCAG	AGTCCCACTA	GCCAGCGGCC	TCAGCCAGGG	ACGAAGGCTC	CAAGCTGAG	1080
AGGCCCTCAG	CGGTGGGTGA	TGGATATCAT	CCCGAAGCAG	GTGAAGGGAC	AACCTGACTG	1140
CAGCCCGAGA	GCCTTACCC	TGGGATCCCG	AGCTTAAAG	ACACCAAGAG	CCTCAGCTAT	1200
GGAGCCCTTC	GGACCACTT	CTCAGACTG	CTGGCACTGG	CCAGGCTCTG	AACCTGGGAC	1260
CCCTCCTCTG	ATGAACACTA	CAGTGGCTGA	GGCATCAGCC	CCCGCCAGG	CCCTGTAGGG	1320
ACAGCATTTG	AAGGACACAT	ATTGCAGTTG	CTTGGTTGAA	AGTGCTGTGT	CTGGAACCTG	1380
CCTGTACTCA	CTCATGGGAG	CTGGCCCC				

Seq ID NO: 402 Protein sequence

Protein Accession #: NP\_003967.1

40  
45

1	11	21	31	41	51	
MELGLGLST	LSHCPWPRRQ	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPVLAS	60
PAGHLPGGRT	ARWCSGRARR	PPQPSPRPAP	PPFAPPSALP	RGGRARARAG	PGSRARAAGA	120
RGCRRLSQLV	FVRALGLGHR	SDELVRFRFC	SGSCRRARSP	HDLSLASLLG	AGALRPFPFGS	180
RPVSPQCCRP	TRYEAVSFMD	VNSTWRTVDR	LSATACGCLG			

Seq ID NO: 403 DNA sequence

Nucleic Acid Accession #: NM\_057091.1

Coding sequence: 783..1445

50  
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1	11	21	31	41	51	
ACTGCCGCT	GAGAGAAGAA	TGGGTGGAG	CAGAGAGCAG	CTGCTGCAGG	GCAGACAGCC	60
GGACCCCAAA	ATCTGCAGCT	ACCAGCAGTC	AGCCGCCCA	CGCAGGGACC	GGCTTACCCC	120
TGCTCTCCCG	CCCTCACTCA	CTTCTCCCG	CCCTCGGCC	GGCTTCCAG	CTCTCTACTT	180
CGCGTGTCTA	CAAACTCAAC	TCCCGGTTTC	CGTGCCTCTC	CACCGCTCGA	GTTCCTACT	240
CTCATATCC	GAGGGGCCCC	TCCAGCATC	TACCCCTC	CCAACCTCGG	GGGACCTAGC	300
CAAGCTAGGG	GGGACTGGAT	CCGACGGGTG	GAGCAGCCAG	GTGAGCCCCG	AAAGGTGGGG	360
CGGGGCGGG	GGCTCCCGG	CCCCACCCG	GGATCTGGTG	ACGCTGGGGC	TGGATTTGA	420
CACCGGACGG	CTGGGGGGG	GGGCGAGAG	CTGCTGAGGG	ATGGAGTTGG	GCCCGGCCCC	480
CAGACAAGGC	CCGGGGGGTC	CGCCAGCAGC	AGGTCCCTCG	GGCCCCAGCC	CTGCTGCCA	540
CCCGGGCCTG	GAGCCCCACA	CCGAGGGGTG	CAGACTGGCT	GCCAGGCCCA	CACCTTTGGC	600
TAAAGAGGCG	ACTGCCAGGT	GTACAGTCTT	GGCATGCGC	TGTTTGAAGT	TGGGGGAGA	660
GCCAGCACT	GGTCCCCGGA	AAGGTGCCTA	GAAGAACAAG	GTGCAGGACC	CGTGCTGCC	720
TCAACAGGAG	GGTGGGGGAA	CAGCTCAACA	ATGGCTGATG	GGCGCTCCTG	GTGTTGATAG	780
AGATGGAAGT	TGGACTTGGG	GGCTCTCCCA	CGCTGTCCCA	CTGCCCTGG	CCTAGGCGGC	840
AGCTGCTCCT	GTGGCCCAAC	CTGGCCGCTC	TGGCTCTGCT	GAGCAGGCTC	GCAGAGGCTC	900
CCCTGGGCTC	CGCGCCCGG	AGCCTTGCCC	CCCGGGAAGG	CCCGCCCTCT	GTCTGGGCT	960
CCCCCGCCGG	CCAAGTGGG	GGGGGAGCCA	CGCCCGCTG	GTGCAATGGA	AGAGCCCGGC	1020
GGCGCGCGCC	GCAGCTTCT	CGCCCGCGGC	CCCGCCCGCC	TGCACCCCA	TCTGCTCTTC	1080
CCCGGGGGGG	CGCGCGGGG	CGGGCTGGGG	GCCCGGGCAG	CGCGCTCGG	GCAGCGGGGG	1140
CGCGGGGCTG	CGCGCTGGC	TGCACTGGG	TGCGGGTGG	CGCGCTGGC	CTGGGCCACC	1200
GCTCGAGCA	GCTGGTGGT	TTCCGCTTCT	GCAGCGGCTC	CTGCGCGGC	CGCGCTCTC	1260
CACACGACCT	CAGCTGGGG	AGCCTACTGG	GCGCGGGGC	CCTGCGAGCG	CCCGGGGGCT	1320
CCCGGCCCGT	CAGCCAGCCC	TGCTGCCGAC	CCAAGCGCTA	CGAAGCGGTC	TCCTTCATGG	1380
ACGTCAACAG	CACCTGGAGA	ACCGTGGACC	GCCTCTCGGC	CACCGCTGCG	GGCTGCCTGG	1440
GCTGAGGGCT	CGCTCCAGGG	CTTTCAGAC	TGGAACCTTA	CGGTTGGCTC	TTCTGCTCTG	1500
GGACCTTCCC	GCAGAGTCCC	ACTAGCCAGC	GGCCTCAGCC	AGGAGCGAAG	GCCTCAAAGC	1560
TGAGAGGCC	CTACCGGTGG	GTGATGGATA	TGATCCCGGA	ACAGGTGAAG	GGACAACTGA	1620
CTAGCAGCCC	CAGAGCCCTC	ACCTTGCGGA	TCCAGCCCTA	AAAGACACCA	GAGACCTCAG	1680
CTATGGAGCC	CTTGGAGCCC	ACTTCTACA	GACTCTGGCA	CTGGCCAGGC	CTGAACTCTG	1740
GGACCCCTCC	TCTGATGAAC	ACTACAGTGG	CTGAGGCATC	AGCCCCCGCC	CAGGCCCTGT	1800
AGGAGCAGCA	TTTGAAGGAC	ACATATTGCA	GTGCTTGGT	TGAAAGTGCC	TGTGCTGGAA	1860
CTGCTCTGTA	CTCACTCATG	GGAGCTGGCC	CT			

Seq ID NO: 404 Protein sequence

Protein Accession #: NP\_003967.1

1 11 21 31 41 51  
5 MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60  
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120  
RGCLRLSQLV PVRALGLGHR SDELVRPRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180  
RPVSQPCCRP TRYEAUSFMD VNSTWRTVDR LSATACGCLG

10 Seq ID NO: 405 DNA sequence  
Nucleic Acid Accession #: NM\_057160.1  
Coding sequence: 1..714

1 11 21 31 41 51  
15 ATGCCCGGCC TGATCTCAGC CCGAGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC 60  
CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACCTGGTC TCTCCGCGCA GCCTGCGCTG 120  
TGGCCACCCG TGGCGGCTCT GGCTCTGCTG AGCAGCGCTG CAGAGGCTTC CCTGGGCTCC 180  
GCGCCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCCTGCTG TCTGGCGTTC CCGCGCGGCG 240  
20 CACCTGCCCG GGGGACGAC GGGCGCTGG TGCACTGGAA GAGCCCGCGG GCGCGCGCGG 300  
CAGCCTTCTC GGGCGCGGCC CCGCGCGCTG GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360  
CGCGCGCGCG GGGCTGGGGG CCGCGGCGAG CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420  
CGCCTGCGCT CGCAGCTGGT GCGGTGCGCG GCGCTCGGCC TGGGCCACCG CTCGACGAG 480  
CTGGTGGGTT TCGCTTCTG CAGCGGCTCC TCGCGCGCGG CGGCTCTCC ACACGACCTC 540  
25 AGCCTGGCCA GCCTACTGGG CGCGGGGGCC CTGCGACCGC CCGCGGGCTC CCGCGCGGTC 600  
AGCCAGCCCT GCTGCGGACC CAGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660  
AOCCTGGAGA CCGTGGAGCG CCTCTCGGCC ACCGCTCGCG GCTGCGTGGG CTGAGGGGCTC 720  
GCTCCAGGGC TTGTGAGACT GGACCCCTAC CGGTGGCTCT TCTGCTGCTG GACCCCTCCG 780  
CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGGCCC 840  
30 TACCGGTGGG TGATGGATAT CATCCCGGAA CAGGTGAAGG GACAACGAC TAGCAGCCCC 900  
AGAGCCCTCA CCTCTGGGAT CCGAGCCTAA AAGACACCG AGACCTCAGC TATGGAGCCC 960  
TTGAGACCCA CTCTCAGAC ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020  
CTGATGAACA CTACAGTGGC TGAGGCATCA GCGCCCGGCC AGGCCCTGTA GGGACAGCAT 1080  
35 TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140  
TCACTCATGG GAGCTGGCCC C

Seq ID NO: 406 Protein sequence  
Protein Accession #: NP\_476501.1

40 1 11 21 31 41 51  
MPGLISARQG PLLEVLPPQA HLGAFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60  
APRSPAPREG PPPVLASPAH HLPGRRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120  
45 RAARAGGPGS RARAAGARGC RLRSQLVPVR ALGLGHRSD ELVRFRCGSG CRRARSPHDL 180  
SLASLLGAGA LRPPPGSRPV SQPCCRPTR EAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 407 DNA sequence  
Nucleic Acid Accession #: NM\_057090.1  
Coding sequence: 29..715

1 11 21 31 41 51  
50 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTGGAGGCC TCTCCAGCT 60  
GTCCCACTGC CCCTGGCCTA GCGGCGAGGC TCCACTTGGT CTCTCGGCG AGCCTGCCCT 120  
55 GTGGCCACCC CTGGCGGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCTC CCCTGGGCTC 180  
CGGCCCCGCG AGCCCTGCCC CCGCGGAAGG CCCCCTGCTG GTCTGGCGGT CCGCGCGGCG 240  
CCACCTGCCG GGGGGACGCA CGGCGGCTG GTGCACTGGA AGAGCCCGCG GCGCGCGGCC 300  
CGAGCCTTCT CGGCCCGGCG CCGCGCGGCC TGCACCCCA TCTGCTCTTC CCGCGGGGGG 360  
60 CGCGCGCGCG CGGCTGGGG GCGCGGCGAG CCGCGCTCGG GCAGGGGGG CGCGGGGCTG 420  
CGCCTGCGC TCGCAGCTGG TCGCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCGACGA 480  
GCTGGTGGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCG GCGGCTCTC CACACGACCT 540  
CAGCCTGGCC AGCCTACTGG GCGCGGGGCG CTGCGACCG CCGCGGGCTC CCGCGCCGCT 600  
CAGCCAGCCC TGCTGCGGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG AGCTCAACAG 660  
65 CACCTGGAGA ACCGTGGACC GCCTCTCGCG CACCGGCTGC GGCTGCCTGG GCTGAGGGCT 720  
CGTCCAGGG CTTTGCAGAC TGGACCCCTA CCGGTGGCTC TTCTGCTG GACCCCTCCC 780  
GCAGAGTCCC ACTAGCCAGC GGCTCAGGCC AGGGAAGAAG GCCTCAAAGC TGAGAGGGCC 840  
CTACCGGTGG GTGATGGATA TCATCCCGGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900  
CAGAGCCCTC ACCCTGGGGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960  
70 CTTCGAGACC ACTTCTACA GACTCTGGCA CTGGCCAGGC CTGAAACCTG GGAACCCCTC 1020  
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCGCGCC CAGGCCCTGT AGGGACAGCA 1080  
TTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140  
CTCACTCATG GAGCTGGGCC C

75 Seq ID NO: 408 Protein sequence  
Protein Accession #: NP\_476431.1

1 11 21 31 41 51  
80 MELGLGGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60  
GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPPP PAPPSPALPRG GRAARAGGPG 120  
SRARAAGARG CRLRSQLVPV RALGLGHRSD ELVRFRCPSG SCRRARSPHD LSLASLLGAG 180  
ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 409 DNA sequence  
Nucleic Acid Accession #: Bos sequence  
Coding sequence: 1..1746

5	1	11	21	31	41	51	
	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCCAGGT	GGAGTGCACC	120
	GGGGCAGCGA	TTGTGGGGGT	GCCCCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
10	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTCC	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
	GGCTCGCTGC	GCTATCTCAG	CCTGCCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGT	GTTGCAGATC	420
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCCAC	480
15	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCCCTCGGC	TTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACITT	TGATGGGCTT	660
	GTAAACCTGC	AGGAACCTGC	TCTACAGCAG	AAOCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAAACCAT	CTCCAGCTG	780
20	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTGGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCGGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCCGTATTC	TTAGCGGCAA	TCAGATCAGC	TTCACTCTCC	CGGGTGCCTT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATTGC	1080
25	TTCCGCATGT	TGGCCAACTC	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCCGCCAA	CGTCAATGCG	CTCATGGCCA	TCCAGCTGCA	GAACAACCCAG	1200
	CTGGAAGACT	TGCCCTCGGG	CATCTTGGAT	CACCTGGGGA	AACGTGTGTA	GCTGGGCTG	1260
	TATGACAATC	CCTGAGGAGT	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
	AACCGACCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCGAGC	CAATGTCCGA	1380
30	GGCCAGTGCC	TCATTATCAT	CAATGTCAAC	GTTCCTGTTT	CAAGCGTCCA	TGTCCCTGAG	1440
	TGCCCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCGGTCTCTT	CTACCACTGA	GCTAACCCAGC	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTCAAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCACAGG	CGGGCTGGCC	1620
	ATTGCCGCCA	TTGTAATTGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTGGCC	1680
35	TGTTGCTGCT	GCAAGAAAGAG	GAGCCAAAGCT	GTCTGTATGC	AGATGAAGGC	ACCCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAAATGATG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGAATTCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCCTAC	CTCTTCCTGA	CTTGCTGAT	TCTCCCGTAG	AGAAGCAGGT	1920
	CGTGCCGGAC	CTTCTTACAA	TCAGGAAGAT	AGATCCCACT	GGCCATGGCA	AAAGCCCTGG	1980
40	GGATTTCGGA	TTCAATAACCC	TGGGCTTCCT	TCGAGAGGGC	TCTTCTCCCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAGAACACGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCCTGCTC	ACTTGTGGGG	AATAGTTCTC	CGCTGAGATA	GCCCCCTCTG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
	ACCCAGCATG	TCCCTCATAA	TGAAAGTTCT	CCCCTTGATT	TTCTGTCTCT	GAAGGCAGGG	2280
45	TGAGTTCTCT	GCTATACAGC	GACTTCAAAC	CATTTAACTG	GTTCCTTAAG	AGCCGTCAT	2340
	CAGCCTGGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAGA	GCGGTCTATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAAGAAACA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACTTTGCTT	2520
50	TGAAAGTTT	AGCCCTTTAA	GGAAATGAAAT	CATGTAGAAT	TTTGCACTTC	TAAAAACATT	2580
	AAAATCAGCT	TATTAATAAG	GGATAGAGAA	AGAAATCTGG	TGCCCTGGGG	TCCTGTGTTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TTGAAGCATG	TGAAGTGTAC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCGAGA	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGGA	GCCAGGACGG	2880
55	TCCCCCCACA	GTACAGCTGT	GCAAAGGCCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCTTG	3000
	AGAGACCCCT	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCGCTGACG	CCACACCCCT	TTCCCTGGCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
	TCCGCTGGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTTAATT	TTCAATCTTC	3180
60	ACTTGTGGGA	AGTGAATGCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAAAG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAATCTCAG	AATCTCAGTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTAGTG	3360
	GTCTGGGGGG	TCCCTGGAGC	TCCTCCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
	TCAGGGGTTA	TTCTCCTCCT	CGAGTCACAG	TCACAAGAAAT	ACCTGCCTTC	TCGTGGCTTC	3480
65	CTGCTATACA	CATATTTCACA	TGGGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGCTTTT	3540
	CTCTGGACAA	TTGGCCCACT	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAAC	TTCACTGAC	TCCAAGGGGA	TCTGGAATTC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TGGGCTCTTA	TAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAATTC	TACCACCAAT	3780
70	CCCGATCGGC	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCACG	TGCTGACCCAG	TTTTCCCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CACCTAGTGA	CTTTGTAGCT	TTTCACTCTC	TGTCACAGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAAGGTC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAG	GCATTTCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAAAC	GGAAGTGAGC	4080
75	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCTT	GGTGCCAAAC	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGGCCAC	AGACCTGTGG	4200
	GGTGTCTCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAAGTG	GCCAGGGCTG	4260
	GAGGAGGGTG	GGAAACCTCA	TCAATCCGTC	GGCCCTGCCA	ATCTTAACCC	AGAACCCCTTA	4320
	GGTATTCTCT	GCAGTAGCCA	TGACATTGGA	GCACCTTCCT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTCAGATG	GACACCAACC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
80	CCTTATGTGA	ACCTCTTGCC	TCTTCCCTTC	TCCCATCAGA	GTGGTGTGAT	GGAGCCATTG	4500
	GCCTCTCTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGA	GTCTCTTTTC	CAACAGGATG	ATGCATTTCG	TCAATTCCTA	4620
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CCTCTCTGTT TACAGTCTCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA 4740
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GGTGTTCAT AGGCTGGGAG TTTTATTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
TTGTCTTGGG CTTCCTGTCAT TAAACCAAAG GAAATGGAAG CCAITCCCCT GTTGCTCTCC 5040
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AGTTGGTCGA CAGATGTTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA 5400
GCCCCAGAT CCCACAGTCA GAACTGAATC TGGCTGTGTT GGAAGCCAGC AGTGGCCCTG 5460
GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520
CTCCTTCCGC CCCAGGTTTC TTCTTCTCTT AAGGAGAGAT TGTCTCACC AACCCGCTGC 5580
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GCCCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCC TCAGGGTTT GTAGAGTGTG 5700
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Seq ID NO: 410 Protein sequence

Protein Accession #: BAB84587.1

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LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFNRL GSLRYLSLAN NKLQVLPGL 120
FQGLDLSLESL LLSSNQLLQI QPAHFSCQSN LKELQLHGNH LEYIPDGAPD HLVLGLTKLNL 180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTDFGL VNLQELALQO NQIGLLSPGL 240
FHNHNLRL SLNNHISQL PPSIFMLPQ LNRLTLFGNS LKELSLGIFG PMPNLRLELNL 300
YDNHISLLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGDNV 360
FRMLANLQNI SLQNNLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCBLRL 420
YDNFWRCDSD ILPLRNWLLL NQPRIGTDTV FVCFSPANVR GQSLIIINNV VAVPSVHVPE 480
VPSYPETPMY PDTSPYDPT SVSSTTELTS PVEDITDLTT IQVTDERSVH GMTQAQSGLA 540
IAAIVIGIVA LACSLAACVP CCCCCKRSQA VLMQMKAPNE C
  
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Seq ID NO: 411 DNA sequence

Nucleic Acid Accession #: XM\_098151

Coding sequence: 1..447

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TCTGGAGTGG GAGCTGGGAG TCAGTGTGG AGAAGAAACA ACAAAAGCCA ATTAGAACCA 180
CTATTTTAA AAAGTGCTTA CTGTGCACAG ATACTCTTCA AGCACTGGAG GTGGATTCTC 240
TCTCTAGCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCCTC TACCCACTTG TGATGGGTA 300
CAGAGGCACT TGCTCTCTG CATGGTGTTC AATAGGCTGG GAGTTTATT TATCTCTTCA 360
AACTTTGTAC AAGAGCTCAT GGCTTGTCTT GGGCTTCTG CATTAACCA AAGGAAATGG 420
AAGCCATTCC CTTGTGCTC TCCTTAG
  
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Seq ID NO: 412 Protein sequence

Protein Accession #: XP\_098151

55  
 60

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1 11 21 31 41 51
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LFLKSAQCAQ ILPKHWIWL SLALSTPAVG VPPLPTCDGV QRHLLFCMVF NRLGVLFISS 120
NFVQELMACL GLSSLNQKRW KPFPCCSP
  
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Seq ID NO: 413 DNA sequence

Nucleic Acid Accession #: NM\_002658.1

Coding sequence: 77..1372

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GAGCGACTCC AAAGCGAGCA ATGAACCTCA TCAAGTTCCA TOGAAGTGT ACTGTCTAAA 180
TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCACATT CACTGCTGCA ACTGCCCAA 240
GAAATTGCGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360
CTCTGCCACT GTCCCTTCAGC AAAGCTACCA TGCCACAGA TCTGATGCTC TTCAGTGGG 420
CCTGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGCGACCCCT GGTGCTATGT 480
GCAGGTGGCG CTAAAGCGCG TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
AAAGCCCTCC TCTCCTCCAG AAGAATTAAA ATTTCAAGT GTGCAAAAGA CTCTGAGGCC 600
CCGCTTTAAG ATTATTGGGG GAGAAATCAC CACCATCGAG AACCAAGCCCT GGTTTGCGGC 660
CATCTACAGG AGGCACCGGG GGGGCTCTGT CACTAOGTG TGTGGAGGCA GCCTCATCAG 720
CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCATTGAT TACCCAAAGA AGGAGACTA 780
CATGCTTAC CTGGGTGCTG CAAGGCTTAA CTCACACAG CAAGGGGAGA TGAAGTTTGA 840
GGTGGAAAAC CTATCTCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAAGA 900
CATTGCCCTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCGGACTAT 960
ACAGACCATT TGCTGCGCCT CGATGTATAA CGATCCCGAG TTTGGCACA GCTGTGAGAT 1020
CACTGGCTTT GGAAGAGAGA APTCTACGA CTATCTCTAT CCGGAGCAGC TGAATATGAC 1080
  
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TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG 1500
CACCACCAAG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC 1560
CAGACCCCTC GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620
TGTCTTTTTC TGGACTGAAG CTGCAAGGAG TTAAGGAGGG CAGGGCATCT CCTGTGCATG 1680
GGCTCGAAGG GAGAGCCAGC TCCCCCGACC GGTGGGCATT TGTGAGGCC ATGTTTGAGA 1740
AATGAATAAT TTCCCAATTA GGAAGGTGAA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800
AATGTGGGAG CAGCGGTTTG GGGAGCAGAG AACTAACGA CTTAGGGCA GGGCTCTGAT 1860
ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTGG 1920
GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCTTT 1980
AAACTGTGTG GACTGTGTAG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC 2040
CTGGGGCCCT TTGGGTCCCC CAGGTGACAG TGCCCTGGAA TGTACTTATT CTGCAGCATG 2100
ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCTTTTC TTGGCCAGTT 2160
ATCCCTTCTT TTAGGCTCAT TTCAATCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
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ATCAATAAAA TGTGATTTTT CTGA

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Seq ID NO: 414 Protein sequence  
Protein Accession #: NP\_002649.1

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HCEIDSKRKC YEGNGHFYRG KASTDTMGPR CLPWNSATVL QQTYHAHERSD ALQLGLGRHN 120
YCRNPDRRRR PWCYVQVGLK PLVQECMVHD CADGKPKSSP PEELKPKCGQ KTLRPRFKII 180
GSEFTTIENQ FWFPAIYRRH RGGSVTVYCG GSLISPCWVI SATHCPIIDY KKEDYIVYLG 240
RSLRNSNTQG EMKFEVENLI LHKDYSADTL AHNDLALLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCEITGPGK ENSTDYLYPE QLMQIVVKLI SHRECQPHY YGSEVTTKML 360
CAADPQWKTD SCQDSSGGPL VCSLQGRMTL TGIVSWGRGC ALKDKPGVYT RVSHFLFWIR 420
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Seq ID NO: 415 DNA sequence  
Nucleic Acid Accession #: NM\_024422.1  
Coding sequence: 202..2907

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GCTCCGSCCG CGGCCCTGCG CCGCGGAGC CCTCCTACCC CGGCCGACG CTGCGGCGCG 180
GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCTC CGGCTCCTG GAACGGAGCC 240
CTCTGCGCGC TGCTCCTGCT GACCCCTGCG ATCTTAATAT TTGCCAGTGA TGCCCTGAAA 300
AATGTGACAT TACATGTTCT CTCCAACTA GATGCGGAGA AACTTGTGG TAGAGTTAAC 360
CTGAAGAGAG GCTTTACAGC TGCAAACTA ATTCAATCAA GTGATCCTGA CTTCCAAATT 420
TTGGAGAGTG GTTCAGTCTA TACAACAAAT ACTAATCTAT TGTCCTCGGA GAAGAGAAAT 480
TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAGA AGAAATATT TGTCTTTTGG 540
GAGCATCAA CAAGGTCTCT AAAGAAAAGA CATACTAAG AAAAGTTCT AAGGCGCGCC 600
AAGAGAAGAT GGGCTCCAAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
CTTTTCTCTC AACAGGTTCA ATCTGACAGC GCCCAAAACT ATACCATATA CTATTCCATA 720
AGAGGTCTCG GAGTTGACCA AGAACCTCGG AATTATTTT ATGTGGAGAG AGACACTGGA 780
AACTGTGATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
TTTGCAACAA CTCCAGATGG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900
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GACACAGATG ACACACGCTC GAAGTACTCC ATCAATGGGC AGGTGCCACC ATCACCCACC 1080
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CGTCTTTCTT ATCAGAATTA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
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TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGGAGG ACACCAGACC 2580  
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 15 AATTAAGTGT TCATGTGGTG CTTGGAACCT GTTGTTTTCC TGAACATCTA AAGTGTGTAG 3360  
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 TTTCTAGCCA GGCATTGACT ATTACAAATT CATT

Seq ID NO: 416 Protein sequence

Protein Accession #: NP\_077740.1

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 ANLIHSSDPD FQILEDGSVY TTNITLLSSE KRSPTILLSN TENQEKKIP VFLEHQTKVL 120  
 25 KRRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQVQV SDTAQNYTII YSIRGPGVDQ 180  
 EPRNLFYVER DTGNLYCTRP VDREQYESPE IIAFATTPDG YTPRLPLPLI IKIEDENDNY 240  
 PIFTEETTF TIFENCRVGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300  
 TGVITTTSSQ LDRELIDKYO LKIKVQMDMG QYFGLQTTST CIINIDVDND HLPFTTSTY 360  
 30 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNPKIVTDA KTNESVLCV 420  
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 35 VTSLDVTLCD CITENDCTHR VDPRIKGGGV QLGKMAILAI LLGIALLPFI LEFTVCGASG 720  
 TSKQPKVID DLAQNLIVS NTEAPGDDKV YSANGPTTQT VGASQGVGC TVSGSIKNGG 780  
 QETIEMVKGQ HQTSESCRGH GHHTLDSR GGHTEVDNCR YTYSEWSFT QPRLGEKVYL 840  
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Seq ID NO: 417 DNA sequence

Nucleic Acid Accession #: NM\_004949.1

Coding sequence: 202..2745

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 50 GACCTGCCCC GAGCCCTCTC CATGAGAGGA GCCCGCCCTC CGGCTCTCTG GAACGGAGCC 240  
 CTCGCGCGCG TGCTCTGCTG GACCTCGCG ATCTTAATAT TTGCCAGTGA TGCCCTGCAA 300  
 AATGTGACAT TACATGTTCC CTCCAAACTA GATGCGGAGA AACTGTGTGG TAGAGTTAAC 360  
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 TTTATAGTGC AATAAAATGT AATTAATCA AGTCCTTATT ATAGACTATT TGAAGCACAA 3300  
 CCTAATGAAA AATTGTAGAG ACCTTGCTTT AACATTATCT CCAGTTAATT AAGTGTTCAT 3360  
 GTGGTGCTTG GAAACTGTTG TTTTCTGAA CATCTAAAGT GTGTAGACTG CATCTGTGCT 3420  
 20 ATTATTTTAT TCTTGTAAAG TGACCTTTTC ACTGTGCAA GGGAGATTTC TAGCCAGGCA 3480  
 TTGACTATTA CAATTTCATT

Seq ID NO: 418 Protein sequence  
 Protein Accession #: NP\_004940.1

25 1 11 21 31 41 51  
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFDA 60  
 ANLIHSSDPD FQILEDGSVY TINTILLSSE KRSPTILLSN TENQEKKKIP VFLEHQTKVL 120  
 30 KRRHTRKEKVL RRAKRNRWAPI PCSMLENSLG PFFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180  
 EPRNLFFYVER DTGNLYCTRP VDREQYESPE ILAFATTPDG YTPFLPLPLI IKIEDENDNY 240  
 PIFTEETTYF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSLIGQVPP SPTLFSMHPY 300  
 TGWITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360  
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNB NGNFKIVIDA KTNBGLCVV 420  
 35 KPLNYBEKQO MILQIGVVNE APPSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480  
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540  
 KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SABIYVAVDP 600  
 EPIHGPPFDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFSGYVVPF TVRDLRGMSS 660  
 VTSLDVTLCD CITENDCTHR VDPRIIGGGV QLGKMAILAI LLGIALLLPCI LPTLVCGASG 720  
 40 TSQKPKVIPD DLAQQLNLIYS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780  
 QETIEMVKGQ HQTSESCRGA GHHHTLDSR GGHTEVDNCR YTYSEWHSFT QPRLGEESIR 840  
 GHTLIKN

Seq ID NO: 419 DNA sequence  
 Nucleic Acid Accession #: NM\_002722.1  
 Coding sequence: 14..301

45 1 11 21 31 41 51  
 ACTCTGGACT COGGATGGCT GCGGCACGCC TCTGCTCTC CTGCTGCTC CTGTCCACCT 60  
 50 GGTGGCTCT GTTACTACAG CCACTGCTGG GTGCCCAGG AGCCCCACTG GAGCCAGTGT 120  
 ACCCAGGGGA CATGCCACA CCAGAGCAGA TGGCCAGTA TGCAGCTGAT CTCCTAGAT 180  
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAGACA CAAAGAGGAC ACGCTGGCCT 240  
 TCTCGGAGTG GGGGTCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGACTTAT 300  
 55 AATGCCACTT TCTGCTCTCT ACAGCTCCAT GAGCAGCGCC AGCCAGCTC TCCCTCTGC 360  
 ACCCTTGGCT CTGGCCAAAG CTTGCTCCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420  
 AAGCC

Seq ID NO: 420 Protein sequence  
 Protein Accession #: NP\_002713.1

60 1 11 21 31 41 51  
 MAAARICLSL LLLSTCVALL LQPLLAGAQA FLEPVYPGEN ATPBQMAQA ADLRRYINML 60  
 65 TRPRYGRKHK EDTLAFSEWG SPFAAVPREL SPLDL

Seq ID NO: 421 DNA sequence  
 Nucleic Acid Accession #: NM\_032545.1  
 Coding sequence: 46..718

70 1 11 21 31 41 51  
 AAAGTGAATC TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAATGA CCTGGAGGCA 60  
 CCATGTCAGG CTCTGTGTTA CGGTCAAGTT GGCATTACAG ATCATCAATT TGGGAACAG 120  
 75 CTATCAAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGTTG CCACTCAGAA 180  
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCAATTC GGAGAGGTGA CTGGGAGGCG 240  
 OGAGGCGTGG GGGCGGAGG AGCCGCTCCC CTACTCCCGG GCTTTCGAG AGGGTGGGTC 300  
 CGGCGGGCGG CGCTGCTGCA GGAAOCCGGG TACTGGGTG CTGGGAGCT TCTGCGTGTG 360  
 CCGGCGCCAC TTCACCGGCC GCTACTGCGA GCATGACCAG AGGCGCAGT AATGCGGCGC 420  
 CCTGGAGCAC GGAGCCTGGA CCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGCG 480  
 80 CCTGCACTGC CTCCCTCTCC AGACGCTGCA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540  
 CCAAGCTCAC GGGCGGAGCG CGGGGGGCGC GCCAGGCTG CTACTCTTGC TGCCCTGCGC 600  
 ACTCTGCAC CGCTCTCTGC GCCCGGATGC GCCCGGCGC CCTGGGTCCG TGGTCCCTTC 660  
 CGTCTCTCAC CGGAGCGGCG GCCCTGCGG AAGGCGGGA CTGGGCGATC GCCTTTAATT 720  
 TTCTATGTTG TAAATAATAG ATGTGTTAG TTTACGTAA GCTGAAGCA TGGGTGAATA 780



TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840  
AAAAAA

Seq ID NO: 422 Protein sequence  
Protein Accession #: NP\_115934.1

1 11 21 31 41 51  
| | | | |  
10 MTRHHVRLR FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSEHGE 60  
VTGSAEGWGP EEPFYPSRAF GEGASARPRC CRNGGTCVLG SFCVCPAHPF GRYCEHDQRR 120  
SEGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHANGP SAGGAPSLLL 180  
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPGRPLGLG HRL

Seq ID NO: 423 DNA sequence  
Nucleic Acid Accession #: NM\_006533.1  
Coding sequence: 72..467

1 11 21 31 41 51  
| | | | |  
20 AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60  
CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120  
TCTCCGGACC TGGTGTGAGG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180  
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240  
CGAGTCCCG ATTCTGAGC ATTACCCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300  
25 AGGGCCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360  
CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAAGCC CTGAAACCTG 420  
GCAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CAGTGAGCT CAGCCTACCG 480  
CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAATAC AATCAGCCCA GTGCAAAC

Seq ID NO: 424 Protein sequence  
Protein Accession #: NP\_006524.1

1 11 21 31 41 51  
| | | | |  
35 MARSLVLCGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LDYMAPDCR 60  
FLTIHRGQVY YVFSKLKGRG RLPWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120  
VKTDKWFYFC Q

Seq ID NO: 425 DNA sequence  
Nucleic Acid Accession #: NM\_080870.1  
Coding sequence: 3..710

1 11 21 31 41 51  
| | | | |  
45 AGATGACACA AGTCACAGAA AAGTCCACAG AACACCCAGA AAAGACCAG TCAACCCAG 60  
AGAAAACACC AAGAACCACA GAAAAGCCTA CGCTATACTC AGAGAAGACC ATATGCACCA 120  
AAGGGAAAAA CACACCACTG CCAGAAAAGC CTACAGAAAA CTGGGGAAAC ACCCACTGA 180  
CCAATGAGAC CATAAAAAGC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240  
TCACAAAGAC TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300  
50 CTCTCTCATCT AAATAAAACT GAAGTTACTC ATCAGGTGCC CACTGGTTCT TTCACCTCA 360  
TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAAGC CACAGGAAAC GAGAGCCATC 420  
CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAATG 480  
ATTCACTCC TGCAATGGGC ATAGTTATTG TGGTCTTGGT GGCTGTGATT CTCCTCCTGG 540  
TGTTCTTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACACGCCCG ACATAAACC 600  
55 AGAARACCCA GTACAATGAT GCAGAGGATG AGGGTGGGCC CAATTCTCTAC CCGGTCTACC 660  
TGATGAGCA GCAGAACTCT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGGAGTA 720  
GGCGCCACGC CCTGGCTCTT CCATGCTCTG CCCCCTTCTT GGATGAGGAA COGGACTCAC 780  
AATTTCATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAACC 840  
CTTCATCTGT TCTTGAAACT GGTGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT 900  
60 AGGGGACAAA GAAGAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGGT 960  
CTGAGAATGA AAAGGTGTTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC 1020  
TGAGTCTTAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080  
GGTTTATGGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140  
TTATTTCCAT TCACTATTAC TTAAGAGTTT GTGTGTAAC AGGCTCATCT CTGAGTTCTC 1200  
65 AGGACCCCTG CCCCACCCC CATTTTTFTA ATGAAAAAA AAAACAAAAA AAACGGATCC 1260  
AAGAAGAAAA GAGAATTAT TFCCTTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAGT 1320  
CCAGAAGAAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTTCTT CCAAAATCCC 1380  
TTAGTTTTC TAAATGTCTA CAGTGGACGC CCTGTGGT TGGCTTGCTG GGTGTGGGT 1440  
70 GGACACGCAA GGAGGGGATT TTTATTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500  
GACCTTCCCT GATTGGTGTG TCAGCATTFA TTTTCTGTG TCTTCCACCA AAAGCCAGCT 1560  
GTAGCTTTAT CTGGTAAAG TTACCATCT TCTCTACTGT CCCCATTCTC TCTCCTOCCA 1620  
CCTTCACCCC AGATTCAAGT TTCTCTCTT GTAGGCATT CATCTGTGTG TGTTTCTGG 1680  
75 ATTTTCTCTC TCTCTCTTA TGGCATTTT ACCTTATTAC TGATTGGGTA GAGGGGAAA 1740  
AGGAGATGA TGATGATAGT TTCTTCTGT CTATTGACCT TTTTATAAT AAAGTATAAC 1800  
ATGT

Seq ID NO: 426 Protein sequence  
Protein Accession #: NP\_543146.1

1 11 21 31 41 51  
| | | | |  
80 MTQVTEKSTE HPEKITSTTE KTRTPKEPT LYSEKTICTK GRNTFVPEKP TENLGNITLT 60  
TETIKAPVKS TENPETAARV TKTIKPSVKV TGDKSLTTTS SHLAKTEVTH QVPTGSFTLI 120  
TSRTELSSIT SEATGNESHV YLNRDGSQKQ IHAGQMGEND SPPAWAIVIV VLVAVILLLV 180

FLGLIFLVSY MMRTRRTLQ NTQYNDAEDB GGPNSYFVYL MBQQNLGMGQ IPSPR

Seq ID NO: 427 DNA sequence

Nucleic Acid Accession #: XM\_069480.1

Coding sequence: 1..4383

5

1	11	21	31	41	51	
1	ATGGACACTG	TGCTGGTGCT	GCTCCTGGGC	CTGCAGGCCT	TGGCOGGACC	CAGTCCGAAG 60
10	CCCCAGAAGG	ACTCTGTCTC	AGACTGGGCC	ATTGTGTGTA	TCACCTCTAC	TTTGGTGGCA 120
	GCAATTGTCA	GCCTAATGTA	CGGTATCAAG	AAGGCCTGCC	AGTTCCGGAG	GGAGATGAGT 180
	CTGGGGTGTG	GCTGTGGCTC	TGTGACCCCT	TACAGCAGCC	ACCATGAGGG	GGAGGCTGCC 240
	AGCCAGCGCT	ACTCTGTGTA	AATGAAAGCT	TCTTGGGGGG	CAGGTGCTAC	TACATTCCAA 300
15	GAATATCAGA	AAACTGGGGA	ACTCTCAACA	TCOGATCACA	TATTTCCCTT	CACTCCAGGC 360
	CTTGTTTATA	GTATCCCTTT	TGATCACAAT	GTTCTGCATT	CAGGACAAAG	ACCTCCAGAG 420
	CTCCCTAAAT	CTACAGAAAT	CCATGAGCAA	AAACGCCACT	GCAACACCAC	ACGCCATTCT 480
	AAGCCAACTG	ACAAGCCCTAC	AGGCCAACTCC	AAAACATAG	ACCACAAAAG	CTCTACAGAT 540
	AATCATGAGG	CTCCTCCAC	TTCTGAAGAA	AACTCCAGCA	ACCAAGGGAA	AGACCCAATG 600
20	ATCOGGAACC	AGCGCTCTGT	TGATCCTGCT	GACTCCACTA	CCACACATAA	AGAATCCGCT 660
	GGAAAAAACC	ATATAACGCC	AGCACCCAAG	AGCAAAATAA	ACTGTGCTAA	GTCCACAACA 720
	GGCAAAATCAA	CGGTAAACAAG	AAAATCAGAT	AAAACCTGAA	GACCTTTGGA	AAAGTCCATG 780
	AGTACTTTGG	ATAAGACAAG	TACCAGCTCA	CATAAGACTA	CAACTTCCTT	CCACAACCTA 840
	GGCAATTTCAC	AGACCAAGCA	AAAAAGCACA	TCTTTTCCAG	AAAAAATCAC	AGCAGCCTCA 900
25	AAAAACAAT	ACAAGACCAC	AGGAACCCCA	GAAGAGTCAG	AAAAAATGTA	AGATTCCAGA 960
	ACAACAGTTG	TCCAGACAAA	GCTCCTGACA	AAAACCTACA	AAAACATACA	AGAGACCTATA 1020
	TCAGCCAAATG	AGCTCACACA	ATCTCTAGCA	GAGCCTACAG	AACATGGAGG	AAGGACAGCC 1080
	AATGAGAACA	ACACACCATC	CCCAGCAGAG	CCTACAGAAA	ATAGAGAAAG	GACAGCCAAT 1140
	GAGAACAACA	CACTATCCCC	AGCAGAGCCT	ACAGAAAATA	GAGAAAGGAC	AGCCAATGAG 1200
30	AACACCCGAC	CATTCCCAGC	AGGGCCTACA	GAATAATAGAG	AAATGACAGC	CAATGAGATG 1260
	ACCACTATAT	TCCAGACAGA	GCCTACAGAA	CATGGAGAAA	GGACAGCCAA	TGAGAACACC 1320
	ACACCATCCC	CAGCAGAGCC	TACAGAACAT	GGAGAAAGGA	CAGCCAATGA	GAACACTACA 1380
	CCATCCCCAG	CAGAGCCTAC	AGAACATGGA	GAAAGGACCC	CATTGGCCAA	TGACAAAACC 1440
	ACATCATCTT	CAGCAGAGTC	TACAGAACAT	GGAGAAAGGA	CCCCACTGSC	CAACGAGAAC 1500
35	ACCAACCATAT	CCCCAGCAGA	GCCTACAGAA	AATAGAGAAA	GGACAGCCAA	TGAGAACACC 1560
	ACACCATCCC	CAGCAGGCCC	TACAGAAAAC	AGAGAAAACG	CAGCCAAACG	GAAGACCAAC 1620
	CTATCCCCAG	TAGAGCCTAC	AGAAAATAGA	GAAACAACAG	CCAATGAGAA	GACCACACCA 1680
	TCCCCAGCAG	AGCCTACAGA	AAATGGACAA	AGGACCCCAT	TTGCCAATGA	GAAAACCAAC 1740
40	TCATCCTCAG	CAGAGCCTAC	AGAACACGGA	GAAAGGACCC	CACTGGCCAA	TGAGAACACC 1800
	ACACCATCCC	CAGCAGAGCC	TACAGAAAAT	AGAGAAAGGA	CAGCCAATGA	GAAGACCAAC 1860
	CCATCCCCAG	CCTCAGCAGA	AGAAAATGGA	GACAGGACTC	CTTTGGCCAA	TGAGAAGACC 1920
	ACGCCATCTC	TAGCAGAGCC	TACAGAAAAT	GGACAAAGGA	CCCCATTGTC	CAATGAGAAG 1980
	ACCAATCAT	CCTCAGCAGA	GCCTACAGAA	CACGAAGAAA	GGACTCCACT	GGCCAATGAG 2040
45	AACACACAT	CATCCCOCGC	AGAGCCTACA	GAAAATAGAG	AAAGGACAGC	CAATGAGAAC 2100
	ACCAACCAT	CCCCAGCAGG	GCCTACAGAA	AATAGAGAAA	TGACAGCCAA	CGAGAAGACC 2160
	ACACTATTCC	CAGCAGAGCC	TACAGAAAAT	AGAGAAAGGA	CAGCCAATGA	GAAGACCAAC 2220
	TCATCCCCAG	CAGAGCCTAC	AGAAAATGGA	CAAAGGACCC	CATTGGCCAA	TGAGAAAACC 2280
	ACATCATCCC	CAGCAGAGCC	TACAGAACAC	GGAGAAAGGA	CCCCACTGTC	CAATGAGAAC 2340
50	ACCACTATAT	TCCAGACAGA	GCCTACAGAA	AATAGAGAAA	GGACAGCCAA	TGAGAAGACC 2400
	ACACCATTCC	CAGCAGAGCC	TACAGAAAAT	AGAGAAAGGA	CAGCCAATGA	GAACACCAAC 2460
	CCATCCCCAG	CAGAGCCTAC	AGAAAATGGA	GACAGGACTC	CATTGGCCAA	TGAGAAGACC 2520
	ACACCATCTC	TAGCAGAGCC	TACAGAAAAT	GGAAAAGGGA	CCCCATTGTC	CAATGAGAAG 2580
	ACCACTATAT	CCTCAGCAGA	GCCTACAGAA	CACGCAGAAA	GGACTCCACT	GGCCAATGAG 2640
55	AACACACAT	CATCCCOCGC	AGAGCCTACA	GAAAATAGAG	AAAGGACAGC	CAATGAGAAG 2700
	ACCACTATAT	TCCAGACAGA	GCCTACAGAA	AATAGAGAAA	GCACAGCCAA	TGAGAAGACC 2760
	ACACCATTCC	CAGCAGAGCC	TACAGAAAAT	AGAGAAAGGA	CAGCCAATGA	GAACACCAAC 2820
	CTATCCCCAG	CAGAGCCTAC	AGAACATGAA	GAAATGACCC	CATTGGCCAA	TGAGAAGACC 2880
	ACACTATCCC	CAGCAGAGCC	TACAGAAAAT	GGAGAAAGGA	CCCCATTGTC	CAATGAGAAG 2940
60	ACCACTATAT	CCTCAGCAGA	GCCTACAGAA	CATGGAGAAA	GGACCCCACT	GGCCAATGAG 3000
	ATCACCCAC	CATCCCOCGC	AGAGCCTACA	GAACATGGAG	AAAGGATAGC	CAATGAGAAG 3060
	GCCACACCAT	CCCCAGCAAA	GCCTACAGAA	CATGGAGAAA	CGACAGTCAA	TGAGGACACC 3120
	ACACCATCTT	CAGCAGAGCC	TACAGAAAAT	GGAGAAAGGA	CCCCACTGTC	CAATGAGAAG 3180
	ACCACTATAT	CCCCAGCAGA	GTCTACAGAA	CATGGAGAAA	GGACAGCCAA	TGAGAAGACC 3240
65	ACACCATCCC	CAGCAGAGCC	TACAGAACAT	GGAGAAAGGA	CAACATCAGC	CAATGAGAAG 3300
	ACCATACCAT	CTCCAGCAAA	GCCTACAGAA	CACGAAGAAA	TGACCCCATC	GGCCAATGAG 3360
	AACACACAC	CATCCCOCGC	AGAGCCTACA	GAACATGGAG	AAAGACTTAC	ATTGGCCAAT 3420
70	GAGAAGATCA	CACTATCCCC	AGAAAGGCTT	ACAGAACATG	GAGCAAAAAC	TAGTGGGCC 3480
	AATGAGAAGA	TCACACCATC	CCTAGCAAAG	CCTACAGAAC	ATGGAGAAAG	GACCACTACA 3540
	CCCAATGACA	AGATCACCTC	ATCTGCAGCA	GAGTCTACAG	AACATAGAGA	TAGGGCTACA 3600
	TCAGCCCAATG	TGATCACACC	AGCCCCAGCA	GAGCCTATAA	AACATGCAAA	AAGGAACACA 3660
	TTGGCCCATG	AGAAGATGAC	ACAAATGACA	GAAAAGTCCA	CAGAACACCC	AGAAAAGACC 3720
75	AGCTCAACCA	CAGTCAAAAAC	CACAGAAACC	CCAGAAAAGC	CTACGCTATA	CTCAGAGAAG 3780
	ACCATATGCA	CCAAAGGGGA	AAACACACCA	GTCCAGAAA	AGCCTACAGA	AAACCTGGGG 3840
	AAACACACAC	TGACCACTGA	GACCATAAAA	GCCCCAGTAA	AGTCCACAGA	AAACCCAGAA 3900
	AAACACAGCAG	CAGTCAAAAAC	GACTATAAAA	CTTTCAGTCA	AGGTACACAG	AGACAAATCT 3960
	CTCACTACTA	CCTCTCTCTA	TCTAAATAAA	ACTGAAGTTA	CTCATCAGGT	GCCCACTGGT 4020
80	TCTTTACCCC	TCATTACATC	TAGAAAGGAG	CTGAGTTCTA	TCACATCAGA	AGCCACAGGA 4080
	AACGAGAGCC	ATCCATACCT	CAATAAAGAT	GGCTCAGAGA	AAGGTATCCA	CGCTGGACAG 4140
	ATGGGAGAGA	ATGATTTCAT	CCCTGCATGG	GCCATAGTTA	TTGTGGTCTT	GGTGGCTGTG 4200
	ATTCTCCTCC	TGGTGTCTCT	TGGCCTGATC	TTCTTGGTCT	CCTATATGAT	GCGGACACGC 4260
	CGCACACTAA	CCAGAAACAC	CCAGTACAA	GATGCAGAGG	ATGAGGCTGG	CCCAATTCTC 4320
	TACCCGGTCT	ACCTGATGGA	GCAGCAGAA	CTTGGCATGG	GCCAGATCCC	TTCACACCG 4380

TGA

Seq ID NO: 428 Protein sequence  
Protein Accession #: XP\_069480.1

	1	11	21	31	41	51	
5	MDTVLVLLLG	LQALAGPSPK	PQKDSVSDWA	IVLITLTLVA	AIVSLMYGIK	RACQFRREMS	60
	LGCGCGSVTP	YSSHHEGEAA	SQRYSCQMK	SWGAGATTFO	EYQKTGELST	SDHIFPLTPG	120
	LVYSIPFDHI	VLSHGQRPPE	LPKSTEIHEQ	KRHQNTTRHS	KPTDKPTGNS	KTIDHKSSTD	180
10	NHEAPPTSEE	NSSNQGDPM	IRNQSVDP	DSTTHKESA	GKQHITPAK	SKINCRKSTT	240
	GKSTVTRKSD	KTGRPLEKSM	STLDKSTSS	HKTITSPHNS	GNSQTKQKST	SPPEKITAAS	300
	KTTYKITGTP	EESEKTEDSR	TTVASDKLLT	KTTKNIQETI	SANELTQSLA	EPTEHGGRTA	360
	NENNTSPAE	PTENRERTAN	ENTTLSPAEP	TENRERTANE	NTAPFPAGPT	ENREMTANEN	420
	TTLPFAEPT	EGERTANENT	TPSPAEPTEH	GERTANENTT	PSPAEPTEHG	ERTPFANDKT	480
15	TSSSAESTEH	GERTPLANEN	TPSPAEPTE	NRERTANENT	TPSPAGPTEN	RETTANEKTT	540
	LSPVEPTENR	ETTANEKITT	SPAPTEENGQ	RTPPANEKTT	SSSAEPTENG	ERTPLANENT	600
	TPSPAEPTE	RETTANEKTT	TPSPAEPTE	DRTPANEKTT	TPSLAEPTE	QRTPPANEK	660
	TTSSSAEPTE	HEERTPLANE	NTTPSPAEP	ENRERTANEN	TPSPAEPTE	NREMTANEK	720
	TLFPAEPTE	RETTANEKTT	SSPAEPTE	QRTPPANEK	TSSPAEPTEH	GERTPLANEN	780
20	TTLSPAEPTE	NRERTANEK	TPFPAEPTE	RETTANENTT	PSPAEPTE	DRTPANEK	840
	TPSLAEPTE	GRTPPANEK	TTSSSAEPTE	HAERTPLANE	NTSSPAEPTE	ENRERTANEK	900
	TTQFPAEPTE	NRESTANEK	TPFPAEPTE	RETTANENTT	LSPAEPTE	EMTPLANEN	960
	TLSPAEPTE	GERTPFNEK	TPSSAEPTE	HGERTPLANE	ITPSRAEPTE	EHGERTANEK	1020
	ATPSPAKPT	HGETTVNEDT	TPSSAEPTE	GERTPLANEN	TTSPTESTE	HGERTANEK	1080
25	TPSPAEPTEH	GERTPSANEK	TPSPAEPTE	HEMTPSANE	NTTPSPVKPT	EHGERTLAN	1140
	EKITLSEPG	TEHGAKTSA	NEKITPSLAK	PTHEGERTTS	PNDKITSSAA	ESTEHDRAT	1200
	SANVITPAPA	EPIKHAKTSA	LAHEKMTQVT	EKSTHEPEKT	TSTTEKTRT	PEKPTLYSEK	1260
	TICTKGKQTP	VPEKPTENLG	NTLITSTIK	APVKSTENPE	KTAAVTKTIK	PSVKVTGDKS	1320
	LTTTSSHLNK	TEVTHQVPTG	SFTLITSRTK	LSSITSEATG	NESHPLYLND	GSQKGHAGQ	1380
30	MGENDSPFAM	AIVIVLVAV	ILLVFLGLI	FLVSYMMRTR	RTLQNTQYN	DAEDSGGPN	1440
	YFVYLMQQN	LGMGQIPSPR					

Seq ID NO: 429 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..10674

	1	11	21	31	41	51	
35	ATGTGGCCTC	GCTTGGCCTT	TTGTTGCTGG	GCTTGGCCTC	TGTTTTCGGG	CTGGGCGACC	60
	TTTCAGCAGA	TGTCCTCCCTC	GCGCAATTC	AGCTTCCGCC	TCTTCCCGCA	GACCGCGCCC	120
40	GGGGCCCCCG	GGAGTATCCC	CGCGCCGCC	GCTCCTGGCG	ACGAAGCCGC	GGGGAGCAGA	180
	GTGGAGCGGC	TGGGCGAGGC	GTTCCGCGCA	CGCTGGCGC	TGCTGCGGGA	GCTCAGCGAG	240
	CGCTGGAGC	TTGTCTTCTC	GTTGGATGAT	TGTTCCAGCG	TGGGCGAAGT	CAACTTCCGC	300
	AGCGAGCTCA	TGTTCTGCTG	CAAGCTGCTG	TCCGACTTCC	CGTGGTGGCC	CACGCGCAGC	360
	CGCGTGGCCA	TGCTGACCTT	CTGTTCCAG	AACCTAGTGG	TGCGCGCGGT	CGATTACATC	420
45	TCCACCGGCC	GCGCGCGCCA	GCACAAGTGC	GCGCTGCTCC	TCCAAGAGAT	CCCTGCCATC	480
	TCTACCGAG	GTGGCGGCAC	CTACACCAAG	GCGCCTTCC	AGCAAGCCGC	GCAAACTCTT	540
	CTTCATGCTA	GAGAAAACCT	AACAAAAGTT	GTATTTCTCA	TCACTGATGG	ATATTCCAAT	600
	GGGGGAGACC	CTAGAACCAAT	TGCAGCGTCA	CTGCGAGATT	CAGGAGTGGG	GATCTTCACT	660
50	TTTGGCATAT	GGCAAGGGAA	CATTGAGAG	CTGAATGACA	TGGCTTCCAC	CCCAAGGAG	720
	GAGCACTGTT	ACCTGCTACA	CAGTTTGAA	GAATTTGAGG	CTTTAGCTCG	CCGGGCAATT	780
	CATGAAGATC	TACCTTCTGG	GAGTTTAT	CAAGATGATA	TGTTCCACTG	CTCATATCTT	840
	TGTGATGAAG	GCAAGGACTG	CTGTGACCGA	ATGGGAAGCT	GCAAAATGTT	GACACACACA	900
	GGCGATTCTG	AGTGCATCTG	TGAAAAGGGG	TATTACGGGA	AAGGTCTGCA	GTATGAATGC	960
	ACAGCTTGCC	CATCGGGGAC	ATACAAACCT	GAAAGCTCAC	CAGGAGGAAT	CAGCAGTTGC	1020
55	ATTCCATGTC	CTGATGAAA	TCACACCTCT	CCACCTGGAA	GCACATCCCC	TGAAGACTGT	1080
	GTCTGACAG	AGGGATACAG	GGCATCTGGC	CAGACCTGTG	AACCTGTCCA	CTGCCCTGCC	1140
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	ACATGTTTGG	TTCCTGTGTA	TGAAGGTATC	AGACTAGAA	GCAGTGATA	GCTTACTTGT	1440
	CAAGGAACA	GCCAGTGGGA	TGGGCCAGAA	CCCGGTGTG	TGGAGCGCCA	CTGTTCACCC	1500
	TTTCAGATGC	CCAAAGATGT	CATCATATCC	CCCCACAAT	GTGGCAAGCA	GCCAGCCAAA	1560
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	GACGTGGAGG	CTCCTCAAA	CAACTGTCTC	AAGGACATAG	AGGCTAAGAC	TCGTGAACAG	1740
	CAAGATTCTG	CCAATGTTAC	CTGGCAGATT	CCAACAGCTA	AAGACAACCT	TGTTGAAAAG	1800
	GTGTCACTCC	AGCTTTCATC	AGCTTTCACC	CCACCTTACC	TTTTCCCAAT	TGGAGATGTT	1860
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	GTCTCGGAGA	AGGTACATGC	CGCAAGCTGG	GATGAGCTCT	AGTTCTCAGA	CAACTCAGGG	2040
	GCTGAATTGG	TCAATTACAG	AAGTCATACA	CAAGGAGACC	TTTTCCCTCA	AGGGGAGACT	2100
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	GAAGGGTCTA	CTGCAAGTA	TTATTGTGCT	TATGAAGATG	GCGTCTGGAA	ACCAACATAT	2340
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	GAAGATGCT	TTGCAATTGG	ACCAGGTGGC	TGGGGTGCG	CTAATAGGCT	GGATTAATCT	2640
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 20 TPUVIEGTVN GTDFDCGKAA RIQCFKGFKL LGLSEITCEA DGQWSSGPPH CEHTSCGSLP 3060  
 MIPNAFISST SSWKENVITY SCRSGYVIQ SSDDLICTEK VWSQYPVCE PLSCGSPSPV 3120  
 ANAVATGRH TYSEVILRC LEGYTMDDT DTFTQKDKR WFFERISCSP KRCPLPENIT 3180  
 HILVHGDDFS VNRQVSUSCA EGYTFEGVNI SVCQLDGTWE PPFSEDESCP VSQGPESPE 3240  
 HGFVVGSKYT FSTIIYQCE PGYELGNRE RVCQENRQWS GGVAICKETR CSTPLEFLNG 3300  
 25 KADIENTTGT PNVAYSCNRG YSLEGPSEAH CTENGWSPH VPLCKPNPCP VPFVIPENAL 3360  
 LSEKEFVVDQ NVSICKREGL LLQGEHIITC NPDETWTQTS AKCEKISOGP PAHVENAIAR 3420  
 GVHYQYQDMI TYSCYSGYML EGFRLSVCLC NGTWTSPIC RAVCRFPQCN GGICORFNAC 3480  
 SCPEGWNGRL CHEPICILPC LMGGRCVAPY QCDCEPFWTG SRCHTAVQCS PCLNGGKCVR 3540  
 30 PNRCHCLSSW TGHNCSR

Seq ID NO: 431 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..390

35 1 11 21 31 41 51  
 | | | | | |  
 ATGAGGTTCA GTGTCTCAG CATGAGGACC GACTACCCCA GAGTGTGTCT GGCTCCTGCT 60  
 TATGTGTCTAG TCTGTCTCT CCTCTTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA 120  
 40 GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTGGGAG 180  
 CAGTGTCTGT ACAATGAGCG CATCGTGTCC CTGAGGAGCA CCGCCCAATG TGGTCCCCC 240  
 TGCACCTTCT GGCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAACGAT 300  
 TTTGTGTGA AGCTGAAGGT TCAGGGGTGTG AATTCACAGT GCCACTATC TCCATCTCC 360  
 AGTAAATGTG AAAGAGGCGG GATATGTTAG

45 Seq ID NO: 432 Protein sequence  
 Protein Accession #: FGENESH predicted

50 1 11 21 31 41 51  
 | | | | | |  
 MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLQCPAPR CGDKIYNPLE 60  
 QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLVQGV NSQCHSSPIS 120  
 SKCERGRIC

55 Seq ID NO: 433 DNA sequence  
 Nucleic Acid Accession #: NM\_007231.1  
 Coding sequence: 89..2017

60 1 11 21 31 41 51  
 | | | | | |  
 TAGGAACAGG GGAGAGTGCA CTGTCTACCA GTCAAGCTCA GCCAGACTGC AAGAGGAGGC 60  
 GAGGCGGAGC CAGCGAGGAG AGTGAAACAT GGACAAGTTG AAATGCCOGA GTTCTTCAA 120  
 GTGCAGGGAG AAGGAGAAAG TGTCCGCTTC ATCAGAGAAT TTCCATGTTG GTGAAATGA 180  
 TGAGAATCAG GACCGTGGTA ACTGGTCCAA AAAATCGGAT TATCTTCTAT CTATGATTGG 240  
 65 ATACGCACTG GGATTAGGAA ATGTGTGAGG ATTTCCATAT CTGACCTACA GCAATGGTGG 300  
 AGGCGCCTTC TTGATACCTT ATGCAATTAT GTTAGCATTT GCTGGTTTAC CTTTGTCTCT 360  
 TCTGGAGTGT TCACTGGGAC AATTGTCTAG CTTAGGTCCA GTTTCAGTTT GGAGGATTCT 420  
 TCCATTGTTT CAAGGTGTGG GAATTACAAT GGTCCTGATC TCCATTTTGT TGACAATCTA 480  
 TTACAATGTC ATAATTGCCT ATAGTCTTTA CTACATGTTT GCTTCTTTTC AAAGTGAAC 540  
 70 ACCATGGAAA AATTGTTCTT CGTGGTCTGA TAAAACTGT AGCAGATCAC CAATAGTAAC 600  
 TCACTGTAAT GTGAGTACAG TGAATAAAGG AATACAAGAG ATCATCCAAA TGAATAAAG 660  
 CTGGGTAGAC ATCAACAATT TTACCTGCAT CAACGGCAGT GAAATTTATC AGCCAGGGCA 720  
 GCTTCCACAGT GAACAATATT GGAATAAAGT GCGCTCCAAA CGGTCAAGTG GAATGAATGA 780  
 GACTGGAGTA ATTGTTTGGT ATTTAGCACT TTGTCTTCTT CTGGCTTGGC TCATAGTTGG 840  
 75 AGCAGCACTA TTTAAAGGAA TCAATCGTC TGSCAAGGTG GTATATTTTA CAGCTCTTTT 900  
 CCCCATGTGT GTCCCTACTCA TCTCTGTAGT ACGAGGTGCA ACTCTGGAGG GTGCTTCAAA 960  
 AGGCATTGTC TACTATATTG GAGCCCACTC AAATTTTACA AAACCTAAGG AAGCTGAGGT 1020  
 ATGGAAGAT GCTGCCACTC AGATATTTTA CTCCCTTCA GTGGCTTGGG GTGGCTTAGT 1080  
 TGCTCTATCA TCTTACAATA AGTTCAAAAA CAACCTGCTC TCTGATGCCA TTGTGTTTGG 1140  
 80 TTTGACAAA TGTCTCACTA GCGTGTGTC TGGATTGCTT ATTTTCTCTA TATTGGGACA 1200  
 CATGGCCCAT ATATCTGAAA AGGAAGTTTC TCAAGTTGTA AAATCAGGTT TTGATTGGC 1260  
 ATTCTATGCC TATCCAGAGG CTCTAGCCCA ACTCCAGGT GGTCCATTIT GTCCCAATT 1320  
 ATTTTCTTTC ATGCTTTTAA CTTTGGGTCT CGATTCTCAG TTTGCTTCCA TTGAAACGAT 1380  
 CACAACAACA ATTCAGATT TATTTCCCAA AGTGATGAAG AAAATGAGGG TTCCCAATAAC 1440  
 TTTGGGCTGC TGCTTGGTTT TGTTCCTCTT TGGTCTGCTC TGTGTGACTC AGGCTGGAAT 1500

5 TAATTATGGC GCAATTCAC ACCCTGACTG GGGAGTTGCT TTAGGCTGCT GTATGATTGT 1800  
 TTCTGCAATT ATTTGGATAC CAATTATGCG TATCATAAAA ATAATTCAGG CTAAGGAAA 1860  
 CATCTTTCAA CGCCTTATAA GTTGTGTCAG ACCAGCTTCT AACTGGGGTC CATAOCTGGA 1920  
 10 ACACATCGT GGGGAAAGAT ATAAAGACAT GGTAGATCCT AAAAAAGAGG CTGACCATGA 1980  
 AATACCTACT GTTAGTGCCA GCAGAAAACC GGAATGAGAT CTCATTGAAA AAAATATATG 2040  
 ATTGTATAAT GTGATTTTTT TTAGAATAGG GGGAACTTAA TTTATTGTG TGTAACTGA 2100  
 ATAGGAAAAAT GTACATACTA TGTTCATGAT AGTGTGATT TTTTCACATT TAAGCAGGAA 2160  
 TGCAATATAA AAATGTGAAT CTCTTAATTC TCAGCCATGT GCTTATTATA TTTCTTTTTA 2220  
 GATTGTCTAT CTGTATAACA CACACACACA CACCTAAGAG TCTCTATTTC ACAATTATAT 2280  
 15 TTTTGTAAAT AGTATATGCA TTTTAAATAC ATTGGAGGCT TTATTTTGAA CTAATTTCTT 2340  
 AGAGAATAGT TATATTTTCT ATTACACAAG TTTAAAAATA TTATTAACTT GTATTTTCTT 2400  
 AATATACAACT CTATCTTTTC CACAAATATG AGTGGGAAAT AAATCAGCAC ATTTGGAAGA 2460  
 AAGTGTAAAA AACTGAAGCC TCACTTAATT AGAAAACGTGA TAAATATATG GACAAATGGA 2520  
 CTATACATAC TATAAGAGGA CTGTAGTTTA ATACTTTTTA CCCAAATATG TTTAAAAACA 2580  
 20 TCGTGCATTG GTTACAGCTC ATGTTTTCTA TATGAACCTA GTCATTAAAT TTTCTTTATA 2640  
 AAAGTGAAT AAAGATGGAA AATTAGGATC CTACAGCCAG TACGTGATAA ATCTAGAAAA 2700  
 TTGAGTTTGG AGTACCTCTT TTCCCATATA CAATCTTCCT TCCTTAGGTA ATTTGGAAGA 2760  
 AAATATGAC CCATTTAATT TCTATTGTGT TTCACCAAT TCAGTGTGTG TCATTATACC 2820  
 TCTCTGAAAT ATAGGTTTAA TTTCAAATAG AATATGGACT TAAATGTTAA TGAGAAACCTG 2880  
 25 GCTTTAATCA ATTCTAGCAT TTTATTACTG TAATACAGGG CTGATAGAGT GATTTTGTCT 2940  
 TATATGAGTC AGTTACTACT TACAGGTGAT AACTTGCATA CTATTGGAAG ATAAAGTTGT 3000  
 CAACTGTGTC AAGAAATGAGA AAAGCCAAAT TAGAAAATCC TATGTCCTAG TTTCTTACC 3060  
 AAGGATAATT AAATATATCA CTAAGAGCTT TATATATTGA TTATATATTG TTGCAACTG 3120  
 GTTTAAGCAT CATAGCCTAT GATGATAAAC ACTGCCTATA TATGTAAATA GCTTTTCATC 3180  
 30 AATCTCTAAA TTTCTTAAAC TAGGCTTCAG GGAGCATATG AAACCAAAAT TATATGGAAC 3240  
 ATTTCTGTG TGTACATGTA CATGCATTTT TCTAGGGAGA GAGTCCGTAG GTTTATCAGA 3300  
 ATATCAAGGA AAATGTGAC CCAAGAAAGT TTAAGAAATCA CATACAGTGC TGCTGGCTTT 3360  
 TTGTGCTTGG CAAATGAGTG ACAAAGAAG AAATAATTTT TCTTACACAT TTTAAACGT 3420  
 TTTCTCTCC TTGTGATTGA AGATGAAAGG AGTAAGAAAT TAAGGCATT GTTTAATTTA 3480  
 35 TACTGGTAAC TTATTAGGG GGGAGGGGAC ATGAAGGTAG GTAAATAGGT AGGCCCTTAA 3540  
 TTGAACCAAC CTCCTAAGTT ATGTACGTAT ATATAAGCTG AAATGTGTGT TGACATTCTG 3600  
 AGGGTTTTCT TTTCTTTTTT CCTTTTTTTT TTTTGTGCT GGGGGCTGG GGGTCAGAGT 3660  
 CTGTCTCTGT TGCCCTGGCT GGGATGCGCT GGCATGATCT CAGCTCACTG CAACCTCTGC 3720  
 40 TTCTCGGATT CAAGTGATTC TCCTGCCTCA GCCTCTTGAG TAGCTGGGAG TACAGGTGCC 3780  
 CGCCACCACA CCAGCTAATT TTTGTATTTT TAGTAGAGGC GAAGTTTCCC CATGTGGGCC 3840  
 AGGCTGCTCT TGAACCTCCG ACCTCAAGTG ATCTGTCTAC CTCGGCTCC TAAAGTGCTG 3900  
 AGATTACAGG TGTAGCCAC CGTGCCCGGC CCAATCTAAG GGTTTTCTTT GAAGCAGGT 3960  
 CAAATGCTGT TAGTAAGTTT CAGGAGATTG TTAATTCCTC AGTTATACCA GATTTTATAA 4020  
 45 AATATTTGAG AATAGATGGC TAACAGAGGG TTAGAAAATAC TTTTCTTAA TTTAATCCA 4080  
 CAGTATGTTA CATGCATCTC ACCACTACAT TTTGGTGCTA TTTAAGGTGT GCAATTTTCT 4140  
 ATAGGTGACT TTTGCAATTC AGGGAAGATT TGGGCATATT AAATGAAAGA ATATCTAATT 4200  
 GGGGGAGGTG TGAAGGGAAA GAAATTCITT TCAAAAGCTG ACCACAAGA GTAGTTAAAA 4260  
 GTTTTGTGCA CTATCTTCAC AAGTGTGTA AGCACAGATT TCAACAGAGT GCTTGGCATA 4320  
 50 TTGTAGGGTG CTCATGGTGT GTTTTATTAT TTATTACTCA GATTCCACAG TGGCAAGAAA 4380  
 CATCATCTCA CATAATGGAA AACATTACA TCAAATCCCA CTTACTTTAA TGCGAACTG 4440  
 GAGATAATTT ATGGTATTGT ATTGTAACAC ATTAATGAAA ACTTTTTTAC AGTTGAGTGA 4500  
 AATTAAAAATC ACTATATCTC

Seq ID NO: 434 Protein sequence  
 Protein Accession #: NP\_009162.1

55 1 11 21 31 41 51  
 MDLKLCPSEF KCREKEKVSA SSENPHVGEN DENQDRGNWS KKS DYLLSMI GYAVGLGNVW 60  
 RPPYLTYNSG GGAFLIPYAI MLALAGLPLF FLECSLGQFA SLGPVSVNRI LPLPQGVGIT 120  
 60 MVLISIPVTI YNVIYIAYSL YMFASFQSE LPWKNCSWS DENCSRSPIV THCNVSTVNK 180  
 GIQEIIMNK SWVDIINFCT INGSEIYQPG QLPSEIYWNK VALQRSSGMN ETGVIVWYLA 240  
 LCLLLAWLIV GAALFKGIKS SGKVVPYPTAL PYPVLLILL VERATLEGAS KGISYIYGAQ 300  
 SNPTKLKEAE VKDAATQIP YSLSVANGGL VALSSYNKPK NNCPSDAIVV CLTNCLTSVF 360  
 65 AGPAIFSIILG HMAHISGKEV SQVVKSGFDL APIAYPEALA QLPGGPPWSI LFFFMILLTG 420  
 LDSQFASIEI ITTTIQDLFP KVMKMRVPI TLGCLLVFL LGLVCVTQAG IYVHLIDHF 480  
 CAGWGLLIAA ILELVGIWI YGNNRPIEDT EMMIGAKRWI FNLWHRACWF VITPILLIAI 540  
 PIWSLVQFHR PNYGAIPYPD WGVALGWOMI VFCIIWIPIM AIKIIQAKG NIFQRLISCC 600  
 RPASNWGPYL BQHRGERYKD MVDPKKEADH EIPTVSGSRK PE

70 Seq ID NO: 435 DNA sequence  
 Nucleic Acid Accession #: M18728.1  
 Coding sequence: 51..1085

75 1 11 21 31 41 51  
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
 CCTCAGCCCC TOCCTGCAGA TTGCATGTCC CCGGAAGGA GGTCTGCTC ACAGCCTCAC 120  
 TTTAAACCTT CTGGAACCCA CCCACCACCT CCAAGCTCAC TATTGAATCC AOCGCATTCA 180  
 80 ATGTGACAGA GGGGAAGGAG GTTCTTCTAC TOGCCACAA CCGGCCACAG AATCGTATTG 240  
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
 TAGGAATCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TOGAGAGACA ATATACCCCA 360  
 ATGCATCCCT GCTGATCCAG AAGGTACACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
 TCATAAAGTC AGATCTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGAGC 480  
 TGCCCAAGCC CTCATCTCC AGCAACAAC CCAACCCCT GGAGGACAAG GATGCTGTG 540



5 CCTTCACTG TGAACCTGAG GTTCAGAAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600  
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCT ACTCTACTCA 660  
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
 ACCGCACTGA CCGAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780  
 CCTCAAGGCG CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840  
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
 10 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140  
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGCTCTG 1200  
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260  
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320  
 15 GCAAAACCATG GTGAGAAAT GAOGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380  
 AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440  
 TGCCCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAATAAAG 1560  
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620  
 AATGTACAG TGGTCTCTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT 1680  
 20 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800  
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860  
 CTGACTCATT CTTTATTCTA TTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
 25 CTCTTGGTAT TACCTCCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
 CTCTAAAGAG TTTAAATGTC TGCAATGCAG CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
 GGCTGGAATT ACAAAACCTA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
 ATAAAGCCCG CAATGTGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATCTC CAACTGAAAT 2220  
 30 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTAAAAA AAAAAAAGA 2280  
 ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340  
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400  
 TGTTCCTGT TCCCAATTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460  
 35 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520  
 TAGTCTTATA ACT

Seq ID NO: 436 Protein sequence

Protein Accession #: AAA59907.1

40 1 11 21 31 41 51  
 | | | | |  
 MGPFSAFPCR LHVPWKEVLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLAHNLQP 60  
 NRIGVSWYK ERVDGNLSIV GVVIGTQQT PGPAYSGRET IYPNASLLIQ NVTONDTGFY 120  
 TLQVIKSDLV NEEATGQPHV YPELKPSPIS SNNSNFVEDK DAVAFTEPE VQNTYLVWV 180  
 45 NGQSLPVSFR LQLSNGNMTL TLLSVKRND GSYECEIQNP ASANRSDPVT LNVLYGPDVP 240  
 TISPSKANYR PGENLNLSC AASNPPAQYS WFINGTFQOS TQELFIPNIT VNNSGSYMCO 300  
 AHSNATGLNR TTVTMITVSG SAFVLSAVAT VGITIGVLAR VALI

Seq ID NO: 437 DNA sequence

Nucleic Acid Accession #: M18728.1

Coding sequence: 1355..1657

55 1 11 21 31 41 51  
 | | | | |  
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
 CCTCAGCCCC TCCTTCGAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120  
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180  
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGGCCACAA CCTGCCCCAG AATCGTATTG 240  
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
 TAGGAACCTA ACAGACTACC CCAGGGCCCC CATACAGTGG TCGAGAGACA ATATACCCCA 360  
 60 ATGCATCCCT CGTATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480  
 TGCCCAAGCC CTCCTCTCC AGCAACAACCT CCAACCCCGT GGAGGACRAG GATGCTGTGG 540  
 CCTTCACCTG TGAACCTGAG GTTCAGAAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600  
 65 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCTC ACTCTACTCA 660  
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
 ACOGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780  
 CCTCAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840  
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
 70 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140  
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGCTCTG 1200  
 75 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260  
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320  
 GCAAAACCATG GTGAGAAAT GAOGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380  
 AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440  
 80 TGCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAATAAAG 1560  
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620  
 AATGTACAG TGGTCTCTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT 1680  
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800  
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860



5 CTGACTCATT CTTTATTCTA TTTTAGTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
CTCTTGGTAT TACCCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
CTCTAAAAGC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAC CAATTTAAAA AAAAAAAGA 2280  
ACACAGGAGA TTCCAGTCTA CTTGAGTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340  
10 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC 2400  
TGTTTCCCTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460  
CTATCACTGT ACTTGTAGAG TGGTGTCTCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520  
TAGCTCTATA ACT

15 Seq ID NO: 438 Protein sequence  
Protein Accession #: AAA59908.1

1 11 21 31 41 51  
20 MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SFAMQDDAVI SISQEVASEG NLTECQIYLV 60  
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELD

25 Seq ID NO: 439 DNA sequence  
Nucleic Acid Accession #: M18728.1  
Coding sequence: 2370..2501

1 11 21 31 41 51  
30 GGAGCTCAAG CTCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
CCTCAGCCCC TCCTCTCAGA TTGCATGTCC CTTGGAAGGA GGTCTGCTC ACAGCCTCAC 120  
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180  
ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATGTTATTG 240  
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
TAGGAATCTA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360  
ATGCATCCCT GCTGATCCAG AACGTACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
35 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGAGC 480  
TGCCCAAGCC CTCCATCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540  
CCTTCACCTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600  
GCCTCCCGGT CAGTCCCGAG CTGCAGCTGT CCAATGGCAA CATGACCCCTC ACTCTACTCA 660  
40 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAT ACAGAACCCA GCGAGTGCCA 720  
ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCTC 780  
CCTCAAGGCG CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCCAC GCAGCCTCTA 840  
ACCCACCTCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
TCTTATATCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
45 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
TCCTCTCAGC TGTTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
TATAGCAGCC CTGGTGTATT TTGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140  
GAATCTCTCT AGCTCTCTCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200  
CTCTGCTCCT GAAGCCCTAT ATGCTGAGGA TGGACAATC AATGAAAAAT TAAAGGGAAA 1260  
50 ACCCTCAGCG CTGAGGTGTG TGCCACTCAG AGACTTCACC TAAGTAGAGA CAGTCAAACT 1320  
GCAAAACATG GTGAGAAATT GACGACTTCA CACTATGAC AGCTTTTCCC AAGATGTCAA 1380  
AACAGAGCTC CTATCATGTA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440  
TGCTCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
GGGTAACTTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560  
55 AGATCCTTTA GTGCACCCAG TGAATGACAT TAGCAGCATC TTTAACACAG CGTGTGTTC 1620  
AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTTCTAGACT CACCTGTCTT CACTCCCTGT 1680  
TTTAATTCAA CCCAGCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800  
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATAGG CTACACTCAT 1860  
60 CTGACTCAIT CTTTATTCTA TTTTAGTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
CTCTTGGTAT TACCCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
CTCTAAAAGC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
65 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAC CAATTTAAAA AAAAAAAGA 2280  
ACACAGGAGA TTCCAGTCTA CTTGAGTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340  
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC 2400  
TGTTTCCCTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460  
70 CTATCACTGT ACTTGTAGAG TGGTGTCTCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520  
TAGCTCTATA ACT

75 Seq ID NO: 440 Protein sequence  
Protein Accession #: AAA59909.1

1 11 21 31 41 51  
MLTNVPISVV LPFCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

80 Seq ID NO: 441 DNA sequence  
Nucleic Acid Accession #: NM\_002381.2  
Coding sequence: 64..1524

1 11 21 31 41 51

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		ACCATGCCGC	GCCCGGCCGC	CGCGGCGCGC	CTCCGCGGAC	TCCTCCTGCT	GCTCTGGCGG	120
5		CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCCGGCTT	COGGAGGCTG	180
		GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCCGCCCTT	CTCCTGCGGC	TCCCGACGGC	240
		GCGCCCGCTT	CCGGGACGAG	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
		AGACCCCTGG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GCGTACGGCC	CCTGGAATTC	360
		ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
10		ACGCGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TOGAGTTCCA	ACTCCAGGCC	480
		TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGCGA	TCACACCCCT	GTCAACAGGC	540
		ACCATGTCAG	GCTGAGCCAT	CCAGACAGCA	ATGGACGAAG	CCTTCACAGT	GGAGGCGAGG	600
		GCTCGAGAGC	CCTCTCTTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCC	660
		CAGGACCAGG	TGAATGAAGT	GGCGGCTCGG	GCCCCAAGCAT	CTGGTATTGA	GCTCTATGCT	720
15		GTGGGGGTGG	ACCGGGGAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCCTAGAG	780
		GAGCATGTTT	TCTACGTGGA	GACCTATGGG	GTCAATTGAG	AACTTTCTCT	TAGATTCCAG	840
		GAAACCTTCT	GTGGCTGGA	CCCTGTGTGT	CTTGGAAACAC	ACCAAGTGCCA	GCACTGTCTG	900
		ATCAGTGATG	GGGAAGGCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
		GACAAGAAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
20		ATCTGTGTGA	ATGAACAGAG	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
		AATGAAGACA	GGAAAACTTG	TTCAGCTCAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
		CAGCACAATT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
		ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
		GGTTGCCAGC	ACATTTGTGT	GAGTGTAGGG	GCGCATCCTT	ACCACGTGTA	TTGCTATCCT	1320
25		GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTCAAGCCA	CTGAGGAAGC	ACGAAGACTT	1380
		GTTTCCACTG	AAGATGCTTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTGAGC	1440
		TCGTATCTTC	AAAGACTGAA	CACTAAACTT	GATGACATTT	TGGAGAAGTT	GAAAAATAAT	1500
		GAATATGGAC	AAATACATCG	TTAAATTGCT	CCAATTTCTC	ACCTGAAAAT	GTGGACAGCT	1560
		TGGTGTACTT	AATACTCATG	CAITCTTTTG	CACACCTGTT	ATTGCCAATG	TTCTGCTTAA	1620
30		TAATTTGCTA	TTATCTGTAT	TAATGCTTGA	ATATTAAGTG	ATAAATTTGA	TGAAGATCTT	1680
		CTGCAGAAAT	AGCATGATTT	TTCCAAGGAA	ATACATATGC	AGATACTTAT	TAAAGACAAA	1740
		CTTTAGTGTC	TCTAAGTTAT	GACTGTGAAA	TGATGGTAG	GAATAGAAAT	GAAAAGTTTA	1800
		GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AATTTTAAAT	TGTTTATATT	AGATAACCAT	1860
		ATTCACAATG	GAAACTTTAG	GTCTAGTTTC	TTTGTAGATG	ATTTATAATA	TAAATCAATC	1920
35		TTATTTAGTA	GAGTGCAAAT	TGTACAAGGT	ATTTACACAT	ACAACCTTCA	ATAACTGAGA	1980
		TGAATGTAAT	TTTGAACGTG	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
		TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAT	ACAGATCAAG	2100
		TGAACATTTAC	ATTGCCATTT	TTAATTCATT	CTGGCTTTTG	AAAGAAATGT	ACTACTAAAG	2160
		AGCACTAGTT	GTGAATTTAG	GGTGTAAAC	TTTITACCAA	GTACAAAAAT	CCCAAAATCA	2220
40		CTTTATTATT	TGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATAAA	ATTGCTATAA	2280
		ATCCGACAAA	TCTAATGTTG	TCTTTTTAAT	GTTAGTGATC	CACCTGCCTC	AGCCTCCCAA	2340
		AGTGCTGGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTTTTTA	CTTATATATT	TGATACATAT	2400
		AAATCTTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCCTTA	AATTTTGAC	2460
		TGCTCAATTC	TGTTTTTCGT	TTGCATTGTC	TTAATATAA	TAAAGTTTAT	TACCTTTACA	2520
45		TATTATCATG	TCTATTTTGG	ATGACTCATC	AATTTTGCTC	ATTAAAGATA	TTTCTTTAAA	2580
		TTAAAAAAA	AAAAAAA					

Seq ID NO: 442 Protein sequence  
Protein Accession #: NP\_002372.1

50	1	MPRPAPARRL	PQLLLLLLWPL	LLLPSAAPDP	VARPGFRRLR	TRPGGSGPR	RPSAAPDGA	60
		PASGTSEPR	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFFVSRII	DTLDIGPADT	120
55		RVAVVNYAST	VKIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTVRAGA	180
		REPSSNIPKV	AIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMASEPLEE	240
		HVFYVETYG	IEKLSRRFQE	TFCALDPCVL	GTHQCOHVCI	SDGEGKHCE	CSQGYTLNAD	300
		KKTCALDRD	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCQSAQ	KCALGTHGQ	360
		HICVNDRTGS	HHCECYBGYT	LNADKKTCVS	RDKCALGSHG	CQHICVSDGA	ASYHCDYCPG	420
60		YTLNEDKKT	SATEEARRLV	STEDACGCEA	TLAPQDKVSS	YLQRLNTKLD	DTLERLKINE	480
		YQYHR						

Seq ID NO: 443 DNA sequence  
Nucleic Acid Accession #: NM\_016639.1  
Coding sequence: 40..429

65	1	GCGGGGGGGG	CAGACAGCGG	CGGGGCGCAG	ACGTGCACCTA	TGGCTCGGGG	CTGCTGCGC	60
		CGGTTGCTGC	GGCTCTCTGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCGGGG	120
70		GAGCAAGCGC	CAGGCAACGC	CCCTGCTCC	CGCGGCAGCT	CCTGGAGCGC	GGACCTGGAC	180
		AAGTGCATGG	ACTGCGGCTC	TTGCAGGGCG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
		GCTGCAGCAC	CTCCTGCCCC	CTTCCGGCTG	CTTTGGGCCA	TCCTTGGGGG	CGCTCTGAGC	300
		CTGACCTTGG	TGCTGGGGCT	GCTTTCTGGC	TTTTTGCTGT	GGAGACGATG	CGCAGGAGGA	360
		GAGAAGTTCA	CCACCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCACGC	TGTGGCGCTG	420
75		ATCCAGTGTG	TAATGTGCC	CTGCCAGCG	GGGCTCGCCC	ACTCATCATT	CATTCTATCA	480
		TTCTAGAGCC	AGTCTCTGCC	TCCAGACGC	GGGGGAGGCC	AAGCTCTCTC	AACCACAAGG	540
		GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTTCAGG	GAACCTTCCA	600
		AGGTGCTTGG	TGCTGGGGCT	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
80		ACAAACACAG	TGACACTGAC	TAAGGAACTG	CAGCAATTGC	ACAGGGGAGG	GGGGTGCCTC	720
		CCTTCTCTT	GAATGCGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
		TCACCTAGAT	GTCCTGAAAT	TCCACCAAGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
		TTAACACTAG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCACTC	900
		CCCAAGCGG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT	960

AATAAAAGAA TCCTTAACTT TAAAAAATA AAAAAAA

Seq ID NO: 444 Protein sequence  
 Protein Accession #: NP\_057723.1

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1 11 21 31 41 51  
 | | | | |  
 MARGSLRRL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRRAPH 60  
 SDFCLGCAAA PPAFRLWLP ILGGALSLTP VLGLLSGFLV WRRRCRRREKF TTPIEETGGE 120  
 GCPAVALIQ

Seq ID NO: 445 DNA sequence  
 Nucleic Acid Accession #: AF322916.1  
 Coding sequence: 50..4300

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1 11 21 31 41 51  
 | | | | |  
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 CAAGTCCCGC CTGAGGAGGC AGGACGTGCC CGGCCCGCG TCGTCTGGCG CCGCCGCGCG 120  
 CAGCGCGCAT GCAGCAGATT GGAATAAATA TGATGACCGA TTGATGAAAG CAGCAGAAAG 180  
 GGGGGATGTA GAAAAAGTGA CCTCAATCCT TGCTAAAAAG GGGGTCAATC CAGGCAAACT 240  
 AGATGTGGAA GGCAGATCTG TCTTCCATGT TGTGACCTCA AAGGGGAATC TTGAGTGTIT 300  
 GAATGCCATC CTTATACATG GAGTTGATAT TACAACCACT GACACTGCAG GGAGAAATGC 360  
 TCTTCACCTG GCTGCTAAGT ATGGACATGC ATGTGCTCTA CAAAACTTC TACAGTACAA 420  
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 AGATTGTCTT TCTAGCATAC AGCTGCTTTG TGACCATGGG GCCTCTGTGA ATGCCAAAGA 540  
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 ACTGCTGATA GATAGAGGAG CGGATGTTAA TTCCAGAGAC AAACAAAACA GAACTGCCCT 660  
 CATGCTAGGT TCGCAATATG GTTGCAGAGA TGCAGTAGAA GTCTTAATTA AAAATGGTGC 720  
 TGATATAAGC TTGCTGGATG CGCTTGGCCA TGATAGTTCT TACTATGCAA GAATTGGTGA 780  
 CAATCTGGAC ATTCTAACCT TGTGGAAGAC TGCACTCGAA AATACCAACA AAGGGAGAGA 840  
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 AAATGTGAAG TCACATCAGA GGGAGCATCA AAATATTGAG GATTGGAGA TTGAAAATGA 960  
 AGATTGAAA GAGAGGTTGA GAAAAATCA GCAAGAACAA AGAATACITTT TGGATAAAGT 1020  
 CAATGGTTTA CAGTTACAGC TGAATGAGGA AGTTATGGTT GCTGATGATC TGGAAAGCGA 1080  
 GAGAGAAAGC CTGAAGTCCC TTTTGGCAGC TAAAGAAAG CAACATGAAG AAAGCTTAAG 1140  
 GACTATTGAG GCTCTGAAA ATAGATTAA ATATTTGAG AGTGATCATT TAGGATCAGG 1200  
 AAGTCATTTT AGTAACCGAA AAGAAGATAT GCTTCTTAAA CAAGGTCAGA TGTATATGGC 1260  
 AGACTCACAG TGTAATCTCC CAGGTATACC AGCCCATATG CAAGCAGAT CTATGTTAAG 1320  
 ACCTCTGGAA CTATCTTTAC CCACTCAAAAC GTCATACTCT GAAAATGAAA TTTTAAAGAA 1380  
 AGAGTTAGAA GCAATGCGAA CTTTCTGTGA GTGAGCAAAA CAAGACCGAC TGAAGCTCCA 1440  
 AAATGAAGT GCACACAAGG TGGCAGAAAT CAAAGCTTTA GCATTAGAAT GTGAAGGGT 1500  
 CAAGGAGGAT TCAGATGAAC AGATAAAGCA ATTAGAAGAT GCATTAAAAG ATGTGCAGAA 1560  
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 AGAACACTTA CCAAGTGAAG CAGCCTCAGG GAATCACAGA CTAACCGAGG AACTGAAGGA 1680  
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 ATTGCTACTG GAAATAGCA GCTTAAGTAA GGATGTAAAG CGCTAGAAA CTGTGTTTGT 2460  
 ACCTCCTGAG AAACATGAAA AAGAGATAAT AGCTCTGAAA TCCATATTTG TTGAACCTTA 2520  
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 AGATGTGAAG AAAAAATTTG AAGATATAAA TCAGGAATTT GTAAAAATAA AAGATAAGAA 2760  
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 TGCCGAATTT AAAGCCCGAG AGAAGGAGCT CGACACAATA CAAGAATGCA TTAAGGTAAA 3000  
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 AAGAAGAATA GAGAAATCTG CTAACAAAT AGAAGCAAAA GATAATAAGA TAAGTGAAC 4020

5 GCTTAATGAT GTGGAAAGAT TAAACACAGG ACTCAATGGC CTTTCCCAAC TCACCTACAC 4080  
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 TCGGACACAC CTTCTTAGTG CTGCACAGGG TCACATGGAT GAAGATGTTT AGGAGGCTCT 4260  
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 TATCTGTTT ATCTTGCTGG TGCTGAACAT TCITTTGTGCA ACTCCATGGT CTTTCTGGGC 4380  
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10 Seq ID NO: 446 Protein sequence  
 Protein Accession #: AAG49577.1

1 11 21 31 41 51  
 15 MKSLKSLRLR QDVPGPASSG AAAASAHAA WNKYDDRLMK AAERGDVERV TSILAKKGVN 60  
 PGKLDVEGRS VFHVVTSGKN LECINAILIH GVDITTSOTA GRNALHLAAK YGHALCLQKL 120  
 LQYNCPTEHA DLQGRITLQK KAMADCPSSI QLLCDHGASV NAKDVKGRTP LVLATQMSRP 180  
 TICQLLIDRG APVNSRDQKN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSYYA 240  
 RIGDNLIDLT LLKTASENTN KGRRLWKQGP SLQQRNLTHM QDEVNVKSHQ REHQNIQDLE 300  
 IENEDLKERL RKIQQEQRL LDKVNLGLQ LNEEVMVADD LESEREKLS LLAKEKEQHE 360  
 20 ESLRTIEALK NRKFYFESDH LGSGSHFSNR KEDMLLKQGG MYMADSQCTS PGIPAHMQSR 420  
 SMLRPLELSL PSQTSYSENE ILKKELEAMR TFCESAKQDR LKLQNELAHK VAECKALALE 480  
 CERVKEDSDE QIKQLEDALK DVQKRMVSEB GKVKQMTHF LALKEHLTSE AASGNHRLTE 540  
 ELKDQLKDLK VKYEGASAEV GKLRNQIKQN EMIVEEFKRD EGKLEENKR LQKELSMCEM 600  
 25 EREKGRKVT EMEGQAKELS AKLALSIPAE KFNEMKSSLS NEVNEKAKKL VEMEREHEKS 660  
 LSEIRQLKRE LENVKAKLAQ HVKPEEHEQV KSRLEQKSGE LKKITELTL KNQTLQKEIE 720  
 KVLNDNLKLL EQAHNLTIEM KNHYVPLKVS EDMKSHDAI IDDLNRKLLD VTQRYTEKKL 780  
 EMEKLLLEND SLKQDVSRLE TVPVPPEKHE KEIIALKSNI VELKKQLSEL KKKCGEDQEK 840  
 30 IHALTSENIN LKQMSNQYV PVKTHEEVRM TINDTLAKTN RELLDVKKKP EDINQEPVKI 900  
 KOKNEILKRN LENTQNIKA EYISLAHEA KMSSLSQSMR KVQDSNAEIL ANYRKGQEEI 960  
 VTLHAEIKAQ KKLSDTIQEC IKVKYAPIVS PRECERKFA TEKELDKLSE EQTKYVSVE 1020  
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 35 EVKNVKEKLV EENAKOTSEI LAVQNLLQKQ HVPLEQVEAL KKSNGTIEK LKEBLKSMQR 1140  
 CYEKEQQTVT KLHQLLENQK NSSVPLAEHL QIKEAPEKEV GIIKASLREK EESQNRKME 1200  
 VSKLQSEVQN TKQALEKLET REVVDLSKYK ATKSDLETQI SSLNEKLANL NRKYEEVCEE 1260  
 VLHAKKKEIS AKDEKELLHF SIEQEIKDQK ERCDKSLTTI TELQRRIQES AKQIEAKDNK 1320  
 ITELLNDVER LKQALNGLSQ LTYTSGNPTK RQSQLIDTLQ HQVKSLEQQL ADADRQHEV 1380  
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40 Seq ID NO: 447 DNA sequence  
 Nucleic Acid Accession #: NM\_003020.1  
 Coding sequence: 29..664

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 CCCTGACCCG GTCTCAGAAG CAGATATCCA GAGGCTGCTT CATGGTGTGA TGGAGCAATT 180  
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 50 CCGAGACATT GAAGGTGGAG CTCATGAAGG ACTTCAGCAT TTGGGTCTCT TTGGCAACAT 300  
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 55 GAAGGGAGGA GAGAGACGAA AGCGGAGGAG TGTCAATCCA TATCTACAAG GACGAGACT 600  
 GGATAATGTT GTTGCAAGA AGTCTGTCCC CCAATTTTCA GATGAGGATA AGGATCCAGA 660  
 GTAAAGAGAA GATGCTAGAC GAAAACCCAC ATTACCTGTT AGGCCTCAGC ATGGCTTATG 720  
 TGCACGTGTA AATGGAGTCC CTGTGAATGA CAGCATGTTT CTACATAGA TAATTATGGA 780  
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 60 AAATTAGATT AAGAGCTTTT TTGTTTCTTG GGTTTTAAAT ATGTGAATCT GCAATGATCA 900  
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 65 GCTGTACTCA AGAGGAGGAG CTGACACATT TCACCTGGCT GGTCTTAAAT AAACATGAAT 1140  
 GCAAGCATTG GC

Seq ID NO: 448 Protein sequence  
 Protein Accession #: NP\_003011.1

70 1 11 21 31 41 51  
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 PVGKTDDGCL ENTPDTABFS REFQLHQHLP DPEHDYPLGL KWNKLLYEK MKGGERRKRR 180  
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80 Seq ID NO: 449 DNA sequence  
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 Coding sequence: 79..2538

1 11 21 31 41 51  
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 CCTGCCGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCTGTCT 120  
 CGGTGGTTGC TGTGTCTTGG CCTGGTGGGC CCACTGCTCG GTGCGGCGCG GCCAGGCTTT 180

5	CAACAGACCT	CACATCTTTC	TTCTTATGAA	ATTATAACTC	CTTGGAGATT	AACTAGAGAA	240
	AGAAGAGAAG	CCCTTAGGCC	CTATTCAA	CAAGTATCTT	ATGTTATTCA	GGCTGAAGGA	300
	AAAGAGCATA	TTATTCACTT	GGAAAGGAAC	AAAGACCTTT	TGCTGAAGA	TTTTGTGTTT	360
	TATACTTACA	ACAAGGAAGG	GACITTAATC	ACTGACCATC	CCAATATACA	GAATCATTGT	420
	CATTATCGGG	GCTATGTGGA	GGGAGTTTAT	AATTTCATCCA	TTGCTCTTAG	CGACTGTITT	480
	GGACTCAGAG	GATTGCTGCA	TTTAGAGAA	GCGAGTTATG	GGATTGAACC	CCTGCAGAAC	540
	AGCTCTCATT	TTGAGCACAT	CATTATTCGA	ATGGATGATG	TCTACAAAGA	GCCTCTGAAA	600
	TGTGGAGTTT	CCAACAAGGA	TATAGAGAAA	GAAACTGCAA	AGGATGAAGA	GGAAAGACCT	660
	CCACAGCATG	CTCAGCTACT	TCGAAGAAGA	AGAGCTGTCT	TGCCACAGAC	COGGTATGTG	720
10	GAGCTGTTCA	TTGTCGTAGA	CAAGGAAAGG	TATGACATGA	TGGGAAGAAA	TCAGACTGCT	780
	GTGAGAGAAG	AGATGATTCT	CCTGGCAAA	TACTTGGATA	GTATGTATAT	TATGTTAAAT	840
	ATTGCAATTG	TTGAGTTGG	ACTGGAGATT	TGGACCAATG	GAAACCTGAT	CAACATAGTT	900
	GGGGTGTCTG	GTGATGTGCT	GGGGAACCTC	GTGCAGTGGC	GGGAAAAGTT	TCTTATCACA	960
	CGTCGGAGAC	ATGACAGTGC	ACAGCTAGTT	CTAAAGAAAG	GTTTTGGTGG	AACTGCAGGA	1020
15	ATGGCATTTG	TGGGAACAGG	GTGTTCAAGG	AGCCACGAG	GCGGATTAA	TGTGTTTGGG	1080
	CAATCACTG	TGGAGACATT	TGCTTCCATT	GTGCTCATG	AATTGGGTCA	TAATCTTGGG	1140
	ATGAATCATG	ATGATGGGAG	AGATTGTTCC	TGTGGAGCAA	AGAGCTGCAT	CATGAATTCA	1200
	GGAGCATCGG	GTTCAGAAA	CTTTAGCAGT	TGCAGTGCAG	AGGACTTTGA	GAAATTAACT	1260
20	TTAAATAAAG	GAGGAAACTG	CCTTCTTAAT	ATTCCAAAGC	CTGATGAAGC	CTATAGTGCT	1320
	CCCTCCTGTG	TGAATAAGTT	GGTGGACGCT	GGGGAAGAGT	GTGACTGTGG	TACTCCAAAG	1380
	GAATGTGAAT	TGGACCTCTG	CTGCGAAGGA	AGTAACCTGT	AGCTTAAATC	ATTGTCTGAG	1440
	TGTGCATATG	GTGACTGTGT	TAAAGACTGT	CGGTTCTTTC	CAGGAGGTAC	TTTATGCGGA	1500
	GGAAAAACCA	GTGAGTGTGA	TGTTCCAGAG	TACTGCAATG	GTCTTCTTCA	GTCTGTCTAG	1560
25	CCAGATGTTT	TTATTCAGAA	TGGATATCCT	TGCCAGAAAT	ACAAAGCCTA	TTGCTACAAC	1620
	GGCATGTGCC	AGTATTATGA	TGCTCAATGT	CAAGTCATCT	TTGGCTCAAA	AGCCAAAGGT	1680
	GGCCCAAGAG	ATTGTTTCTG	TGAAGTGAAT	TCTAAAGGTG	ACAGATTGCG	CAATTGTGGT	1740
	TCTCTCGGCA	ATGAATACAA	GAAGTGTGCC	ACTGGGAATG	CTTTGTGTGG	AAAGCTTCAG	1800
	TGTGAGAATG	TACAAGAGAT	ACCTGTATTT	GGAATGTGTC	CTGCTATTAT	TCAAAGCCTC	1860
30	AGTCGAGGCA	CCAAATGTTT	GGGTGTGGAT	TTCCAGCTAG	GATCAGATGT	TCCAGATCCT	1920
	GGGATGTATG	TCGAAGGCAC	AAAATGTGGT	GCTGGAAAGA	TCTGTAGAAA	CTTCCAGTGT	1980
	GTAGATGCTT	CTGTCTGAA	TTATGACTGT	GATGTTTCTG	AAAAGTGTCA	TGGACATGGG	2040
	GTATCTAATA	GCAATAAGAA	TTGTCACTGT	GAAAATGGCT	GGGCTCCCCC	AAATTGTGAG	2100
	ACTAAAGGAT	ACGGAGGAAG	TGTGGACAGT	GGACCTACAT	ACAAATGAAT	GAATCTGTCA	2160
35	TTGAGGGACG	GACTTCTGGT	CTTCTTCTTC	CTAATTGTTC	CCCTTATTGT	CTGTGCTATT	2220
	TTTATCTTCA	TCAAGAGGGA	TCAACTGTGG	AGAAGCTACT	TCAGAAAGAA	GAGATCACAA	2280
	ACATATGAGT	CAGATGGCAA	AAATCAAGCA	AACCCTTCTA	GACAGCCGGG	GAGTGTCTCT	2340
	CGACATGTTT	CTCCAGTGAC	ACCTCCCAAG	GAAATTCCTA	TATATGCAAA	CAGATTGTGA	2400
	GTACCAAGCT	ATGCAAGCAA	GCAACCTCAG	CAGTTCCCAT	CAAGGCCACC	TCCACCACAA	2460
40	CGAAAGATAT	CACTTCAGGG	AAACTTAATT	CCTGCCCTGC	CTGCTCCTGC	ACCTCCTTTA	2520
	TATAGTTCCC	CACTTGATT	TTTTTAAOCT	TCTTTTGTCA	AATGTCTTCA	GGGAACGTAG	2580
	CTAATACTTT	TTTTTTTTCT	TGATGTTTTC	TTGAAAAGCC	TTTCTGTGTC	AACTATGAAT	2640
	GAAACAAAAA	CACCAAAAAA	CAGACTTCAC	TAACACAGAA	AAACAGAAAC	TGAGTGTGAG	2700
	AGTTGTGAAA	TACAAGGAAA	TGCAGTAAAG	CCAGGGAAAT	TACAATAACA	TTTCCGTTTC	2760
45	CATCATTGAA	TAAGTCTTAT	TCAGTCATCG	GTGAGGTTAA	TGCACTAATC	ATGGATTTTT	2820
	TGAACATGTT	ATTGCASTGA	TTCTCAAAAT	AACGTATATG	GTGTAAGATT	TTTGTCAAT	2880
	AGTGTTTAAG	TGTTATTCTG	AATTTTCTAC	CTTAGTTATC	ATTAATGTAG	TTCTCATTG	2940
	AACATGTGAT	ATCTTAATAC	CTGTGAAAAC	TGACTAATCA	GCTGCCAATA	ATATCTAATA	3000
50	TTTTTCAATC	TGCACGAATT	AATAATCATC	ATACTCTAGA	ATCTTGTGTC	TCACTCACTA	3060
	CATGAATAAG	CAAAATATGT	CTTCAAAAGA	ATGCACAAGA	ACCACAATTA	AGATGTCATA	3120
	TTATTTTGA	AGTACAAAAT	ATACTAAAAG	AGTGTGTGTG	TATTCACGCA	GTTACTCGCT	3180
	TCATTTTCTA	TGACCTTTCA	ACTATAGGTA	ATAACTCTTA	GAGAAATTAA	TTTAATATTA	3240
	GAAATTTCTAT	TATGAATCAT	GTGAAAGCAT	GACATTGTTT	CACAATAGCA	CTATTTTAAA	3300
55	TAAATTATAA	GCTTTAAGGT	ACGAAGTATT	TAATAGATCT	AATCAAAATAT	GTGTAATCAT	3360
	GGCTATAATA	AAGCAGGAGC	AATATAAAAA	TCTTCAATCA	ATTGAACTTT	TACAAAACCA	3420
	CTTGAGAATT	TCATGAGCAC	TTTAAAAATCT	GAACTTTCAA	AGCTTGCTAT	TAAATCATTT	3480
	AGAAATGTTA	CTTTACTTAA	GGTGTGCTGG	GTGATGTAAA	ATATTAGACA	CTAATATTTT	3540
	CATAGAAATT	AGGCTGGAGA	AAGAAGGAAG	AAATGGTTTT	CTTAAATACC	TACAAAAAAG	3600
60	TTACTGTGGT	ATCTATGAGT	TATCATCTTA	GCTGTGTTAA	AAATGAATTT	TTACTATGGC	3660
	AGATATGGTA	TGATCGTAA	AATTTTAAGC	ACTAAAAATT	TTTTTATAAC	CTTTCATAAT	3720
	AAAGTTTAA	AATAGGTTTA	TAACTGAAT	TTTATTAGTT	TTTTAAAGT	GTTTTGTGTT	3780
	TGTGTATATA	TACATATACA	AATACACAT	TTACAATAAA	TAAATACTT	GAAATTTCTA	3840
	AAAAAAA	AAAAAAA	AAAAA				

Seq ID NO: 450 Protein sequence  
 Protein Accession #: NP\_003807.1

70	1	11	21	31	41	51	
	MGSGARFPPSG	TLRVRWLLLL	GLVGPVLGAA	RPGFQQTSHL	SSYEIITPWR	LTRRERREAPR	60
	PYSKQVSYVI	QABGKEHIIH	LERNKDLLPE	DFVVYTYNKE	GLTIDHFNH	QNHCHYRGYV	120
	EGVNSSIAL	SDCFGLRGLL	HELENASYGIE	PLONSSHFEB	IYRMDDVYK	EPLKCGVSNK	180
	DIEKETAKOE	EEEPPEMTQL	LRRRAVLPO	TRYVELFIVV	DKERYDMNGR	NOTAVREEMI	240
	LLANYLDSMY	IMLNIIRVLV	GLEIWTNGNL	INIVGGAGDV	LGNFVQWREK	FLYTRRRHDS	300
75	AQLVLKKGFG	GTAGMAPVGT	VCSRSHAGGI	NVFGQITVET	PASTVAHEL	HNLMNHDDG	360
	RDSCGAKSC	IMNSGASGR	NFSSCSAEDF	EKLTLNKGKN	CLLNIPKPE	AYSAPSOGNK	420
	LDVAGEECD	GTPKCELD	CEBGSCTCLK	SFAECAYGDC	CKDCRFLPGG	TLRCRGTSEC	480
	DVPEYCNSS	QFQPDVFIIQ	NGYPOQNKKA	VCYNGMCQYY	DAQCQVIFGS	KAKAARPKDCF	540
	IEVNSKGRDF	GNGCFSGNEY	KKCATGNALC	GKLQCNQVE	IPVFGIVPAI	IQTPSRGKTC	600
80	MGVDFQLGSD	VDPGMVNEG	TKCGAGKICR	NFQCDVASVL	NYDCDVQKCK	HGHVCNSNK	660
	NCHCENGWAP	PNCTCKGYGG	SVDSGPTYNE	MNTALRDGLL	VFPFLIVPLI	VCAIFIFIKR	720
	DQLWRSYFRK	KRSQTYESDG	KIQANPSRQP	GSVPFHVSFV	TPPREVPYIA	NRPVAVPTAA	780
	KQPQPPSRP	PPPQPKVSSQ	GMLIPARPAP	APPLYSSLT			

Seq ID NO: 451 DNA sequence  
Nucleic Acid Accession #: NM\_016650.1  
Coding sequence: 196..789

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      GGTTCACATA TATGCAGATG TCTCGATATA GGAATGAAAT TACGTCTTTG GAACCACTTA 60
      AATAAGTCAA ATATACTTGG AGCTTTAAAA ATTAAAAGGA GAGAGATTCG AGCACCTTTT 120
      CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGGTGTG 180
10     CCCCAGCTGG GAAACATGGC TGTCATACAT TCACATCTGT GGAAAGGATT CCAAGAGAAG 240
      TTCTGAAGG GAGAACCCAA AGTCTTGGG GTTGTGCAGA TTCTGACTGC CCTGATGAGC 300
      CITAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCTTATT 360
      TCGTGCATTA TCGGTACAC AATTGCGGGG TCAGTAATGT TTATTATTTC AGGATCCTTG 420
      TCAATTGCAG CAGGAATTAG AACTACAAAA GGCCTGGTCC GAGGTAGTCT AGGAATGAAT 480
15     ATCACCAGCT CTGTACTGCG TGCATCAGGG ATCTTAATCA ACACATTTAG CTTGGCGTTT 540
      TATTCACTCC ATCACCCTTA CTGTAACATC TATGGCAACT CAAATRAATG TCATGGGACT 600
      ATGTCCATCT TAATGGGTCT GGATGGCATG GTGCTCCTCT TAAGTGTGCT GGAATTCCTG 660
      ATGTCTGTGT CCTCTCTGCG CTTTGGATGT AAGTGCTCT GTTGTACCCC TGGTGGGGTT 720
      GTGTTAATTC TGCCATCACA TTCTCACATG GCAGAAACAG CATCTCCAC ACCACTTAAT 780
20     GAGGTTTGAG GCCAACAAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG 840
      ACACAAGAGC CTCACATGAG AAATTACCAG TATCCAACCT CGATAGTAGT AGACGTGTG 900
      ATATTATTAT TATATGTAAAT CCAATTATGA ACTGTGTGTG TATAGAGAGA TAATAAATTC 960
      AAAAATTATG TCTCATTTT TTCCCTGGAA CTCAATAACT CACTTCACTG GCTCTTTATC 1020
25     GAGAGTACTA GGAGTTAAAT TAATAAATAA TGCATTAAAT GAGGCCACAG GAAAAA

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Seq ID NO: 452 Protein sequence  
Protein Accession #: NP\_057734.1

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MAVIHSMLWK GLQEKFLKGE PKVLGVVQIL TALMSLSMGI TMMCMASNTY GSNPISVHIG 60
      YTIWGSVMFI ISGSLSIAAG IRTTKGLVRG SLGMNITSSV LAASGILINT FSLAFYSFHH 120
      PYCNYYGNSN NCHGTMSILM GLDGMVLLLS VLEFCIAVSL SAFGCKVLCC TPGSVVLILP 180
35     SLSHMAETAS PTPLENEV

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Seq ID NO: 453 DNA sequence  
Nucleic Acid Accession #: NM\_002091.1  
Coding sequence: 56..503

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTCTCTGCT CTTCCAGGCC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GACCATGCG 60
      CGGCAGTGAG CTCCCGCTGG TCCTGCTGCG GCTGGTCTCT TGCCTAGCGC CCCGGGGGCG 120
      AGCGGTCCCG CTGCTGCGCG GCGGAGGGAC CGTGTGACCC AAGATGTACC CGCGCGGCAA 180
      CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
      TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
      GAATTGTGCT GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCACCCCAA 360
      GGCCTTGGGC AATCAGCAGC CTTGCTGGGA TTCAGAGGAT AGCAGCAACT TCARAAGATG 420
      AGGTTCAAAA GGCAGAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
      CCCCAGCTG AACCAAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACMAAACCCC 540
      TAAGAGACTG AGTTCTGCAA GCATCAGTTC TAOGATCATC CAACAGATT TCCTGTGTGA 600
      AAATAITTTA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
      CTTCTGTTT AAACCTGTGT GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTAATGCT 720
      TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAGGCCCC CGAGCTGTTA CCATTCACAA 780
55     TAAAAGCTTA AACACAT

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Seq ID NO: 454 Protein sequence  
Protein Accession #: NP\_002082.1

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKSTGESS 60
      VSRGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPQ PKALGNQPPS WDSSEDSNFK 120
65     DVGSKGKVR LSAFGSQRER RNPQLNQ

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Seq ID NO: 455 DNA sequence  
Nucleic Acid Accession #: NM\_016522.1  
Coding sequence: 265..1299

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70     1      11      21      31      41      51
      |      |      |      |      |      |
      GCGAAGCAG CAGGAGGGA GCCCCTTTG GCGTCTCTCC GTGGAACCGG TTTTCOGAGG 60
      CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGAGGA GTCTGCGCGC 120
      TTTTCTCTC CCGCGCCTC CCGGTGCGCG GGGTTCAAC GCTCAGTCCC CGCGCTCGCT 180
      CCGCACCCA CCACTTCTC GTGCTGCGCC GGGGGCGTG TCGGTGCGG CTGCGGAGT 240
      TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCTT GCCCTGGAAG 300
      TGCTCTGTG TCGTGTCTCT CAGGCTGCTG TTCTTGTATC CCACAGGAGT GCCGTGTGCG 360
      AGCGGAGATG CCACTTCCC CAAAGCTATG GACAACTGTA CGGTCCGCA GGGGGAGAGC 420
      GCCACCTCA GGTGACTAT TGACAACCGG GTCAACCGG TGGCTCGCT AAAACGCAAG 480
      ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCTGGATC CTCGCTGGT CTTTCTGAGC 540
      AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
      TACACCTGCT CGGTGAGAC AGACAACAC CCAAGACCT CTAGGGTCCA CCTCATTTG 660
      CAAGTATCT CCAAAATTGT AGAGATTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
80     ATTAGCCTCA CCTGCATAGC AACTGGTAGA CCAGAGCCTA CGTTACTTTG GAGACACATC 780

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5  
10  
15  
20

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TCTCCCAAAG CGTTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTC A GGGCATCACC 840
CGGGAACAGT CAGGGGACTA CGAGTGCACT GCCTCCAATG ACGTGGCGC GCCCGTGGTA 900
CGGAGAGTAA AGGTCAACGT GAACTATCCA CCATACATTT CAGAAGCCAA GGGTACAGGT 960
GTCCCGGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
TTCCAGTGGT ACAAGGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
AACAGACCTT TCCTCTCAAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
TACACTTGGG TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTTGGT 1200
CCAGGCGCGC TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260
CTGCTCTTTC TGGTCTTGCA CCTGCTTCTC AAATTTTGAT GTGAGTGCCA CTTCGCCACC 1320
CGGAAAGGCG TGCCGCCACC ACCACCACCA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
CCATTCAGAT ATATACAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA 1440
GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAAATTG 1500
CCTTGAGATC ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560
CCCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGSCAAG 1620
GGCTCAGCCT CTCTGCCCCA AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
AAATTCAATC AGTCCATAGA GAOGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
CGGGCCCAAG CGTGGCGCTG CGGGCACTTT GGTAGACTGT GCCACCAAGG CGTGTGTTGT 1800
GAAACGTGAA ATAAAAGAG CAAAAAAGAG AAAAAAAGAG

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Seq ID NO: 456 Protein sequence  
Protein Accession #: NP\_057606.1

25  
30

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1 11 21 31 41 51
| | | | |
MGVOGYLFLP WKLVVVSRLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
NRVTRVAMLN RSTILYAGND KWCLDPRVVL LSNQTQYYSI BIGNVDVYDE GPYTCSVQTD 120
NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCIAT GRPEPTVTWR HISPRAVGFV 180
SEDEYLEIQG ITRREQSDYE CSASNDVAAP VVRVVKVTVN YPPYISEAKG TGVFVGQKGT 240
LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VERNRPFSLK IFFNVSEHDY GNYTCVASNK 300
LGHTNASIML FGPFAVSEVS NGTSRRAGCV WLLPLLVLHL LLKPF

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Seq ID NO: 457 DNA sequence  
Nucleic Acid Accession #: NM\_012261.1  
Coding sequence: 203..1045

35  
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45  
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60  
65  
70

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1 11 21 31 41 51
| | | | |
GATTTGCTCT GCCAGCAGCT GTGGGTGCGG CGCTGACAC CGAGTCTAG CTAGGGGCTC 60
ACAGAATACG CGCTCCCTCC CTCGCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120
CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
CCTCATTCGG GGCAGTGCAG GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGCAG 240
ACTTCGAGTT CTCTGTATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAAAGAGT 300
GGAAATCTCT TCAGGCCCTT CCACTAACCC TGAAAAGAT ATATTGTGG TGGGGGAAA 360
TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCGGAT ATGCAATGA CCGGGGAGC 480
TGAGGTGAAG GGCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGTGGATCG 540
CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA 600
GGGAGCTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
CAAAAGCGCA GTCACTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT 720
CACCCCGCTC GGAAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780
TGATCCGCGA AAGAGCGTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTGTACAT 840
TATCTCAGAT TTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
GGAAAGAAAC TTGGCCCTGA TTTTGGGGCT CATCTTGGGC CTGCTCATCA TGGTAACACT 960
CGCGATTAC CAGTCCACC ACAAAATGAC TGCCAACAG GTGCAGATCC CTCGGGACAG 1020
ATCCCAATAT AAGCATATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGCTCCC 1080
CCAATCGAT CAGGTAGAAC AACAAAAGCA CTTTTCATC TTGTACAGCA GATACACCAA 1140
CATAGCTACA ATCAAAACAG CCGTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
AACCCACGGA AGGGGGAGAG AGGGTCTCAG ACAGCTTTCG TGCTCATGCT GGCTTGGCTT 1320
ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGCT GGCTTGGCTT 1320
TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA 1380
TTGAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCCT 1440
TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC 1500
TCATGCTCCC TGCAGCAAGA CCGCTGAAAG TGATTCAATG TTCTGGCTGG CATCTGCAAT 1560
GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
AAAAAGACTA ATGTAACATAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
GGGGAGCTCG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AATGAAATA AAACACACTA 1740
TTCTCTGGC

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Seq ID NO: 458 Protein sequence  
Protein Accession #: NP\_036393.1

75  
80

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1 11 21 31 41 51
| | | | |
MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60
EPAAKFIPVY DVHASNYYDL ITEQADIALT RGAEVKRCRG HSQSELQVFW VDRAYALKML 120
FVKESHNMKS GPETATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHELS ALVTPAGKSY 180
EQQAQQTISL ASSDPQKVTM MILSAVHIQF FDIISDFVFS BEHKCPVDER EQLBETLPLI 240
LGLILGLVIM VTLAIYHVHH KMTANQVQIP RDRSQYKHM

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Seq ID NO: 459 DNA sequence  
Nucleic Acid Accession #: NM\_001169.1  
Coding sequence: 85..870

1 11 21 31 41 51

5  
10  
15  
20  
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TAGGAGATAA	GAGTATCTTG	CACAGCAGGT	GCAGGTTTCC	CAGCAGCTCA	GGCAAGAGTC	60
CGATGTTTGT	GCCTATCTGAT	CCTGATGTCT	GGAGAGATAG	CCATGTGTGA	GCCTGAATTT	120
GGCAATGACA	AGGCCAGGGA	GCCGAGCGTG	GGTGGCAGGT	GGCGAGTGTG	CTGGTACGAA	180
CGGTTTGTGC	AGCCATGTCT	GGTGGAACTG	CTGGGCTCTG	CTCTCTTCAT	CTTCATCGGG	240
TGCCTGTGCG	TCATTGAGAA	TGGGACGGAC	ACTGGGCTGC	TGCAGCCGGC	CCTGGCCAC	300
GGGCTGGCTT	TGGGGCTCGT	GATTGCCACG	CTGGGGAATA	TCAGTGGTGG	ACACTTCAAC	360
CCTGCGGTGT	CCCTGGCAGC	CATGCTGATC	GGAGGCCCTCA	ACCTGGTGAT	GCTCCTCCCG	420
TACTGGGTCT	CACAGCTGCT	CGGGGGGATG	CTCGGGGCTG	CCTTGGGCAA	GGTGGTGAGT	480
CCTGAGGAGA	GGTTCCTGAA	TGCATCTGGG	GCGGCCTTTG	TGACAGTCCA	GGAGCAGGGG	540
CAGGTGGCAG	GGGCGTGGT	GGCAGAGATC	ATCCTGACGA	CGCTGTGGC	CCTGGCTGTA	600
TGCATGGGTG	CCATCAATGA	GAAGACAAAG	GGCCCTCTGG	CCCGTTCTC	CATCGGCTTT	660
GGCCTCACCG	TGGATATCCT	GGCTGGGGG	CCTGTGTCTG	GAGGCTGCAT	GAATCCCGCC	720
CGTGCCTTTG	GACCTGCGST	GGTGGCCAAC	CACTGGAACT	TCCACTGGAT	CTACTGGCTG	780
GGCCCACTTC	TGGCTGGCCT	GCTTGTGGA	CTGCTCATTA	GGTGTCTCAT	TGGAGATGGG	840
AAGACCCGCC	TCATCTGAA	GGCTCGGTGA	GCAGAGCTCG	TGGGATTCTT	GCTGCTCCAG	900
GTGTCTCTAG	CTACCTGTG	CCAGACTGAG	GACAGGGGAG	TTCCTGCATT	TCTGCCCAGG	960
GCAGAGGCC	AGAGGAGCGA	CCCCCTGCTT	CCACTGCTTG	GGCCTGCTTT	CTCAGATAGA	1020
CTGACTGCTG	AGGAGGCTCT	AGGTTCTTGG	AATTCTTTTG	TGCTCATCAG	AGACCCAGC	1080
CTGGGAACA	CGCTGCCCG	ACTGCCAGA	GAGCAGTGCA	AACACCAAA	CACGAGCGTG	1140
TTTCTTGAGA	GGAATGTCCC	CGAGTTGGAC	AAGGAGGCTG	TTTCTGCACA	TCAGCTCATT	1200
TCCCGCACCC	CATTCTTGC	TTGATTGCTT	TGTTGGGGG	CTGGCCACTT	CCTTGTCTCT	1260
CAAGCTGACA	ATTCTCACTT	TGCAATAAAT	AGTCCAGTGT	TTCCTTCAT		

Seq ID NO: 460 Protein sequence  
Protein Accession #: NP\_001160.1

30  
35

MSGEIAMCEP	EFGNDRKREP	SVGGRRWRVSW	YERFVQPCLV	ELLGSALFIF	IGCLSVIENG	60
TDITGLLQPAL	AHGLALGLVI	ATLGNISGGH	FNPVSLAAM	LIGGLNLVLM	LPYVWSQLLG	120
GMLGAALAKV	VSPERFWNA	SGAAPVTQVE	QGVAGALVA	EIILTLALL	AVCMGAINEK	180
TKGPLAPPSI	GFATVVDILA	GGPVSGGCMN	PARAFGPVAV	ANHNWPHWY	WLGPLLALGL	240
VGLLIRCFIG	DGKTRLILKA	R				

Seq ID NO: 461 DNA sequence  
Nucleic Acid Accession #: NM\_003226.1  
Coding sequence: 2..226

40  
45  
50

GATGCTGGGG	CTGGTCTGG	CCTGTCTGTC	CTCCAGCTCT	GCTGAGGAGT	ACGTGGGCCT	60
GCTGCAAAAC	CAGTGTGCGG	TGCCGGCCAA	GGACAGGGTG	GACTGCGGCT	ACCCCCATGT	120
CACCCCCAAG	GAGTGCAACA	ACCGGGGCTG	CTGCTTTGAC	TCCAGGATCC	CTGGAGTGCC	180
TTGGTGTTC	AAGCCCCCTGA	CTAGGAAGAC	AGAATGCACC	TTCTGAGGCA	CCTCCAGCTG	240
CCCCCTGGAT	GCAGGCTGAG	CACCTTGCC	CGGCTGTGAT	TGCTGCCAGG	CACGTGTCAT	300
CTCAGTITTT	CTGTCCCTTT	GCTCCCGGCA	AGCTTCTGTC	TGAAAGTTCA	TATCTGGAGC	360
CTGATGTCTT	AACGAATAAA	GGTCCCATGC	TCCACCCG			

Seq ID NO: 462 Protein sequence  
Protein Accession #: NP\_003217.1

55

MLGLVLALLS	SSSABEYVGL	SANQCAVPAK	DRVDCGYPHV	TPKECNRRGC	CFDSRIPGVP	60
WCFKPLTRKT	ECTF					

Seq ID NO: 463 DNA sequence  
Nucleic Acid Accession #: NM\_002993.1  
Coding sequence: 64..408

60  
65  
70  
75  
80

GGCAGAGACC	AGTCTCCGG	CCTCCACCCA	GCTCAGGAAC	COGGAACCC	TCTCTTGACC	60
ACTATGAGCC	TCCCGTCCAG	COGCGCGGCC	CGTGTCCCGG	GTCCTTCGGG	CTCCTTGTGC	120
GGCTGCTG	CGCTGCTGCT	CCTGCTGACG	COGCGGGGCG	CCCTGCGCAG	CGCTGGTCTT	180
GTCTCTGCTG	TGCTGACAGA	GCTGCGTTGC	ACTTGTTTAC	CGGTTACGCT	GAGAGTAAAC	240
CCCAAAACGA	TTGGTAAACT	GCAGGTGTTC	CCCGCAGGCC	CGCAGTGCTC	CAAGGTGGAA	300
GTGTAGAGCT	CCCTGAAGAA	CGGGAAGCAA	GTTTGTCTGG	ACCGGAAGC	CCCTTTTCTA	360
AAGAAAGTCA	TCCAGAAAT	TTTGGACAGT	GGAAACAAGA	AAACTGAGT	AACAAAAAAG	420
ACCATGCATC	ATAAAATTGC	CCAGTCTTCA	GCGGAGCAGT	TTTCTGGAGA	TCCCTGGACC	480
CAGTAAGAA	AGAAGGGAAG	GTTTGGTTTT	TTTCCATTTT	CTACATGGAT	TCCCTACTTT	540
GAAGAGTGTG	GGGGAAGCC	TAOGCTTCTC	CCTGAAGTTT	ACAGCTCAGC	TAATGAAGTA	600
CTAATATAGT	ATTTCACATA	TTTACTGTTA	TTTACCTGTA	TAAGTTATTG	AACCCCTTGG	660
CAATTGAACA	TATTGTGAGC	AAAGAATCAC	TGGTTATTAG	TCTTTCAATG	AATATTGAAT	720
TGAAGATAAC	TATTGTATTT	CTATCATACA	TTCCTTAAAG	TCTTACCGAA	AAGGCTGTGG	780
ATTTCGTATG	GAAATAATGT	TTTATTAGTG	TGCTGTTGAG	GGAGGTATCC	TGTTGTTCTT	840
ACTCACTCTT	CTCATAAAT	AGGAAATATT	TTAGTTCTGT	TTTCTTGGGG	AATATGTTAC	900
TCTTTACCTT	AGGATGCTAT	TTAAGTTGTA	CTGTATTAGA	ACACTGGGTT	TGTCATACCG	960
TTATCTGTGC	AGAATATATP	TCCTTATTCA	GAATTTCTAA	AAATTTAAGT	TCTGTAAGGG	1020
CTAATATATT	CTCTTCTAT	GGTTTATGAT	GTTTGAATGC	TTCTTAGTAT	GGCATAATGT	1080
CATGATTTAC	TCATTAAACT	TTGATTTTGT	ATGCTATTTT	TTCACTATAG	GATGACTATA	1140



5  
ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200  
TGATTGCTAA TTTACATAGA AATGTATTCT CTITGGTTTT TAAATAAAG CAAAATTAC 1260  
AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTGAA CAATTGAAAT ATAAATTCAT 1320  
CATTATGTC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380  
TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440  
AAATGCACT TTTATTTTTT CTTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500  
TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA

10  
Seq ID NO: 464 Protein sequence  
Protein Accession #: NP\_002984.1

15  
1 11 21 31 41 51  
MSLPSSRAAR VPGPSGSLCA LLALLLLLTP PGFLASAGFV SAVLTELRCT CLRVTLRVNP 60  
KTIGKLQVFP AGPQCSKVEV VASLRNGKQV CLDPPEAPFLK KVIQKILDSG NKKN

20  
Seq ID NO: 465 DNA sequence  
Nucleic Acid Accession #: NM\_002038.2  
Coding sequence: 108..500

25  
1 11 21 31 41 51  
GAACCGTTTA CTCGCTGCTG TGCCCATCTA TCAGCAGGCT CCGGCTGAA GATTGCTTCT 60  
CTTCTCTCCT CCAAGGTCTA GTGACGGAGC CCGCGCGCGG CGCCACCATG CGGCAGAAGG 120  
CGGTATCGCT TTCTTGTGTC TACCTGCTGC TCTTCACCTG CAGTGGGGTG GAGGCAGGTA 180  
AGAAAAAGTG CTGGAGAGCG TCGGACAGCG GCTCGGGGTT CTGGAAGGCC CTGACCTTCA 240  
TGGCCGTCGG AGAGAGACTC GCAGTCGCGG GGCTGCCCGG GCTGGGCTTC ACCGGCGCGG 300  
GCATCGCGGC CAACTCGGTC GCTGCCTCGC TGTATGAGCTG GTCTGCGATC CTGAATGGGG 360  
CGCGCGTGCC CGCCGGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGGCAGCA 420  
GGGTGTCAT TATTGTAATT GGTGCCCTGA TGGGCTACCG CACCCACAAG TATCTCGATA 480  
GTGAGGAGGA TGAGGAGTAG CCAGCAGCTC CCAGAACCTC TTCTTCCTTC TTGGCCTAAC 540  
TCTTCAGTT AGGATCTAGA ACTTTGCCTT TTTTTTTTTT TTTTTTTTTT TTTGAGATGG 600  
GTTCTCACTA TATTGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC 660  
ACTGACGCT CCAACTCCTA GCCTCAAGTG ATCCTCTCTG CTCACCTCC CAAGTAGGAT 720  
TACAAGCATG GCGGACGAT GCCCAGAAAT CAGAACTTTC TCTATCACTC TCCCAACAA 780  
CCTAGATGTG AAAACAGAAT AAATTCACC CAGAAAA

40  
Seq ID NO: 466 Protein sequence  
Protein Accession #: NP\_002029.3

45  
1 11 21 31 41 51  
MRQKAVSLFL CYLLLFCTSG VEAGKKKCE SSDSGSGFWK ALTFMAVGGG LAVAGLPALG 60  
FTGAGLAANS VAASLMSWSA ILNGGGVPAG GLVATLQSLG AGGSSVVVGN IGALMGYATH 120  
KYLDSSEDEE

50  
Seq ID NO: 467 DNA sequence  
Nucleic Acid Accession #: NM\_003469.2  
Coding sequence: 92..1945

55  
1 11 21 31 41 51  
GAAACGGCCC GAGAAGCTCG CCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60  
CATATAACA AAAAGAGGAA ATCTTTCAA CATGGCTGAA GCAAGACCC ACTGGCTTGG 120  
AGCAGCCCTG TCTCTTATCC CTTTAAATTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180  
TCAGAGAAAC CAGCTGCTCT AGAAGAACC AGACCTCAGG TTGAAAAATG TCCAAAAGTT 240  
TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAG AACCAAGCTCA 300  
TAAGGAAGAA AGCAGCCGCA ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360  
AAAAGAAAT GCGATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420  
GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAT GAGCCTCAGT CTGCACCAAA 480  
AGAAAAAAG CCCTATGCCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540  
TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCTATGTA 600  
TGAAGAGAA TCCAGGGATA ACCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660  
TACTCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCAA GAGCTGGGGA AACTGACAGG 720  
ACCAAAACAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAATTTATA CGGATGATGA 780  
AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG 840  
GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCAGGAA GAGGTGAGAG ACAGCAAGA 900  
GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960  
CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020  
AATTGCCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080  
AAATGGGAAA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140  
GCTGATTGAA ATCTCAAGGA ATTACAGAT ACCCCAGAA GACTTAATTG AGATGCTCAA 1200  
AACTGGGGAG AAGCGAATG GATCAGTGA ACCGGAGCGG GAGCTTGACC TTCTGTGTA 1260  
CTAGATGAC ATCTCAGAGG CTGACTTGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320  
CTCCAAGAGT GGCTACCTTA AAACACCTGG TGTGCTGGG ACTGAGGCC TACCAGACGG 1380  
GCTCAGTGT GAGGATATT TAAATCTTT AGGGATGGAG AGTCAGCAA ATCAGAAAAC 1440  
GTGATATTTT CCAATCCAT ATAACCAGGA GAAAGTCTG CCAAGGCTCC CTTATGTTGC 1500  
TGGAGATCT AGATCGAAC AGCTTCCCAA AGCTGCCTGG ATTCCACATG TTGAAAACAG 1560  
ACAGATGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620  
GATGCTAGTT AAATACCTTG AGATCATTAA TTCAAACCAA GTGAAGCGAG TTCTCGSTCA 1680  
AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAAT GAGCAGGCCA TCAAGAGCA 1740  
TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC 1800  
TGTGGGGCCC CCGAAGAAAT ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860  
AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920

5 TAAGAGAGCA ATGGAATAA TGTAAGCTGC TTTCATTAAT TACCTACTT TCATTCTCTC 1980  
 CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTGA CTTCATCTCT GTTAACACTG 2040  
 TAATATCTTT AAATGATGTA CAGGCAGATG AAACCAGGTC ACTGGGGAGT CTGCTTCATT 2100  
 TCCTCTGAGC TGTATCTCTG TGTATGGATA TGTGTAATG TTATGACTCC TTGATAAAAA 2160  
 ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT 2220  
 GGCTGTGGCA TTGTTGATGC TCACATATGA TAAAAAGTG TCCTATAATT CTATTGAAAG 2280  
 TTTTAAATAT TTATTGAATT ATTTTGTIAC TGTCTGTAGC GTTTTGTGGA GACTCTGGAC 2340  
 AAAAAATAA AGCATTATAA ATATA

10 Seq ID NO: 468 Protein sequence  
 Protein Accession #: NP\_003460.1

15 1 11 21 31 41 51  
 MAEARKTHWG AALSLIPLIF LISGAEAAAF QRNQLQKEP DLRLNVQKF PSEPMIRALE 60  
 YIENLRQQAQ KEESPDPYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120  
 AENEPQSAFK ENKPYALNSE KNPPMDMSDD YETQQWPERK LKHMQFPFMY EENSRENPFK 180  
 RTNBIVEEQY TQSLATLES VFQELGKLTG PNNQKRERMD EQKLYTDEE DDIYKANNIA 240  
 YEDVVGGEW NPVEEKIESQ TQEEVRSKE NIGKNEQIND EMKRSQQLGI QEEDLRKESK 300  
 DQLSDDVSKV IAYLKLRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRNLQI 360  
 PPEDLIEMLK TGEKPNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420  
 RAGTEALPDG LSVEDILNLL GMESAANQKT SYFPNPNQOE KVLPRLPYGA GRSRSNQLPK 480  
 AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPQG GSSEDDIQEE 540  
 EQIEQAIKEH LMQSSSQETD KLAPVSKRFP VGPPKNDDTP NRQYWEDELL MKVLEYLNQE 600  
 KAEKGRSHIA KRAMENM

30 Seq ID NO: 469 DNA sequence  
 Nucleic Acid Accession #: NM\_006398.1  
 Coding sequence: 19..516

35 1 11 21 31 41 51  
 GGCCCCCTGT CTGCAGAGAT GGCTCCCAAT GCTTCCTGCC TCTGTGTGCA TGTCCGTTCC 60  
 GAGGAATGGG ATTTAATGAC CTTTGTATGCC AACCCATATG ACAGCGTGAA AAAAATCATA 120  
 GAACATGTCC GGTCTAAGAC CAAGGTTCTT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180  
 AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240  
 CACCTTACCC TGAAAGTGGT GAAGCCCACT GATGAGGAGC TGCCCTTGTG TCTGTGGAG 300  
 TCAGGTGATG AGGCAAGAG GCACCTCTCT CAGGTGOGAA GGTCCAGCTC AGTGGCACAA 360  
 GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420  
 AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480  
 TTAATCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540  
 AGGGGTCAA AAGCTTATTT CTTTAACTCT CTYACTCAAC GAACACATCT TCTGATGATT 600  
 TCCCAAAATT AATGAGAATG AGATGAGTAG AGTAAGATTG GGGTGGGATG GGTAGGATGA 660  
 AGTATATTGC CCAACTCTAT GTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720  
 TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTC

Seq ID NO: 470 Protein sequence  
 Protein Accession #: NP\_006389.1

50 1 11 21 31 41 51  
 MAPNASCLCV HVRSEWDLM TFDANFYDSV KRIKEHVRSK TKVPVQDQVL LLGSKILKPR 60  
 RLSLSYSGDK ERTIHLTLKV VKPSDEELPL FLVESGDRAK RHLLQVRRSS SVAQVKAMIE 120  
 55 TKTGIIPETQ IVTCNGKRL E DGMADYGI RKGILLFLAS YCIGG

Seq ID NO: 471 DNA sequence  
 Nucleic Acid Accession #: XM\_094741.1  
 Coding sequence: 1..948

60 1 11 21 31 41 51  
 ATGAAGGCCA ACTACAGCGC AGAGGAGCGC TTTCTCTGCT TGGGTTTCTC CQACTGGCCT 60  
 TCCCTGCAGC CGTCTCTCTT CGCCCTTGTC CTCTGTGCT ACCTCTCTGAC CTTGACGGGC 120  
 65 AACTCGGCGC TGTGTCTGCT GGCCTGCGC GACCCGCGCC TGACACGCGC CATGTACTAC 180  
 TTCTCTGCTC ACCTGGCCTT GGTAGAGCGC GGCCTTCACTA CTAGCGTGGT GCGCGCGCTG 240  
 CTGGCCAACC TGGCGGAGAC AGCGCTCTGG CTGCGCGCA GCCACTGCAC GGCCAGCTG 300  
 TGGCATCGC TGGCTCTGGG TTGGGCGGAA TGGCTCTCTC TGGCGGTGAT GGCTCTGGAC 360  
 CGCGCGGCGC CAGTGTGCGC CCGCTGCGC TATGCGGGGC TGTCTCTCCC GCGCTATGT 420  
 70 CGCACGCTGG CCAGCGCCTC CTGGCTAAGC GGCCTCACCA ACTCGGTTGC GCAACCGCG 480  
 CTCTGTGGCT AGCGCGCGCT GTGCGCGCCC CGCTCTGCTG ACCACTTCAT CTGTGAGCTG 540  
 CCGCGCTTGC TCAAGCTGGC CTGCGGAGGC GACGGAGACA CTACCGAGAA CCAGATGTT 600  
 GCGCGCGCGC TGGTCACTCT GCTGCTGCGC TTGCGGTCA TCTGCGCTC CTACGCTGCC 660  
 75 GTGGCGCGAG CTGTCTGTG CATGCGGTTG AGCGGAGGCC GGAGGAGGCC GGTGGGCA 720  
 TGTGGGTCCC ACCTGACAGC CGTCTGCTG TTCTACGGCT CGGCATCTA CACCTACCTG 780  
 CAGCGCGCGC AGCGCTACAA CCAGGCAAGG GCGAAGTTGG TATCGCTCTT CTACACCTG 840  
 GTCAACCTCT CTCTCAACC GCTCATCTAC ACCCTCAGGA ATAAGAAATG GAAGGGGCA 900  
 GCGAGGAGGC TGCTGCGGAG TCTGGGAGGA GGCCAGGCTG GGCAGTGA

80 Seq ID NO: 472 Protein sequence  
 Protein Accession #: XP\_094741.1

1 -11 21 31 41 51  
 MKANYSABER FLLGLPDSWP SLQPVLPALV LLCYLLTLTG NSALVLLAVR DPLRHTPMYY 60

FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASIALGSAB CVLLAVNALD 120  
 RAAAVCRPLR YAGLVSPRLC RFLASASWLS GLTNSVAQTA LLAERPLCAP RLLDHFICEL 180  
 PALLKLACGG DGDTTENQMF AARVVILLIF FAVILASYGA VARAVCCMRP SGGRRRAVGT 240  
 CGSHLTAVCL FYGSAITYYL QPAQRYNQAR GKFVSLFYTV VTPALNPLIY TLRNKKVKGA 300  
 ARRLRLSLGR GQAGQ

Seq ID NO: 473 DNA sequence  
 Nucleic Acid Accession #: NM\_001062.1  
 Coding sequence: 76..1380

1 11 21 31 41 51  
 | | | | |  
 GCTCTCATT CCTTCTGCC ATCACTTAAT AAATAGCCAG CCAATTTCATC AACATTCTGG 60  
 TACACTGTGG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTGT 120  
 TCTTTTATTC CAAGCCAACT ATGOGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180  
 CTAACCACTC TGTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240  
 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCCGTAT GCAAAAGATG 300  
 ATCCAAACAA TCAAAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360  
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACCT AATATATGAT 420  
 TACCACCTGA CTGACAAGCT AGAAAATAAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480  
 CACAATGGCA CTCOCCTGAC TAACACTACT CAGCTCAGCC TGGACGTTTT GGCCTTGTGT 540  
 CTGTTCAATG GGAACACTAC AACCOCGAA GTTGTCAACC ACTTCACTCC TGAAAATAAA 600  
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG 660  
 ACCGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG 720  
 AACATCAGTA TTTATACAAA GTCACCTGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAAT 780  
 GGTCTCATTG GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840  
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAACTC TGAATACAGT GCTCAGCGAA 900  
 ATTTCTCAAG GAGCATCTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960  
 GGAAAAGACT TCTTGATAT TAACAAAGAC TCTTCTGCG TCTCTGCTC AGGTAACCTC 1020  
 AACATCTCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080  
 GTCATTAAT CTGTGAGAA CAATGAAACA TATTTCAACA ATGTCATCTG GCTAAATGGT 1140  
 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200  
 ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACTGTA TTCAGGGCCT ATGTGCCAAC 1260  
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCCTGAG CCAAGGAGCT 1320  
 GGTATGAGC TTGTCCGCAA TGGAGAAAC TTGGAGGTTT GCTGGAGCAA ATACTAATAA 1380  
 GCCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGCACTG GAGTTCATG TTTATTGTCC 1440  
 TTAAGCCTTC TTCTTCATT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500  
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC

Seq ID NO: 474 Protein sequence  
 Protein Accession #: NP\_001053.1

1 11 21 31 41 51  
 | | | | |  
 MRQSHQLPLV GLLLFSPFIP QLCICEVSE ENYIRLKP LL NTMIQSNYNR GTSAVNVVLS 60  
 LKLVGIQIQT LMQRMIQIQL YNVKSRSLSDV SSGELALIL ALGVCRNAEE NLIYDYHLTD 120  
 KLENKPQAEI ENMEAHNGTP LTNYYQLSLD VLALCLFNGN YSTAEVNVHF TPENKNYYFG 180  
 SQFSVDTGAM AVLALTCVKK SLINGQIKAD EGSLKNISYI TKSLVEKILS EKKENGLIGN 240  
 TFSITGEAMQA LPSVSDYVNE NDWNQQTILN TVLTEISQGA FSNPNAAAQV LPALMGKTF 300  
 DINKDSSCVS ASGNFISAD EPITVTPFDS QSYISVNVSV RINETYFTNV TVLNGSVFLS 360  
 VMEKAQKQND TIFGFTMEER SNGPYITCIQ GLCANNNDRT YWELLSGGEP LSQAGSYVYV 420  
 RGENLEVRW SKY

Seq ID NO: 475 DNA sequence  
 Nucleic Acid Accession #: NM\_004852.1  
 Coding sequence: 89..1546

1 11 21 31 41 51  
 | | | | |  
 GCCCCCGCCC GCCCCGGGCC CTGATGAGCT GAATGAAGGC TGCTACACC GCCTATOGAT 60  
 GCCTACACAA AGACCTAGAA CGTGCSCCAT GAACCCGAGG CTGACAATGG AAAGTCTGGG 120  
 CACTTTGCAC GCGCGCGCGC GCGGCGGAGC TGGCGGGGGG GCGGCGGGGG GCGGCGGGGG 180  
 CGGCGGCGGG GCGCGGCGGC ATGAGCAGGA GCTGCTGGCC AGCCCCAGCC CCCACCAOCC 240  
 GCGCGCGGCG CCGCGTGGCT CGCTGCGGGG COCTCCGCGC CCTCCAACCG CGCACCAAGG 300  
 GCTGGGCAOG GCGGCAOGCG GCGCAGCGGC GCGCTGCGGC TCGGCCATGG TCACCAGCAT 360  
 GGCCCTOGATC CTGGACGGCG GCGACTACCG GCCCGAGCTC TCCATCCCGC TGCACCAAGC 420  
 CATGAGCATG TCTTGGAGCT CGTCTCGGCC TGGCATGGGC ATGAGCAACA CCTACACCAC 480  
 GCTGACACCG CTCACGCGCG TGCCAACCAT CTCCACCGTG TCTGACAAAT TCCACCAACC 540  
 TCACCCGCAC CACCATCCGC ACCACCAACA CCACCAACAC CACCAAGCGC TGTCCGGCAA 600  
 CGTCAGCGCG AGCTTCACCC TCATGCGCGA CGAGCGCGGG CTCOCGGCCA TGAACAACTC 660  
 CTACAGTCCC TACAAGGAGA TGCCCGGCAT GAGCCAGAGC CTGTCCCGCG TGGCCGCCAC 720  
 GCGGCTGGGC AACCGGCTAG GCGGCTTCCA CAACGCGCAG CAGAGTCTGC CCAACTACGG 780  
 TCCGCGCGGG CAGGCAAAAT TGCTCAGCCC CAACCTGAGC GCGCACCACA CTGCTATGCT 840  
 GACCGCGGGT GAGCAACACC TGTCCCGCGG CCTGGGCACC CCACCTGCGG CCATGATGTC 900  
 GCACCTGAAC GGCCTGCACC ACCCGGGCCA CACTCAGTCT CAOGGGCGGG TGCTGGCACC 960  
 CAGTGGCGAG CGGCCACCTT CGTCTCATC GGGCTCGCAG GTGGCCACGT CGGGCCAGCT 1020  
 GGAAGAAATC AACACCAAGG AGGTGGCCCA GCGCATCACA GCGGAGCTGA AGCGCTACAG 1080  
 TATCCCCAGG GCGATCTTTG GCGAGGGGT GCTGTGCGGG TCTCAGGGGA CTCTCTCGGA 1140  
 CCTGCTCCGG AATCCAAAAC CGTGGAGTAA ACTCAAACTT GGCAGGGAGA CCTTCCGCGC 1200  
 GATGTGGAAG TGGCTTCAGG AGCCCGAGTT CCAGCGCATG TCCGCTTAC GCGTGGCAGC 1260  
 GTGCAACGCG AAGAGGCAAG AACCAACAA AGACAGGAAC AATTCCAGGA AGAAGTCCCG 1320  
 CCGTGTGTTC ACTGACCTCC AACCGCGAAC ACTCTTGCC ATCTTCAAGG AGAACAAACG 1380  
 CCGTCACAG GAGATGCAGA TCACCAATTTC CCAGCAGCTG GCGCTGGAGC TCACCAACGT 1440  
 CAGCAACTTC TTATGAAGG CCGCGCGCG CAGCCTGGAG AAGTGGCAAG ACGATCTGAG 1500

CACAGGGGGC TCCTCGTCCA CCTCCAGCAC GTGTACCAAA GCATGATGGA AGGACTCTCA 1560  
 CTTGGGCACA AGTCACCTCC AAATGAGGAC AACAGATACC AAAAGAAAAA AAAGGAAAAA 1620  
 GACACCGGAT TCCTAGCTGG GGCCCTTCAC TGGTG

5 Seq ID NO: 476 Protein sequence  
 Protein Accession #: NP\_004843.1

1 11 21 31 41 51  
 10 MNPELTMESL GTLHGARGGG SGGGGGGGGG GGGGGPGHEQ ELLASPSPHH ARRGPRGSLR 60  
 GPPPPPTAHQ ELGTAAAAAA AASRSAMVTS MASILDGGDY RPELSIPLEH AMSMCDSSP 120  
 PGMGMSNTYT TLTPQLPLPP ISTVSDKPHH PHPHRHPPHH HHHHRQLRSG NVSGSFTLMR 180  
 DERGLPAMNN LYSPLYKEMPG MSQSLSPPLAA TPLGNLGLGL HNAQQSLPNY GPPGHDKMLS 240  
 15 PNFDHHTAM LTRGEQHLNR GLGTPPAAMM SHLNLGHPG HTQSHGFLVA PSRERFPSSS 300  
 SGSQVATSGD LEEINTKEVA QRITAEIKRY SIPOAIFAQK VLCRSQGTLS DLLRNPKPWS 360  
 LKSGRETFR RMWRKLEQEP FQMSALRLA ACKRKEQEPN KDRNNSQKKS RLVTDLQRR 420  
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20 Seq ID NO: 477 DNA sequence  
 Nucleic Acid Accession #: NM\_013271.1  
 Coding sequence: 27..809

25 1 11 21 31 41 51  
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45 Seq ID NO: 478 Protein sequence  
 Protein Accession #: NP\_037403.1

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55 Seq ID NO: 479 DNA sequence  
 Nucleic Acid Accession #: NM\_002214  
 Coding sequence: 681..2990

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Seq ID NO: 480 Protein sequence  
Protein Accession #: NP\_002205

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GEVSIQLRPG AEANFMLKVH PLKKYFVDLY YLVDVSASME NNIEKLNSVG NDLSRKMAPP 180
SRDFRLGPGS YVDKTVSPYI SIHPERIHQ CSDYNLDMP PHGYIHVLSL TENITEFEKA 240
VHRQKISQNI DTPEGGFDM LQAAVCESHI GWRKEAKRLI LVMTDQTSHL ALDSKLAGIV 300
VPNDGNCHLK NNIVYKSTTM EHPSLQLSE KLIDNNINVI FAVGQKQFHW YKDLLPLLP 360
TIAGIESKA ANLNLVVEA YQKLISEVKV QVENQVQGIY FNITAI CPDG SRKPGMEGCR 420
NVTISDEVLF NVITVMKKCD VTGGRNYALI KPIGFNETAK IHLHRNCSCQ CEDNRGPKGK 480
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VYGKYCEKDD FSCPYHHGNL CAGHGCEAG RCQCFSGWEG DRCQCPASAA QHCVNSKGQV 600
CSGRGTVCVG RCBCDTFRSI GRFCEHCPTC YTACKENWNC MQCLHPNLIS QAILDQCKTS 660
CALMEQQRHV DQTSBCFSSP SYLRIFPIIF IVTFLIGLLK VLIIRQVILQ WNSNKKISSS 720
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Seq ID NO: 481 DNA sequence  
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Coding sequence: 1..2574

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CAAACTAACA AAATCAAAAC GTCATGCCA TTTGGAAGAG TCCAGTTTAA CCTTCTAAAT 840
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TCCTGTGAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGTG 1020
TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCTGAAA GAATAAAAG 1080

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5 GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGGTTCCA 1140  
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 15 CATGGCATTG TTCACAGTGA TCTTAAACCA GCTAACTTTC TGATAGTTGA TGGAAATGCTA 1980  
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 20 ATTTCTAAAT TACATGCCAT AATTGATCCT AATCATGAAA TTGAATTTCC CGATATTCCA 2280  
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Seq ID NO: 482 Protein sequence  
 Protein Accession #: NP\_003309.1

30 1 11 21 31 41 51  
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Seq ID NO: 483 DNA sequence  
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Seq ID NO: 484 Protein sequence

Protein Accession #: NP\_003658.1

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Nucleic Acid Accession #: NM\_005756.1

Coding sequence: 73..3117

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Protein Accession #: Eos sequence

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Seq ID NO: 493 DNA sequence  
Nucleic Acid Accession #: NM\_015507  
Coding sequence: 241..1902

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5 TCTTGATATA GATATGCCAA TATTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100  
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10 Seq ID NO: 494 Protein sequence  
 Protein Accession #: NP\_056322

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 20 SLRGDVFFPK VNEAGFGLI LVQRKALTSK LEHKDLNISV DCSFNHIGCD WKQDREDDFD 420  
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25 Seq ID NO: 495 DNA sequence  
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Seq ID NO: 496 Protein sequence  
Protein Accession #: NP\_003497.1

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Protein Accession #: NP\_009127

1 11 21 31 41 51

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Seq ID NO: 501 DNA sequence  
Nucleic Acid Accession #: NM\_006103  
Coding sequence: 29..406

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20 CGCAATGGC TGTGGGAAGG TGTCTGTGT CACTCCCAAT TTCTGAGGTC CAGCCACCAC 420  
CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGGTT CCAGCCACC 480  
TGCCCTCCCT TTTTTCGGGA CTCTGTATTC CCTCTGGGC TGACCACAGC TTCTCCCTTT 540  
CCCAACCAAT AAAGTAAACA CTTCAGCAA AAAAAAAAAA AAAA

25 Seq ID NO: 502 Protein sequence  
Protein Accession #: NP\_006094

30 1 11 21 31 41 51  
MPACRLGPIA AALLLSLLLF GFTLVSGTGA EKTGVCPBLQ ADQNCITQECV SDSECADNLK 60  
CCSAGCATFC LLCPNDKEGS CPQVNIFFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVSC 120  
VTFNF

35 Seq ID NO: 503 DNA sequence  
Nucleic Acid Accession #: NM\_002407  
Coding sequence: 65..352

40 1 11 21 31 41 51  
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TTCTGGCTGC AAATCCTCTGG AGGACATGGT TGAAAAGACC ATCAATTCCG ACATATCTAT 180  
ACCTGAATAC AAAGAGCTTC TTCAGAGTT CATAGACAGT GATGCGCTG CAGAGGCTAT 240  
GGGGAATTC AAGCAGTGT TCCTCAACCA GTCACATAGA ACTCTGAAA ACTTTGACT 300  
45 GATGATGCAT ACAGTGTACG ACAGCATTG GTGTAATATG AAGAGTAATT AACTTTATCC 360  
AAGGCGTTTG GCTCAGAGGG CTACAGACTA TGGCCAGAAC TCATCTGTG ATTGTAGTAA 420  
ACCACTTTTC TTCTTGTGT TGTCTTTTA TGTGAAACT GCTAGACAC TGTTGAAACC 480  
TCAATTCAT TTCCATTTC AATACTAAT GCAATC

50 Seq ID NO: 504 Protein sequence  
Protein Accession #: NP\_002398

55 1 11 21 31 41 51  
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KFKQCFNLQS HRTLKNFGLM MHTVYDSIWC NMKSN

60 Seq ID NO: 505 DNA sequence  
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Coding sequence: 171..2126

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TCCGCCCTC AGGTCTCTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180  
ATGATGAAT TCTCAATAT TATGAATTAC ATGAACTAT TGGGACAGT GGCTTTGCAA 240  
AGGTCAAACT TGCTGCGCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300  
AAAACACACT AGGGAGTGAT TTGCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC 360  
70 TGAGACATCA GCATATATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420  
TGGTTCTTGA GTACTGCCCT GSAGGAGAGC TGTTTGACTA TATAATTTC CAGGATGCCC 480  
TGTCAGAAGA GGAGACCGGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540  
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75 ATCTACAGAC ATGCTGTGGG AGTCTGGCT ATGCAGCACC TGAGTTAATA CAAGGCAAT 720  
CATATCTTGG ATCAGAGGCA GATGTTTGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780  
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GAAAATATGA TGTTCOCAG TGGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC 900  
80 TGCAAGTGA CCAAGAAAA CGGATTCTTA TGAATAATCT ATTGAACCAT CCCTGGATCA 960  
TGCAAGATTA CAACTATCCT GTTGAAGTGC AAAGCAAGAA TCCTTTTATT CACTCGATG 1020  
ATGATTGGGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAAAAC ATGAGGAGT 1080  
TAATTTCACT GTGGCAGTAT GATCACTCA CGGCTACCTA TCTTCTGCTT CTAGCCAGA 1140  
AGGCTCGGG AAAACAGATT GGTTAAGGC TTTCTTCTT CTCTGTGGA CAAGCCAGT 1200  
CTACCCCAT CACAGACATC AAGTCAATA ATTGAGTCT GGAAGATGTG ACCGCAAGT 1260

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GATATTATTT TGTGTATGAA TCTAAATCAA GCCATCTGT CATTATGTGA CTGTCTTTT 2340
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Seq ID NO: 506 Protein sequence

Protein Accession #: NP\_055606.1

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AYVHSQQYAH RDLKPEMLLP DEYHKLKLLD FGLCAKPKGN KDYLQCTCCG SLAYAAPELI 180
QKGSYLGSEA DVVSMGILLY VLMCGFLFFD DDNVMALYKK IMRGKYDVFK WLSFSSILL 240
QQMLQVDPKK RISMKNLNPH PHIMQDYNYP VEWQSKNPF I HLDDDCVTEL SVHHRNNRQT 300
MEDLISLWQY DHLTATYLLD LAKKARGKPV RLRLSSPFCG QASATPFPTDI KSNWNSLEDV 360
TASDKNVVAG LLDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTFANKL 420
KNKENVYTPK SAVKNEEYFM FPEPKTPVNK NQHKREILTT PNRYTTPSKA RNQCLKETPI 480
KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
LTRSKRRGSA RDGPRRLKLV YNVTTTRLVN PDQLLNEIMS ILPKKHVDFV QKGYTLKCOQ 600
QSDPGKVTMQ FELEVQQLQK PDVVGIRQR LKGDWVYKR LVEDILSSCK V

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Seq ID NO: 507 DNA sequence

Nucleic Acid Accession #: NM\_000582

Coding sequence: 88..990

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CAGAATCTCC TAGCCCCACA GACCCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCCATG 300
GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATGTACTCG 360
AACGATCTCG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
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TTCCTCCAGC TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
GGACTGAGGT CAAAATCTAA GAAATTTGCG AGACCTGACA TCCAGTACCC TGATGCTACA 600
GACGAGGACA TCACTCACA CATGGAAGGC GAGGAGTTGA ATGGTGATA CAAGGCCATC 660
CCCGTTGCCC AGGACCTGAA CGGCGCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720
GAAACGAGTC AGCTGAGTGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780
TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCGG ATGTGATTGA TAGTCAGGAA 840
CTTTCCAAAG TCAGCCGCTGA ATTCCACAGC CATGAATTTT ACAGCCATGA AGATATGCTG 900
GTTGTAGACC CCAAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA 960
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ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT 1200
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Seq ID NO: 508 Protein sequence

Protein Accession #: NP\_000573

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1 11 21 31 41 51
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DFPTDLPAPE VFTPVVFTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYFDA TDEDITSHME 180
SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
NEHSDVIDSQ ELSKVSREPH SHEPHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN

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Seq ID NO: 509 DNA sequence  
Nucleic Acid Accession #: AB051390.1  
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10	GCCCAGGGCA	CGCGCGCGA	GGGCTACACC	GAGTTCAGCC	TCCGCGTGGA	GGGCGACCCC	240
	GACTTCTACA	AGCGGGGAAC	CAGTACCGC	GTAACACTTT	CAGCTGCTCC	TCCCTCTAC	300
	TTCAGAGGAT	TCACATTAAT	TGCCCTCAGA	GAGAACAGAG	AGGGTGATAA	GGAGAAGAC	360
	CATGCTGGGA	CCCTCCAGAT	CATAGACGAA	GAAGAACTC	AGTTTATGAG	CAATTGCCCT	420
	GTTCAGTCA	CTGAAAGCAC	TCCAOGGAGG	AGGACCGGA	TCCAGGTGTT	TTGGATAGCA	480
15	CCACCAGCG	GAACAGGCTG	CGTGATTCTG	AAGGCCAGCA	TCGTACAAAA	ACGCATTATT	540
	TATTTTCAAG	ATGAGGGCTC	TCTGACCAAG	AAACTTTGTG	AACAAGATTG	CACATTTGAT	600
	GGGGTGACTG	ACAAACCCAT	CTTAGACTGC	TGTGCTGCG	GAAGTGCCTG	GTACAGACTC	660
	ACATTTTATG	GGAATTGCTC	CGAGAACACA	CACCCAAAGG	ATTACCTCTG	TCGGGCCAAC	720
	CAGTGGTCTG	CGATCATCGG	AGGATCCAC	TCCAAGAATT	ATGTACTGTG	GGAATATGGA	780
20	GGATATGCGA	CGGAAGGGCT	CAACAAAGTT	GCAGAATTGG	GCTCACCCGT	GAATAATGGAG	840
	GAAGAAATTC	GACCAACAGG	TGATGAGGTC	CTCACCGTCA	TCAAAGCCAA	AGCCCAATGG	900
	CCAGCTCGC	AGCCTCTCAA	CGTGAGAGCA	GCACCTTCAG	CTGAATTTTC	CGTGGACAGA	960
	AGCGGCCATT	TAATGTCTCT	CCTGACCATG	ATGGGCCCTA	GTCGCCAGTG	GAACGTAGGC	1020
	TTATCTGCAG	AAGATCTGTG	CACCAAGGAA	TGTGGCTGGG	TCCAGAAGGT	GGTGCAAGAC	1080
25	CTGATTCCTT	GGGACGCTGG	CACGACAGC	GGGGTGACCT	ATGAGTCACC	CAACAAACCC	1140
	ACCATTCCTC	AGGAGAAATC	CCGGCCCTCG	ACCAAGCTCG	ACCATCTCTA	GAGTCTCTTC	1200
	TATGACCTCG	AGGGTGGGTC	CATCACTCAA	GTAGCCAGAG	TTGTCTCGA	GAGAATCGCA	1260
	CGGAAGGGTG	AACAATGCAA	TATTGTACCT	GACAATGTCT	ATGATATTGT	AGCTGACCTG	1320
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	CTGAAGCAG	AGCTGGACCT	CAGCGTCCCT	TGCCCTGACA	CCAGGACTT	CCAGCCCTGC	1500
	ATGGGCCCTT	GCTGCCAGTA	CGAAGACGGC	TCCACCTGCA	CCATGTCCGA	GTGGATCACC	1560
	TGGTCCGCTT	GCAGCATCTC	CTGCGGCATG	GGCATGAGGT	CCCGGGAGAG	GTATGTGAAG	1620
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35	GTCAACAGAG	AGTGCTCTCT	CAGCAGCTGC	CTGATGACCG	AGTGGGGCGA	GTGGGACGAG	1740
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40	TGCAATGCTG	ATCTGGAGCA	GGTGAGAGAG	TGCATGCTCC	CTGAATGCCC	CATTGACTGT	2040
	GAGCTCACCG	AGTGGTCCCA	GTGGTCCGAA	TGTAAACAAGT	CATGTGGGAA	AGGCCACGTG	2100
	ATTGGAACCC	GGATGATCCA	AATGAGAGCT	CAGTTTGGAG	GTGCACCCCT	CCCAGAGACT	2160
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	CGCTGAGGAG	AGGCCCGAGA	GAGCCCGCGG	AGTGAGCAGC	TGAAGGAAGA	GTCTGAAGGG	2280
45	GAGCAGTTCC	CAGGTGTAG	GATGCGCCCA	TGGACGGCCT	GGTCAGAAATG	CACCAAACTG	2340
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50	CAGTATCTCT	GTGGATGCCA	GAGACATCCT	TTCTGAATAC	TTCTTGATGG	GTACAGGCTG	2640
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Seq ID NO: 510 Protein sequence  
Protein Accession #: BAB18461.1

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NVDDIVADLA PERKDEDDTP ETCIYSNWSF WSACSSSTCD KGKRMQRML KAQLDLSVPC 480
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15 PTEETEKCTV NEBCSPSSCL MTENGWDEC SATCGMGMKK RHRMIRNMPA DGSMDKAETS 600
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MLPECPIDCE LTEMNQWSEC NKSCGKGHVI RTRMIQMEPQ FGGAPCPETV QRKRCRIRKC 720
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Seq ID NO: 511 DNA sequence  
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Coding sequence: 76..1401

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AACGCGGAGA TCTCCAAGAG GCTGGGCAAG CGCTGGAAGA TGCTGAAGGA CAGCGAGAAG 360
ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGCTCAAGC ACATGGCCGA CTACCCCGAC 420
35 TACAAGTACC GGCCCGGAAA AAAGCCCAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC 480
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GGTGCAGAAG CCTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCCCAGCGGC 600
GCGGCGGCCA AGCGCGGCGC GGGCAAGGCG GCCAGTCCG GGGACTACGG GGGCGCGGGC 660
40 GACGACTACG TGCTGGGCGG CCTGCGCGTG AGCGGCTCGG GCGCGGCGGG CGCGGGCAAG 720
ACGGTCAAGT CGGTGTTTCT GGATGAGGAC GACGACGACG ACGACGACGA CGACGAGCTG 780
CAGCTGCAGA TCAAAACAGGA GCGGACGAGG GAGGACGAGG AACCAACGCA CCAGCAGCTC 840
CTGCAAGCGC CGGGCGCAGC GCGTGCAGC CTGCTGAGAC GCTACAAAGT GCGCAAGATG 900
CCCGCCAGCC CTACGCTGAG CAGCTCGGCG GAGTCCCGCG AGGGAGCGAG CCTCTACGAC 960
45 GAGGTGCGGG CCGGCGCGAC CTGCGGCGCC GGGGCGGGCA GCGGCTCTTA CTACAGCTTC 1020
AAGAAATCA CCAAGCAGCA CCGCGCGCGC CTGCGGCGAG CCGGCTGTC GCCCGGTC 1080
TCGCGCTCGG TGTCACCTC CTGCTCCAGC AGCAGCGGCA GCAGCAGCGG CAGCAGCGGC 1140
GAGGACGCGC AGGACCTGAT GTTCGACCTG AGCTTGAATT TCTCTCAAG GCGCACAGC 1200
GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCGGGGA ACCTGTCCCT GTGCTGCTG 1260
50 GATAAGGATT TGGATTCTGT CAGCGAGGCG AGCCTGGGCT CCCACTTGA GTTCCCGGAC 1320
TACTACGAGC CGGAGCTGAG CGAGATGATC GCGGGGGA CTGCTGGAGG GAACCTCTCC 1380
GACCTGGTGT TCACATATTG AAAGGCGGCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCAG 1440
AGCTGGGTTC CTGGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG 1500
ATGATGGTGG TGTGTATGTT GCGGTGGTGA GGGTGGAGGG GAGAGAAGAA GATGCTGATG 1560
55 ATATTGATAA GATGTCGTGA CGCAAGAAA TTGGAAGAAA TGATGAAAAT TTTGGTGGAG 1620
TTAAAGTGAA ATGAGTAGTT TTTAAACATT TTTCTGTGTC TTTTCTGTGC CCCCCTCCCT 1680
TCCTTTATCG TGCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA 1740
AAAATGTGTT TTTGTAATTA CTATTTCTTT TTCTGAAAT TCGTGATTGC AACAAAGGCA 1800
GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT 1860
60 GTCGCTCTTT GAAAGTCTGA AGACGCTGCG AGAGGAACCT TTTGGCAGCA CAACCTGTAC 1920
TCTAGGAGT TGGTGGAGAT ATTTTITTTT CTTAAGAGAA CTTAAGAAC TGGTGATTTT 1980
TTTTTAACAA AAAAAGGG
```

Seq ID NO: 512 Protein sequence  
Protein Accession #: NP\_003099.1

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65      1      11      21      31      41      51
|      |      |      |      |      |
MVQQAESLEA ESNLPREALD TEEGEFMACS PVALDESDDP WCKTASGHIK RPMNAPMVWS 60
KIERRKIMEQ SPDMHNAREI KRLGKRWKML KDSEKIPFIR EAERLRLLKM ADYPDYKYRP 120
70 RKPKMDPSA KPSASQSPER SAAGGGGSA GGGAGGAKTS KGSSKKCKKL KAPAAAGAKA 180
GAGKAAQSGD YGGAGDDYVL GSLRVSGSGG GGAGKTVKVC FLDEDDDDDD DDELQLQIK 240
QEPDEDEEP PHQQLQPPG QQPQLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVRAG 300
ATSGAGGGR LYYSFRNITK QHPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD 360
75 LMFDSLNFPS QSAHSASEQQ LGGAAAGNL SLSLVDRDL D SPSGSLGSH FEFPDYCTPE 420
LSEMIAGDWL BANFSDLVPT Y
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Seq ID NO: 513 DNA sequence  
Nucleic Acid Accession #: CAT Cluster

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80      1      11      21      31      41      51
|      |      |      |      |      |
GGTGCACCTA AATCTGATAA CTGGCTTATT ATGTAATTTA TTGGTGTAT TATAGTAGAG 60
ATTGGTAATC TACAGTAAGA TTTTCAGTTA GGATTTGAGA TTATGATAAT AACTAATAGA 120
ATATTTCTAA ATTGGAATTA GAAGATTGTT GTATGACAGA GAGTCAGGAC TTGCCATTGG 180
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GCAAAACATCA AAGTCATTGT TTGGTGTGTA ATAGTACAAA ATCATCTTGC TTAACAGAGA 240  
AAGGATATCT GTTGTCTCCCG AATGAAACAA TTTTCTGTAA ATAGAGGGCC CAGAAATGGT 300  
CTCTGACAAAT TAATAAAGAC ATCAAAGATA GCAAAATGAT TTTTATATCT TAGGGCCAAT 360  
ACTACCAATT TAATAATTAA AACAAATTCT GGTGAGCTCT GAACCTGGCA GAATTGGTGG 420  
CAACATAGAC TTTGGATTCT CCAAAATCCC CACATAAAAC AAAGGGGATC AACTAGATAG 480  
AAAAACCAGA AACCTTTGGA AATATCTGTT TAAAAAATAA AAAAAGTCGA CGCGGGCC

Seq ID NO: 514 DNA sequence

Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51  
GGAGCCACAG TGAAGTCAA GAATGTCAGT GATTCCACAT TTAATATCTA CATTITTGCA 60  
GGGCGATTAC TCTTTTGTAG TATAACATTG AGCTGATAGC ACATAGTGTA GACAAGTGAA 120  
TACAGGATTC TCTGGGTTGT ATTCCAGAA GTCTGGAGGT CATTTGGATA TTTGTGGGCC 180  
CTTGGCTTCA CTCTGACTTG TGTGACACAT AAAAATTGTG ATGAAATGTC CTATAGATGT 240  
CCTGCAGGTC TTAAGAAAGC CTTTCCAAAC TATGAAACAG CCCAGCAGCA CTGAGTTAGA 300  
GGTAAATTCT GAACCTTGA AACTATAAAC TATTCTAAT GCACATAGAA TTGGCAAGTA 360  
GCATTCTATG TCTATGAACA GTATGTCCTT TCTATATAAC AGAGAAAATC TTTTAAAGCA 420  
AACTACTCAG TTTAAACCTT AATCTCTCTC ATAATCTCAG TACTTTTGAA TGAAGACATA 480  
TCAATGCAAC AGTACACTCT TATTGAGGCA TTGAAAGAA AGAATTCGAG ATCTAGTTTG 540  
TATCAGATAT TATAAATTAG TATGGTTTAG TCTTTGTCTAT GAAATCTAC TTAATTTTGT 600  
GACTATAGT TTAAGAATGT AAGCAGAAGT TCTGCACCAA TCAGAATAAG CTACATTATG 660  
CTTGAGTGAC AACTACTGTA ATGACAAAAT ATCAGTGGCT TAATACAATG GTTTTCTCT 720  
CATACTTGT CATAAAGAGT CAGCAAGGAC CCTGCTCATT ATGGTCCCTC AGGGACCCAG 780  
GGTTGTGGA AGCTCCACCA TTTTAGATAG CTCCCTTCAA AGTCAGCCAT CTTTGGCAGT 840  
CCATGTCCCC CAACAGGCTG GCAAAATTTG GCTCTGGATG GCTTCAAGGA TTGAGCATCG 900  
GGCAGTTTAA ATGCTTTCAA CATGAAAGT GGACACCGGC CACTCCCTCT CATATCCCTT 960  
GGGCGCAAGC TAGGTCACAG GGGCCGGACC TAACTTCGGA GGGTTGGGGA ATTGTAATTC 1020  
CTCCATGTAC CCAAGTGGGA GAGAAGCCAG ATACTGAGAA ACATCAATAA TGGCTAACAG 1080  
AAATCCATT TACCAATCCC TTTGCCATAA GTGAAAGAT GAGTACTTTC ATCAATTTGT 1140  
AAATCTGACT TTTGAAGTAA ATCCTGGTAG CTGTCATGGG GGCTGGATTT CCAGAAAGCC 1200  
ATATGTAATT TGGGAATGAC ATTCACITAA GCTCATAGAA TATCATTATT TGATGTAAAA 1260  
TGCCCTCAT TGCATACAG GACCAAAATG CACTAACAC AAAACCCCCC TCCCAAGCGG 1320  
GCCCGGGGCT CCTATTCCCC TCCATCCCTT TAAATGAGGC ATTCTATGAT TTGGAATGGA 1380  
AGCCCATGT TAGTGTGAAG AATTTTACTT AATTCAGAA TTATCTCTAC TGAATATGTG 1440  
CCAGTTCTGA AAGGAATGCA AAGTCAAATT TTGCATCTTC TTTGCTCAAG GGCCTTTAGA 1500  
TGTAACACAC CAGACATGAT ACAAGGCTGA CAATGACATT ATGATTTAAA TATGTTAAAC 1560  
AATTATTAA ATTTGTGAATC AACAAAAAAT TATGTTCTTT ATTTATGTTT TTGTCATAGT 1620  
CCTGACTCAC TGCCATACATA CCCCTCTTGT TCCTCAGTTC TTATCCCTGA TTTCTTACAG 1680  
GATGGCTTAA GACAGCTGTA GATGTTTTTA TTAGCAAAA AAAAAAATAA AAAAGTCGAC 1740  
GCGGCCGGA ATTTAGTAG

Seq ID NO: 515 DNA sequence

Nucleic Acid Accession #: NM\_012427

Coding sequence: 43..924

1 11 21 31 41 51  
CTTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGGGG CCATGGCTAC AGCAAGACCC 60  
CCCTGATATG GGGTGTCTGT TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT 120  
GTCTCTGCCA ACAATGATGT TTCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC 180  
AACCAAGACC TGGGAGCTGG GGGCGGGGAA GAGCCCGGCT CGGATGACAG CAGCAGCCGC 240  
ATCATCAATG GATCCGACTG CGATATGCAC ACCCAGCCGT GGCAGGCGCG GCTGTTGCTA 300  
AGGCCCAACC AGCTCTACTG GGGGGCGGTG TTGGTGATC CACAGTGGCT GCTCACGGCC 360  
GCCACTGCA GGAAGAAAGT TTTGAGATC CGTCTCGGCC ACTACTCCCT GTCACCAAGT 420  
TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAAATCCA TCCCCACCC TGGCTACTCC 480  
CACCCGTGCC ACTCTAAAGA CCTCATGCTC ATCAAACTGA ACAGAAGAA TCGTCCCACT 540  
AAGATGTCA GACCATCAA CGTCTCTCT CATTTGCCCT CTGCTGGGAC AAAGTGTCTG 600  
GTGTCTGCTG GGGGACAAAC CAAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC 660  
TTGAATATCA CGTGTCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT 720  
GACACCATGT TCTGCGCCGG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTCTGGG 780  
GGGCCCTGGG TCTGCAATGG CTCCCTGACG GGAATCGTGT CCTGGGGAGA TTACCTTTGT 840  
GCCCGGCCCA ACAGACCGGG TGTCTACAG AACCTCTGCA AGTTCAACAA GTGGATCCAG 900  
GAAACCATCC AGGCCAATCT CTGAGTCATC CCAGGACTCA GCACACCGGC ATCCCCACCT 960  
GCTGCAGGGA CAGCCCTGAC ACTCCTTTCA GACCCCTCAT CTTCCCCAGA GATGTTGAGA 1020  
ATGTTTCTCT CTCCAGCCCC TGACCCCATG TCTCCTGGAC TCAGGGTCTG CTTCCCCAC 1080  
ATTGGGCTGA CGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAAA CTGTCCAGGG 1140  
CGGGGGTGGC GTCTCAATCT CCCTGGGGCA CTTTCATCCT CAAGCTCAGG GCCATCCCT 1200  
TCTCTGAGC TCTGACCCAA ATTTAGTCCC AGAAATRAAC TGAGAAGTGG AAAAAAATAA

Seq ID NO: 516 Protein sequence

Protein Accession #: NP\_036559

1 11 21 31 41 51  
MATARPPWMV VLCAITALL LGVTEHVLN NDVSCDHPSN TVPSGSNQDL GAGAGEDARS 60  
DDSSRIING SDQDMHTQFW QAALLLRPNQ LYCGAVLVHP QWLLTAHCR KKVPRVRLGH 120  
YSLSPVYEG QMFPQGVKSI PEPGYSHPGH SNDLMLIKLN RRIRPTKDV R PINVSSHCP 180  
AGTKCLVSW GPTKSPQVHP PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS 240  
CQDSDGGFVV CNGSLQGLVS WGDYPCARPN RGVYTNLCK FTKWIQETIQ ANS

Seq ID NO: 517 DNA sequence  
Nucleic Acid Accession #: NM\_001719  
Coding sequence: 123..1418

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5      1      11      21      31      41      51
|      |      |      |      |      |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACGGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GSCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCGCACAGC CTTGCTGGCG CTCTGGGCAC 180
10    CCTGTTCCTT GCTGCGCTCC GCGCTGGCGG ACTTCAGCCT GGACAAACAG GTGCACTCGA 240
GCTTCATCCA CCGGCGCTTC CGCAGCCAGG AGCGCGGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
GCCAGGGCTT CTCTACCCC TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
15    GCCTGCAAGA TAGCAATTC CTACCGAAG CGACATGGT CATGAGCTTC GTCAACCTCG 540
TTGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAGATG CCCAGAAGGG GAAGCTGTGA CGGCAGCGGA ATTCCGGATC TACAAGGACT 660
ACATCCGGGA ACGCTTCGAC AATGAGAGCT TCCGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGTACCCTTC TGGGCTCGG 780
20    AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACACGCAA CCACTGGGTG GTCAATCGCG 840
GGCACACCTT GGGCTTCGAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGGGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGAGGC AAACAGCGCA 1020
GCCAGAACCG CTCGAAGCGC CCCAAGAACC AGGAAGCCCT CGGGATGGCC AAGTGGCAG 1080
25    AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTACGCGGCC TACTACTGTG 1200
AGGGGAGAGT TGCCCTTCCCT CTGAACCTCT ACATGAAGGC CACCAACACG GCATCGTGTC 1260
AGACGCTGGT CCACCTTCAT AACCCGGAAG CGGTGCCCAA GCCTGCTGT GCGCCCAAGC 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
30    ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCTTTTG TAGACCTTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
35    TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAACCAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGAGCT GCGATTGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACCAGCCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCGGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAACG AATGAATG
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Seq ID NO: 518 Protein sequence  
Protein Accession #: NP\_001710

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45      1      11      21      31      41      51
|      |      |      |      |      |
MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQRE RREMQRILS 60
ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV PSTQGPPLAS 120
LQDSHFLTDA DMWFSVNLV EHDKEFFPHR YHREPRPDL SKIPEGEAVT AAEFRYIKDY 180
IRERFDNETF RISVTVQLQE HLGRESDLFL LDSRTLWASE EGWLVPDITA TSNHWVNVPR 240
HNLGLQLSVE TLGGGQINPK LAGLIGRHGP QNKQPPMVAE PRATEVHFRS IRSTGSKQRS 300
50    QNRSKTPKQI EALRMANVAE NSSSDQRQAC KRHELYVSPR DLGQDWIIA PEGYAAYYCE 360
GECAFPILNSY MNATNHAIQV TLVHFNPET VPKPCCAPTQ LNAISVLYFD DSSNVILKCY 420
RNMVVRACGC H
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Seq ID NO: 519 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 264..782

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60      1      11      21      31      41      51
|      |      |      |      |      |
CCCTGCTCCA GTCAACCCCG GAAGCTGACT GGTCCAAGCA CAGCTGAAGC ATGAGGAAAC 60
TCATCGCGGG ACTAATTTTC CTTAAATTT AGACTTGCAC AGTAAGGACT TCAACTGACC 120
TTCTCTCAGC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC 180
TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC 240
65    AACTTATCAG CAGGAGCTCT ATCATGCTGA CAGAAGTCAT GGAGGTCTGG CATGGCTTAG 300
TGATCGCGGT GGTGTCCCTC TTCTGTCAGG CCTGCTTCCT CACCGCCATC AACTACCTGC 360
TCAGCAGGCA CATGGCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCCAGGTTT 420
CCAGGCCGAG CCTGCGCCAC CATCATCCAC CTGCTGTCAA AGAGATGAAG GAGACTCAGA 480
CAGAGAGAGA CATCCCAATG TCTGATTCCC TTACAGGCA TGACAGCGAC ACACCCTCAG 540
70    ATAGCTTGGG TAGCTCTGCG AGTTGCGCTC CTGCTGCCA GGCCACAGAG GATGTGGATT 600
ACACACAAGT GGTCTTTTCT GACCTGGAG AACTAAAAAA TGACTCCCG CTGGAATATG 660
AGAACATAAA GGAAATCACA GATTATGTCA ATGTCAATCC AGAAAGACAC AAGCCAGTTT 720
TCTGTTATTT TGTCAACCCG GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGGCCATGT 780
GAATTCCAAA TATTTTAAAT GGGGTCCAGT TCTCTATGGA TTCTTACATT TAAATTTGAG 840
75    GGAATGCCA TTTTTCCTCC TTAACAAGG CATGGGGCTC ACAAGTCTAT GGAGACAGGC 900
CAAAAAGAT GTGAGAAGA AACTGATAA ATACACAGAG GTCTCTAAGA CCCATGGACT 960
CCTGGTCTGT ACCCAAAAAA GCTGTTGGTT CCTCAAAAAA AAAACAAGG CTTGGCTGGG 1020
AAAACAGGCC AATGCCCGCG CAAGAAAGGT TGAGATCAGA TGTTAGGAAG AACTTTCAGG 1080
TAAAGTATGA GAACATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCCAGGGA 1140
80    AAATTTTAAA AAGGTTGAAT CAGCTGTGTG AGAGTTCTAT TTGGCAATCT CATGTTTAAA 1200
TGACTTCCCT TTGAGCTCTT TAATTATTGG CAATAAACAA CTCTTTTAAA AGTTTAAAA 1260
AAAATAGCAA CCACACCA
```

Seq ID NO: 520 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
 5 MLTEVMEVWH GLVIAVVSLE LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGH 60  
 HPPAVKEMKE TQTRRDIPMS DSYLRHSDT PSDSLDSSCS SPPACQATED VDYTQVVFSD 120  
 PGEKNDSP DYENIKIITD YVNVNPERHK PSFWYFVNPA LSEPAEDQV AM

Seq ID NO: 521 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 107..328

1 11 21 31 41 51  
 15 CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTCCA AATATTTT 60  
 ATGGGGTCCA GTTCTCTATG GATTCTTACA TTTAATTGT AGGGAATGC CATTTTTCCC 120  
 CCTTAAACAA GGCATGGGGC TCACAAGTCT ATGGAGACAG GCCAAAAGA ATGTGGAGAA 180  
 GAAACTGAT AAATACACAG AGGTCTCTCA GACCATGGA CTCTGGTCT GTACCCAAA 240  
 AAGCTGTTCG TTCTCAAAA ACAAAAACAA GGCTTGGCTG GGAACACAG CCAATGCCCC 300  
 GGCAAGAAAG GTTGAGATCA GATGTTAGGA AGAAGTTTCA GGTAAAGTAT GAGAAGTATG 360  
 20 GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCACAG GAAATTTTAA AAAAGGTTGA 420  
 ATCAGCTGTT GTAGAGTTCT ATTTGGCAAT CTCATGGTAA AATGACTTCC CTTTGAGCTC 480  
 TTTAATTATT GGCATAAAC AACTTCTTAA AAGTTTAA ATAAATAGC AACCACCACC 540  
 A

Seq ID NO: 522 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 30 MPFFPLKQGM GLTSLWRQAK KNVEKKTDKY TEVLKTHGLL VCTQKSCSFL KNKNKAWLGK 60  
 QANAPARKVE IRC

Seq ID NO: 523 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 211..1895

1 11 21 31 41 51  
 40 GGATCTGAGG GGGGCCAGT CACTTCCTCC ACGTTCTCGT GCTGGCGGG AGGAGCGSAT 60  
 GGGGCTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTT TTGGGTGGA 120  
 GAGGAATTAT CTGATAAAAT TCCTGGGTTA ATATTTTAA AACCGGAGAG TTTTAAAAA 180  
 TGATTTTTTT CCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGT AACCAGCATA 240  
 GTGCTTTTC TTTCTCTTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAG 300  
 45 CACAGGTTC TTGAACAGCT GGATTCGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360  
 CTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCAACATCA CAGCTCAACT CCAGGAGGGA 420  
 GAAGTAAT GTTCCCTGA ATGGGATGGA CTCATTGTGT GGCACGAGG AACAGTGGGG 480  
 AAAATATCGG CTGTTCATG CCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540  
 TTCCGACACT GTAAACCCAA TGGAACATGG GATTTTATGC ACAGCTTAAA TAAACATGG 600  
 50 GCCAATTATT CAGACTGGCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660  
 TTCTTTGAAC GCCTCTATG AATGTATACC GTTGGCTACT CCATCTCTT TGGTTCCTG 720  
 GCTGTGGCTA TTCTCATCT TGGTACTTC AGACGATGTC ATTGCACTAG GAACTATATC 780  
 CACATGACT TATTTGTGTC TTTCTGCTG AGAGCTACAA GCATCTTGT CAAAGACAGA 840  
 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900  
 55 CAAAATTCCT TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960  
 GTTGTGATG TATTTTACTT CTTGGCTACA AATTATATAT GATCCTGCT GGAAGGTCTC 1020  
 TACCTGCATA ATCTCATCT TGTGGCTTC TTTTGGACA CCAATAACCT GTGGGGCTTC 1080  
 ATCTTGATAG GCTGGGGGT TCCAGCAGCA TTTGTGCGAG CATGGGCTGT GGCACGAGA 1140  
 ACTCTGCTG ATGCGAGGTG CTGGGAACCT AGTGTGCGAG ACATCAAGTG GATTATCAA 1200  
 60 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTGT TTCTGAATAC GGTTAGAGTT 1260  
 CTAGCTACCA AATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320  
 AAACGGCCA AATCGACACT GGTCTGCTC CTAGTCTTTG GAGTGCAATTA CATGTGTTT 1380  
 GTATGCTGCT CTCACCTCT CACTGGGCTC GGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440  
 TTCTTCAACT CCTTTCAGGG TTTCTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500  
 65 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAAAT TCTCGTGA CTGGAAGAG 1560  
 ACACCGCAT GTGGCAGCG CAGATGCGGC TCAGTGTCTA CCACCGTGAC GCACAGCACC 1620  
 AGCAGCCAGT CACAGGTGGC GGCCAGCACA GGCATGTGTC TTATCTCTGG CAAAGCTGCC 1680  
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740  
 TCAGAGCAGG ACTGCTGCC ACACCTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800  
 70 CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGAATCTAA CCCAGACACT 1860  
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 524 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 75 MLRSSLSSTI VLFLLFSST INESISSRKR HRFLEQLDSD GTITIEBQIV LVLKAKVQCE 60  
 LNITATQLEG EGNCFPEWDG LICWFRGTVG KISAVPCPPY IYDFNHKQVA FRHCNPNGTW 120  
 80 DFMHSLNKTW ANYSDCRLRL QPDISIGKQE FFERLYVMYT VGYSSISFSL AVAILIIGYF 180  
 RRLHCTNRYI EMHLFVSFPL RATSIPVKDR VVHARIGVKE LESLIMQDDP QNSIEATSVD 240  
 KSYIIGCKIA VVMPIYFLAT NYWILVEGL YLEHLIFVAF PSDTKYLWGF ILIGWGFPA 300  
 PVAANAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILPLNTRV LATKIWNENA 360  
 VGHDTKRYR KLAKSTLVLV LVFGVHYIVF VCLPHSPTGL GWEIRMHCEL PFNSFQGFV 420  
 SIIYCYNGE VQAEVKMWS RWNLSVDWKR TPCCGSRRCG SVLTTVTHST SSQSQAAS 480

RMVLISGKAA KIASRQPD SH ITPGYVSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540  
SRPMESNPDT BGOQGETEDV L

Seq ID NO: 525 DNA sequence  
Nucleic Acid Accession #: NM\_005048  
Coding sequence: 143..1795

1 11 21 31 41 51  
10 GGCCGGTGGC CCGGGCCCGA CCACCCAGC TCGCGTCTGT TACTGGCCAC AAGTTTGCTC 60  
TGGCCAGCC AAGTTGGCAA CTGGGAAGCT TCTCCCGGC TCTGGAGGAG GGTCCCTGCT 120  
TCTTCTTACA GCCGTTCCCG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG 180  
GCTAATGTCT GGCAGCTGCC TCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATAC 240  
15 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300  
AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTCCCTGAA TGGGATGGAC TCATTGTGTG 360  
GCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGC CCTCCTTATA TTTATGACTT 420  
CAACCATAAA CAGGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480  
CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT 540  
20 CAGCATAGG AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600  
CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTACTTCA GAGATTGCA 660  
TTGCATAGG AACTATATCC ACATGCACCT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720  
CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780  
AATAATGCAG GATACCCAC AAAATTCCAT TGAGGCAACT TCTGTGACA AATCACAATA 840  
25 TATCGGTGCG AAGATTGCTG TTGTGATGTT TAATTAACCT CTGGCTACAA ATTATTATG 900  
GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTGGACAC 960  
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Seq ID NO: 526 Protein sequence  
Protein Accession #: NP\_005039

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Seq ID NO: 527 DNA sequence  
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40	CTGGGTAGCA	GAAGAAATGG	AACACTGCAC	CAAACTCTGT	GGAAGTTCTG	GCTATCAGCT	2820
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10 Seq ID NO: 528 Protein sequence  
 Protein Accession #: XP\_036683

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70 Seq ID NO: 530 Protein sequence  
 Protein Accession #: NP\_002765

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80 Seq ID NO: 531 DNA sequence  
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Seq ID NO: 532 Protein sequence

Protein Accession #: NP\_036284

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 LVIAVERHMS | IMRMVHNSL | TKKRVTLIL | LVWAIAPMG | AVPTLGNWCL | CNISACSSLA | 180  
 PIYSRSLVFP | WTVSNLMAFL | IMVVVLYRIY | VYVKRKTINV | SPHTSGSISR | RRTPMKLMKT | 240  
 VMTVLGAFVV | CNTPLGLVLL | LDGLNCRQCG | VQHVKKRWFL | LALLNSVNP | IYISYKDEDM | 300  
 YGTMKGMIC | FSQENPERRP | SRIPSTVLSR | SDTGSQYIED | SISQGAVCNK | STS

Seq ID NO: 533 DNA sequence

Nucleic Acid Accession #: NM\_002821

Coding sequence: 150..3362

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 21  
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 51

AACTCCCGCC | TCGGGAAGCC | TCGGGGTGCG | GCTCCGCTGC | CGGCTGCTGC | TGCGGCGCCC | 60  
 GCGCTCCGGT | GCGTCCGCTC | CCTGTGCGCG | CCGCGAGACA | GTCGCGGCCC | GCGCTGCGCG | 120  
 CCTCAGCTCC | TTTTCTGAG | CCGCGCGCGA | TGGGAGCTGC | GCGGGGATCC | CCGGCCAGAC | 180  
 CCGCGCGGTT | GCTCTGCTC | AGCGTCTCTG | TGCTGCGCGT | GCTGGGCGGT | ACCGAGACAG | 240  
 CCATTGTCTT | CATCAAGCAG | CCGTCTCCCG | AGGATGCACT | GCAGGGGCGC | GCGGCGCTGC | 300  
 TTGCTGTGTA | GGTGAGGCT | CCGGGCCCGG | TACATGTGTA | CTGGCTGCTC | GATGGGCCCC | 360  
 CTGTCCAGGA | CACGAGCGG | CGTTTCCGCC | AGGCAGCAG | CCGTACGCTT | GCAGCTGTGG | 420  
 ACCGCGTCA | GACTCTGGC | ACCTTCCAGT | GTGTGCTCG | GGATGATGTC | ACTGGAGAAG | 480  
 AAGCCCGAG | TGCCAAAGCC | TCCTTCAACA | TCAAATGGAT | TGAGGCAGGT | CCTGTGGTCC | 540  
 TGAAGCATCC | AGCCTCGGAA | GCTGAGATCC | AGCCACAGAC | CCAGGTCA | CTTGTTGCC | 600  
 ACATTATGAG | GCACCTCGG | CCCACCTACC | AATGGTTCCG | AGATGGGACC | CCCCTTCTG | 660  
 ATGGTCAGCA | CAACCAACA | GTCAGCAGCA | AGGAGCGGAA | CCGTACGCTC | CGGCCAGCTG | 720  
 GTCCTGAGCA | TAGTGGGCTG | TATTCTGCT | GCGCCACAG | TGCTTTTGGC | CAGGCTTGCA | 780  
 GCAGCCAGAA | CTTCACTTGG | AGCATTGCTG | ATGAAAGCTT | TGCCAGGGTG | GTGCTGGCAC | 840  
 CCGAGGAGCT | GGTAGTAGCG | AGGTATGAGG | AGGCATGTT | CCATTGCCAG | TTCTCAGCCC | 900  
 AGCCACCCCG | GAGCCTGCG | TGGCTCTTGG | AGGATGAGAC | TCCCATCACT | AACCGCAGTC | 960  
 GCGCCCAACA | CCTCCGAGA | GCCACAGTGT | TTGCCAACGG | GTCTCTGCTG | CTGACCCAGG | 1020  
 TCGGCGCAGC | CAATGCGAGG | ATCTACCGCT | GCATTGGCCA | GGGGCGAGGG | GGCCCAACCA | 1080  
 TCATCTCGGA | AGCCACACTT | CACTAGCAG | AGATTGAAGA | CATGCGCTA | TTTGAGCCAC | 1140  
 GGGTGTTCAC | AGCTGGCAGC | GAGGAGCGTG | TGAACCTGCT | TCCCCCAAG | GGTCTGCCAG | 1200  
 AGCCACGCTG | GTGTGGGAG | CACGCGGAG | TCGGCTGCC | CACCATGGC | AGGGTCTACC | 1260  
 AGAAGGGCCA | CGAGCTGGTG | TTGGCCAATA | TTGCTGAAAG | TGATGCTGGT | GTCTACACCT | 1320  
 GCCACGCGGC | CAACCTGGCT | GGTACAGGGA | GACAGGATGT | CAACATCACT | GTGGCCACTG | 1380  
 TGCCCTCTCG | GCTGAAGAAG | CCCCAAGACA | GCCAGCTGGA | GGAGGGCAAA | CCGGCTACT | 1440  
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 TGGAGGTGTA | TGATGGGACA | TGGTACCGTT | GTATGAGCAG | CACCCAGGCC | GGCAGCATCG | 1620  
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 AGCAGTGCACT | GAGTTTGGAC | AAGGAGGCCA | CGGTGCGCTG | TTCAGCCACA | GGCCGAGAGA | 1740  
 AGCCCACTAT | TAAGTGGGAA | CGGCGAGATG | GGAGCAGCCT | CCGAGAGTGG | GTGACAGACA | 1800  
 ACGCTGGGAC | CCTGCATTTT | GCGCGGTGTA | CTGAGATGA | CGCTGGCAAC | TACACTTGCA | 1860  
 TTGCTTCCAA | GGGCGCGCAG | GGCCAGATTC | GTGCCCATGT | CCAGCTCACT | GTGGCAGTTT | 1920  
 TTATCACCTT | CAAAGTGGAA | CCAGAGGCTA | CGACTGTGTA | CCAGGGCCAC | ACAGCCCTAC | 1980  
 TGCACTGCGA | GGCCAGGGG | GACCCCAAGC | CGCTGATTCA | GTGGAAGGCG | AAGGACCGCA | 2040  
 TCTTGGAACC | CACCAAGCTG | GGACCCAGGA | TGACATCTT | CCAAGATGGC | TCCCTGTGTA | 2100  
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 ACATCAAGCA | CAOGAGGCGC | CCCCTCTATG | TGTGGACAA | GCCTGTGCGG | GAGGAGTGGG | 2220  
 AGGGCCCTTG | CAGCCCTCCC | COCTACAAGA | TGATCCAGAC | CATTGGGTTG | TCGGTGGGTG | 2280  
 CCGCTGTGCG | CTACATCAIT | GCGGTGCTGG | GCCTCATGTT | CTACTGCAAG | AAGCGCTGCA | 2340  
 AAGCCAAGCG | GCTGCAGAG | CAGCCCGAGG | GCGAGGAGCC | AGAGATGGAA | TGCCTCAACG | 2400  
 GAGGGCCCTT | GCAGAACGGG | CAGCCCTCAG | CAGAGATCCA | AGAAGAAGTG | GCCTTGACCA | 2460  
 GCTTGGGCTC | GGGCCCGCG | GGCACCAACA | AAGCCACAG | CACAAGTGAT | AAGATGCACT | 2520  
 TCCACGGTCT | TAGCTGCAG | CCAATCACCA | CGCTGGGGA | GAGTGAGTTT | GGGGAGGTGT | 2580  
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5	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAAGCTGAA	CCAGGCCAAC	GTGGTGCGCG	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCTCTG	AGGATTTCCTA	2820
	AGAGCAAGGT	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAAACA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACTGCCTG	GTCACTGCCC	AGAGACAAGT	GAAGGTGTCT	GCCTGGGGCC	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCACTTCCG	CCAGGCCCTGG	GTGCCGCTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCCTGG	3120
10	CCTTCGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
	CAGATGATGA	AGTACTGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGGCTGTCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCGCTCAGG	ATGGCTTGGG	CAGGGAGGGA	CATCTCTAGA	GGGAAGCTCA	3420
15	CAGCATGATG	GGCAAGATCC	CTGTCTCTCT	GGGCTCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
	TTGTCTAGAG	CTGAGCAGGG	CCTGGCCTTT	CCTCTCTCTC	CTCACCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCTTGCCAC	3600
	CTCTCTCTCT	ATCAGGAGCA	GTGTGGGTGC	CACAGGTAAC	CCCAATTCT	GGCCTTCAAC	3660
	TTCTCCCTCT	GACCGGGTCC	AACTCTGCCA	CTCATCTGCC	AACTTTGCTC	GGGGAGGGCT	3720
20	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCTTAATA	TTCTCAAGTT	CTGGGCACAC	3780
	AGGGTTAATG	AGTCTCTTGC	CCACTGTGCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCTCTC	CCACTCTGGG	CTTGTGCACA	CTGACCCAGA	CCCACTGCTT	3900
	CCCAACCTCT	CTCTCTCTTC	CTCATCTTAA	GTGCTTGGCA	GATGAAGGAG	TTTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACC	GGCCTTTTTC	TATGACCAAC	GGGCGGCTTT	TATATGTAAT	4020
25	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGT	AGGGTGGGGC	CCTGGAGATG	AGGAGGGTGG	4080
	GCCATCCTTA	CCCAACACTT	TTATTGTTGT	CGTTTTTTGT	TTGTTTTGTT	TTTTTGTGTT	4140
	TGTTTTTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTTA		

Seq ID NO: 534 Protein sequence

Protein Accession #: NP\_002812

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	MGAARGSPAR	PRRLPLLVL	LLPLLGGTQT	AIIVFIKQPS	QDALQGRRL	LRCEVEAPGP	60
	VHVYLLDGA	PVQDTERREA	QSSLSFAAV	DRLQDSGTFC	CVARDDVTGE	EARSANASFN	120
35	IKHIEAGPVV	LKHPASEAEI	QPQTQVTLRC	HIDGHPRPTY	QWFRDGTPLS	DQSNBTVSS	180
	KERNLTLRPA	GPEHSGLYSC	CAHSAPQAC	SSQNFLLSTA	DESFARVVLA	PQDVVVARVE	240
	EAMFHCQFSA	QPPPSLQWLF	EDETPITNRS	RPHLRRAIV	FANGSLLLTQ	VRPNAGIYR	300
	CIGQQQRGPP	IILEATLHLA	EIEDMPLFEP	RVPTAGSEER	VTCLPPLKLP	RPSVWHERAG	360
	VRPLTHGRVY	QKQHELVLAN	IAESDAGVYT	CHAANLAGQR	RQDVNITVAT	VPSHLKKPQD	420
40	SQLLEGKFGY	LDCLQVATPK	PTVVWYRNQM	LISEDSRFEV	FKNGTLRLNS	VEVYDGTWYR	480
	CMSSTPAGSI	EAQARVQVLE	KLKFTPPPQP	QQCMFEDKEA	TVPCSATGRE	KPTIKWERAD	540
	GSSLEFWYTD	NAGTLHFARV	TRDDAGNYTC	IASNGPOGQI	RAHVQLTVAV	PITFKVEPER	600
	TTVYQGHATL	LQCEAQGDPK	PLIQWKGKDR	ILDPTKLGR	MHIFQNGSLV	IHDVAPEDSG	660
	RYTCIAGNSC	NIKHTEAPLY	VVDKFPVEES	EGPGSPFFYK	MIQTIGLSVG	AAVAYIIAIVL	720
45	GLMPYCKKRC	KAKRLQKQPE	GEPEMECLN	GGPLQNGQPS	AEIQEEVALT	SLGSGPAATN	780
	KRHSTSDKMH	FFRSLQIPIT	TLGKSEFGEV	FLAKAQGLEE	GVAETLVLVK	SLQTKDEQQQ	840
	LDFRRELFMF	GKLNHANVVR	LLGLCREAEP	HYMWLEYVDL	GDQLQFLRIS	KSKDKELKSG	900
	PLSTKQKVAL	CTQVALGMEH	LSNNRFVHKD	LAARNCLVSA	QRQVKVSALG	LKSDVYNSEY	960
50	YHFRQAWVPL	RHMSPEALIE	GDFSTKSDVN	AFGLVMWEVF	THGEMPHGGQ	ADDEVLLADLQ	1020
	AGKARLPQPE	GCPSLYRLRM	QRCWALSPKD	RPSFSEIASA	LGDSTVDSKP		

Seq ID NO: 535 DNA sequence

Nucleic Acid Accession #: NM\_013952

Coding sequence: 161..1357

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	TTCAGAAGGA	GGAGAGACAC	CGGGCCCGAG	GCACCCCTGC	GGGCGGGGCG	ACCCAAGCAG	60
	TGAGGGCCTG	CAGCCGGCCG	GCCAGGGCAG	CGGCAGGCGC	GGCCCGGACC	TACGGGAGGA	120
60	AGCCCCGAGC	CCTCGGCGGG	CTGCGAGCGA	CTCCCGGGCG	ATGCCTCACA	ACTCCATCAG	180
	ATCTGCCCAT	GGAGGCTGGA	ACCAGCTGGG	AGGGGCCCTT	GTGAATGGCA	GACCTCTGCC	240
	GGAAAGTGTC	CGCCAGCGCA	TCGTAGACCT	GGCCCAACAG	GGTGTAAAGC	CCTGCGACAT	300
	CTCTCGCCAG	CTCGCGTCA	GCCATGGCTG	CGTCAGCAAG	ATCCTTGGCA	GGTACTACGA	360
	GACTGGCAGC	ATCGGCGCTG	GAGTGATAGG	GGGCTCCAAG	CCCAAGGTGG	CCACCCCAAA	420
65	GGTGGTGGAG	AAGATTGGGG	ACTACAAAGC	CCAGAACCTT	ACCATGTTTG	CCTGGGAGAT	480
	CCGAGACCGG	CTCCTGGCTG	AGGGCGTCTG	TGACAATGAC	ACTGTGCCCA	GTGTCAGCTC	540
	CATTAAATGA	ATCATCCGGA	CCAAAGTGCA	GCAACCATTC	AACCTCCCTA	TGGACAGCTG	600
	CGTGGCCACC	GATGTCCTGA	GTCCCGGACA	CACGCTGATC	CCGAGCTCAG	CTGTAACTCC	660
	CCCGGAGTCA	CCCAAGTGGG	ATTCCCTGGG	CTCCAACCTC	TCCATCAATG	GGCTCCTGGG	720
70	CATCGCTCAG	CCTGGCAGCG	ACAAGAGGAA	AATGGATGAC	AGTGATCAGG	ATAGCTGCGG	780
	ACTAAGCAAT	GACTCACAGA	GCAGCAGCAG	CGGACCCCGA	AAGCACCTTC	GCACGATGTC	840
	CTTCAGCCAG	CACCACTCTG	AGCCGCTCGA	GTGCCCATTT	GAGCGGCAGC	ACTACCCAGA	900
	GGCTATGCTC	TCCCCAGAGC	ACAACAAAGG	CGAGCAGGGC	CTCTACCCGC	TGCCCTTGCT	960
	CAACAGCACC	CTGAGCAGCG	GGAAGGCCAC	CCTGACCCCT	TCCACACGCG	CAGTGGGGCG	1020
75	CAACCTCTCG	ACTCACGAGA	CCTACCCCGT	GCTGGCAGCT	CCGCCCTTTT	GGATCTGCAG	1080
	CAAGTCGGCT	CCGGGGTCCC	GCCCTTCAAT	GCCTTTCCCC	ATGCTGCCTC	CGTGTACGGG	1140
	CAGTTCACGG	GCCAGGCCCT	CCTCTCAGGG	CGAGAGATGG	TGGGGCCAC	GCTGCCCGGA	1200
	TACCCACCCC	ACATCCCCAC	CAGCGGACAG	GGCAGCTATG	CCTCCTCTGC	CATCGCAGGC	1260
80	ATGGTGGCAG	GAAAGTGAAT	CTCTGGCAAT	GCCTATGGCC	ACACCCCTTA	CTCCTCTTAC	1320
	AGCGAGGCCCT	GGGGCTTCCC	CAACTCCAGC	TTGCTGAGTT	CCCCATATTA	TTACAGTTCC	1380
	ACATCAAGGC	CGAGTGACCC	GCCCACCACT	GCCAGGCCCT	TTGACCATCT	GTAGTTGCCA	1440
	TGGGGACAGT	G					



1 11 21 31 41 51  
 5 MGARGALLLA LLLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWPMQGSRLR 60  
 LMDSHVQGVV LLSHRNALT AHCFTYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120  
 VSNLYLSPRY LGNSPYDIAL VKLSAPVYTT KHIQPICLQA STFEFENRTD CWTGWGYIK 180  
 EDEALSPHPT LQEVQVAIIN NSMCNHLFLK YSFRKDIFGD MVCAGNAQGG KDACEFGDSGG 240  
 PLACNKNGLW YQIGVVSNGV CGGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSWPLL 300  
 10 PFFLLWALEFL LGPV

Seq ID NO: 541 DNA sequence  
 Nucleic Acid Accession #: NM\_014344  
 Coding sequence: 131..1444

1 11 21 31 41 51  
 15 GCGGCGCGGA TGGGGCCGAA GCGCCCGAAG CCGCGGAGCC CACAAACTGC CGGGCCCGCC 60  
 TCGCCGCGCG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGCGCG ACCGGCACAG 120  
 CCGCGGAGAG ATGGGCGAGG GATGCGGGG CGCCGCGGCC ACCGCGGGGC TCTGGCTGCT 180  
 20 GCGCTGCGGC TCGCTGCTGG CGCTGTGGGG AGGGCTCCTG CCGCGCGGGA CCGAGCTGCC 240  
 CGCCTCCCGG CCGCCCGAAG ACCGACTCCC ACGGCGCCCG GCCCGGAGCG GCGGCCCGCG 300  
 CCGCGCGCCT CGCTTCCCTC TGCCCCCGCC CTGGCGTGG GACGCGCGCG GCGGCTCCCT 360  
 GAAAACTTTC CGGCGCTGCT TCACTCTGCG GGCGCGCGCG GACGCGCGCG CCGGCGAGTC 420  
 CCGGAGGAGC CCGAGGTGGC ACGTGTGAGC CAGGCGAGCC CGGCGGAGG AGAGCGCGCG 480  
 25 GGTGCACGCG GCGCTCTTCT GGAGCGCGCG CTGGAGGAG CAGGTGCCCC CGGGCTTTTC 540  
 GGAGGCCGAG CCGCGCGCGT GGCTGGAGGC GGCTGCGCGC GCCCGGATGG TGGCCCTGGA 600  
 GCGCGGGGCT TCGGGGCGCA GCTCCAACCG ACTGGCCCGT TTTGCCGACG GCACCGCGCG 660  
 CTGCGTGCAG TACGCGATCA ACCGCGAGCA GATTGAGGCG GAGGCGCTGT CTTACTATCT 720  
 30 GCGCGCGCTG CTGGGCTTCC AGCGCCACGT GCGCGCGCTG GCACTGGCTC GGTGGAGGCG 780  
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 35 CCTGACGCGC AACTTCGAGC GGCTGCTAAG CAACCTCTTC AGCCTGCACT GGGACCGCGC 1080  
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 CGAGCGCGCT TTGCACTGCA TGTGCGTGTG CCGCGAGCGG ACCGCGCGCG GGTCTCTGGA 1260  
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 40 TCGCTTCCCC GAGCTGGCGC CCCTTGCAGA CCCCCACGCT CAGCTGCTAC AGCGCGCGCT 1380  
 CGACTTCTCT GCCAAGCACA TTTTGCACGT TAAGGCCAAG TACGGCGCGC GGTCTGGGAC 1440  
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 45 AAAGTTCTGG GAGGACGAAC TCACCGAGGC GAGAAAGTGA ACATTTCTCT CACCCAGCTT 1680  
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 TCCCTTTCCG AAAAAGGAAA ACTTGGCTTT GAGCGGTTGA GCTAATTCTG CAATTTTCTA 1860  
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 50 CTGTGTTCTC CTTTGTGTCC AGCGCGCGGA TGGTGAGATC ACTGTTCCAA GCAGGGGGAC 1980  
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 55 TGTGTTTGAT TTTCAATTTT TATTAAGAAA AAATTTTATT TTACAGAATT TACCTTCTCT 2280  
 GTATATATGT GCATAAAGTG TGGTGTAAT ATACTAAACA AACTTATATT TCAATAAAG 2340  
 GGAGTTTAAA ATTTAAAAA AAAAAA

Seq ID NO: 542 Protein sequence  
 Protein Accession #: NP\_055159

1 11 21 31 41 51  
 60 MGRRMRGAAA TAGLWLLALG SLLALWGGLL PPRTELPASR PPRDLRPRP ARSGGPAPAP 60  
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 65 GVFWSRGLEE QVPPGFSEAQ AAAMLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR 180  
 YGINPEQIQG EALSYYLALR LGLQRHVPL ALARVEARGA QWAVQVEELR AAHWTEGSSV 240  
 SLTRWLPNLT DUVVPAPWRS EDGRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLT 300  
 NFDRLVSNLF SLQWDPVRVQ RATSNLHRGP GGALVFLDNE AGLVHGYRVA GMDKYNELP 360  
 70 LQSVCFRER TARRVLELHR GQDAAARLLR LYRHEPRFP ELAALADPHA QLLQRRDLPL 420  
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 Coding sequence: 1..1290

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 80 TCTCGGTTCA ACACCTTCTG AGTTGTGGTG GCCGATGAGC GTTCCGAAGC CCGGAAAGG 180  
 CCTGTAAAGC GGGCGGACCC GACCTCCAG GCGGACGATG ATTCTTACT TGACCAAGAC 240  
 TTACCTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGGACT CCTGTGACAA CTGCAGCAA 300  
 CAGAGAGAGA TACTGAAGCA GAGAAAGGTG AAAGCCAGGT TGACCATTCG TGCGGTTCTG 360  
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5  
 10  
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ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT 480
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GAAGCTGTGC AAAGAATCAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC 660
ACCGCAGCTG TTGGAGTTGC AGTTAATGTA ATAATGGGCT TTCTGTTGAA CCAGTCTGGT 720
CACCGTCACT CCCATTCCCA CTCCTGCGCT TCAAAATCCC CTACCAGAGG TTCTGGGTGT 780
GAACGTAAAC ATGGGCAGGA TAGCCTG3CA GTGAGAGCTG CATTGTGACA TGCTTTGGGA 840
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TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA 960
TTTCGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTTGAAT 1020
GTAGACTATA TCAAGAAGC CTTGATGAAA ATAGAAGATG TATATTCACT CGAAGATTTA 1080
AATATCTGGT CTCTCACTTC AGGAAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT 1140
GGAAGTTCAT CTAAATGGGA GGAAGTACAG TCCAAAGCAA ACCATTATT ATTGAACACA 1200
TTTGGCATGT ATAGATGTAC TATTCAGCTT CAGAGTTACA GGCAAGAAGT GGACAGAACT 1260
TGTCCAAATT GTCAGAGTTC TAGTCCCTGA
  
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Seq ID NO: 544 Protein sequence

Protein Accession #: XP\_007652.1

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1 11 21 31 41 51
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PVNGAHPFLQ ADDSLLDQD LPLTNSQLSL KVDSCDNCSK QREILKQRKV KARLTIAAVL 120
YLLFMIGELV GGYIANGSLAI MTDALHMLTD LSAIILTLA LMLSSKSPK RFTFGFHRLE 180
VLSAMISVLL VYILMGPLYL EAVQRTIEMV YEINGDIMLI TAAVGVAVNV IMGFLNQSG 240
KRHSHSLSLP SNSPTRGSGC ERNHQDLSLA VRAAFVHALG DLVQSVGVLI AAYIIRFKPE 300
YKIADPTCY VPSLLVAFTT PRIIWDTVVI ILEGVPSHLN VDYIKALMK IEDVSVEDL 360
NIWSLTSGKS TAIVHIQLIP GSSSKWEEVQ SKANHELLNT FGMRYCTIQL QSYRQEVDR 420
CANQSSSP
  
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Seq ID NO: 545 DNA sequence

Nucleic Acid Accession #: AB037765.1

Coding sequence: 1..2478

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1 11 21 31 41 51
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CAACCAGGAA AAGCCTCTTT AGCTTATTTT TGTCAAGCTG ATTCCCAAG AACATCTGTA 180
TTTCTTGAAG CTGTGAATGA GGCTGTTAGA CCTCTGCAGG ACTATGGAAT TTCAGTTGCC 240
AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG GAAAAGAAAA GGATTGTGAT 300
AAAGCATATT TATTCAAGGG CAACATATTG CTCAGAGAA TCCCTACTGA CACCTTGTTT 360
GATGTGAATG CCATTGTGCG CCATGTTCTC TTTGCTCTTC TTTTATAGTA AGTGAATAT 420
ATTACCAACC TGAAGAGCCT TCAGAACATA GAAATGCTC TGAAGAGAAA AGCAATATT 480
ATATTCTCAT ATGTAAGAGC CATTGGAATA CCAGAGCACA GAGCAGTCAT GGAAGCOGCT 540
TTTGTGTATG GGACTACATA CCAATTGTTC TTAACCAACG AAATTGCCCT TTTGAAAAGT 600
ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCAATGTAA ACTAGTCTTG 660
GACTTGACCC AGCAATGTAG AAGAACACTA ATGGAACAGC CATTGACTAC ACTGAACATT 720
CACCTGTTTA TTAAGACAAT GAAAGCACTT CTGTTGACTG AAGTTGCTGA AGATCTCTCA 780
CAAGTTTCAA CTGTCCATCT CCAACTGGGC TTACCACTGG TTTTATTGTT TAGCCAAACG 840
GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTG CTGCGGCTCT TCTGGGAAAA 900
GCAGGAGTTC TACTCTTGT TAAAGGACTCT TTGGAAGTGA ACATTCTCTA AGATGCTAAT 960
GTGGTCTTCA AAGAGCAGA AGAGGGAGTT CCAATGGAAT TTTTGGTATT ACATGATGTT 1020
GATTTAATAA TATCTCATGT GGAAATAAAT ATGCACATTG AGGAATACA AGAAGATGAA 1080
GACAATGACA TGGAAAGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAACTGTT 1140
TTCAAGATA GGAAGAGAAA ATTAACCTTG GAACCTACAG TGAACCTAAC AGAAGAAAAC 1200
TTTAATGCAA CAGTGATGGC TTCTGACAGC ATAGTACTCT TCTATGCTGG TTGGCAAGCA 1260
GTATCCATGG CATTTTGTGA ATCCTATATT GATGTGGCAG TTAAACTGAA AGGCACATCT 1320
ACTATGCTTC TTAAGTAAT AAACCTGTGCA GATTGGTCTG ATGTATGTAC TAAGCAAAAT 1380
GTTACTGAAT TTCTATCAT AAAGATGTAC AAGAAAGGCG AGAACCCAGT ATCTATGCT 1440
GGAATGTAG GAACCGAAGA TCTCTTAAAA TTTATCCAGC TCAACAGGAT TTCTATCCA 1500
GTGAATATAA CATOGATCCA AGAAGCAGAA GAATATTTAA GTGGGGAATT ATATAAGAC 1560
CTCATCTTGT ATTCTAGTGT GTCAGTATTG GGACTATTTA GTCCAACCAT GAAACAGCA 1620
AAAGAAGATT TTAGTGAAGC AGGAAACTAC CTAAAAGGAT ATGTTATCAC TGGAATTTAT 1680
TCTGAAGAAG ATGTTTTGCT ACTGTCAACC AAATATGCTG CAAGTCTTCC AGCCCTGCTG 1740
CTTGCCAGAC ACACAGAAGG CAAATAGAG AGCATCCAC TAGCTAGCAC ACATGCACRA 1800
GACATAGTTC AAATAATAAC AGATGCACTA CTGGAAATGT TTCGGGAAT CACTGTGGAA 1860
AATCTTCCCA GTTATTTTCA ACTTCAGAAA CCATTATTGA TTTTGTTCAG TGATGGCACT 1920
GTAAATCCTC AGTATAAAAA AGCAATATTG AACTGTTAA AGCAGAAATA CTGGATTCA 1980
TTTACTCCAT GCTGGTTTAA TCTAAAGAAT ACTCCAGTGG GGAGAGGAAT CTTGAGGGCA 2040
TATTTTATGC CTCTGCTCTC CCTTCTCTT CTGTGTTTGG TGAATCTGCA TTCAGGTGGC 2100
CAAGTATTTG CATTTCTCTC AGACCAAGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG 2160
AAGAAATTAG AAGCAGGACT AGAAAATCAT ATCACAATT TACCTGTCTA AGAATGGAAA 2220
CCTCTCTCTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC 2280
ACTAGGAAGG TTCCCAAGTG TATGAAGAA ACAGATGTGC AGGAGAATGA TAAGGAACAA 2340
CATGAAGATA AATCGGCAGT CAGAAAAGAA COGATTGAAA CTCTGAGAAT AAAGCATTGG 2400
AATAGAAGTA ATTGGTTTAA AGAAGCAGAA AAATCATTTA GACGTGATAA AGAGTTAGGA 2460
TGCTCAAAAG TGAACATA
  
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Seq ID NO: 546 Protein sequence

Protein Accession #: BAA92582.1

1 11 21 31 41 51

5 MFSGFNVRV GISFVIMCIP YMPTVNSLFE LSPQKYFSTL QPGKASLAYF CQADSPTSIV 60  
 FLEELNEAVR PIQDYGISVA KVMCVKEEIS RYCGKEKDLM KAYLFKGNIL LRBFPTDTLP 120  
 DVNAIVAHVL FALLFSEVKY ITNLEDLQNI ENALKGKANI IPSYVRAIGI PEHRAVMEAA 180  
 FVYGTITYQFV LTTETIALLES IGSEDVEYAH LYFFHCKLVL DLTOQCRRTL MEQPLTTILNI 240  
 HLPKTKMKAP LITEVAEDPQ QVSTVHLQLG LPLVFIVSQQ ATYEADRRTA ESWAVRLLGK 300  
 AGVLLLLRDS LEVNIPOQAN VVFKRAEBSV PVEFLVLHDV DLIISHVENN MHIEIQEDE 360  
 DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVELTEET FNATVMASDS IVLFYAGWQA 420  
 VSMAPLQSYI DVAVKLKQTS TMLLTRINCA DMSDVCTKQN VTEFPIIKMY KKGPNVSYA 480  
 10 GMLGTEDLLK PIQLNRISYP VNITSIQEAE EYLSGELYKD LILYSSVSVL GLFSPMTKTA 540  
 KEDFSEAGNY LRGVYITGIY SBEDVLLST KYAASLPALL LARHTEGKIE SIPLASTHAQ 600  
 DIVQIITDAL LEMFPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKQAIL TLVKQKYLDS 660  
 FTPCNLNLKN TPVGRGILRA YFDPLPPLPL LVLVNLHSGG QVFAPPSDQA IIEENLVNLW 720  
 KKLKAGLENH ITILPAQEWK PPLPAYDFLS MIDAATSQRG TRKVPKCMKE TDQVENDKEQ 780  
 HEDKSAVRKE PIETIRIKHW NRSNWFKEAE KSFRDRKELG CSKVN

15 Seq ID NO: 547 DNA sequence  
 Nucleic Acid Accession #: NM\_033102.1  
 Coding sequence: 1..1662

20 1 11 21 31 41 51  
 ATGGTCCAGA GGCTGTGGGT GAGCCGCGCTG CTGCGGCACC GGAAAGCCCA GCTCTTGCTG 60  
 GTCAACCTGC TAACCTTTGG CCTGGAGGTG TGTTTGGCCG CAGGCATCAC CTATGTGCGG 120  
 CCTCTGTCTG TGGAACTGGG GGTAGAGGAG AAGTTTATGA CCAATGGTCT GGCATTTGGT 180  
 25 CCAGTGTCTG GCTGTGCTCT TGTCCCGCTC CTAGGCTCAG CCAGTGACCA CTGGCGTGA 240  
 GCCTATGGCC GCGCGCGGCC CTTCATCTGG GCACTGTCTT TGGGCATCTT GCTGAGCCTC 300  
 TTCTCATCC CAAGGGCGGG CTGGCTAGCA GGGCTGCTGT GCCCGGATCC CAGGCCCTG 360  
 GAGCTGGCAC TGCTCATCTT GGGCGTGGG CTGCTGGACT TCTGTGGCCA GGTGTGCTTC 420  
 ACTCCACTGG AGGCCCTGCT CTCTGACCTC TTCGGGACCC CGGACCACTG TCGCCAGGCC 480  
 30 TACTCTGTCT ATGCCTTCAT GATCAGTCTT GGGGGCTGCC TGGGCTACCT CCTGCTGCC 540  
 ATTGACTGGG ACACCAAGTC CCTGGCCCCC TACCTGGGCA CCCAGGAGGA GTGCTCTTT 600  
 GGCTGTCTCA CCTCATCTT CCTCACCTGC GTAGCAGCCA CACTGTCTGT GGTGAGGAG 660  
 GCAGCGCTGG GCCCACCGA GCCAGCAGAA GGGCTGTGG CCCCTCTCTT GTGCCCCAC 720  
 TGCTGTCCAT GCCGGGCCCG CTCTGGCTTC CGGAACCTGG GCGCCCTGCT TCCCGGCTG 780  
 35 CACCACTGTG GCTGCGCGAT GCCCGCACCC CTGCGCGCGC TCTTCGTGGC TGAGCTGTGC 840  
 AGCTGGATGG CACTCATGAC CTTCACGCTG TTTTACACGG ATTTCTGTGG CGAGGGGCTG 900  
 TACCAGGGCG TGCCAGAGC TGAGCGGGGC ACCGAGGGCC GGAGACACTA TGATGAAGGC 960  
 GTTCGGATGG GCAGCTGGG GCTGTCTCTG CAGTGCGCCA TCTCCCTGGT CTCTCTCTG 1020  
 40 GTCATGGACC GGCTGGTGCA GCGATTCCGG ACTCGAGCAG TCTATTGGC CAGTGTGGCA 1080  
 GCTTTCCCTG TGGCTGCCGG TGCCACATGC CTGTCCCACTA GTGTGGCGGT GGTGACAGCT 1140  
 TCAGCGCGCC TCACCGGGTT CACCTTCTCA GCCCTGCAGA TCCTGCCCTA CACACTGGCC 1200  
 TCCCTCTACC ACCGGGAGAA GCAGGTGTTT CTGCCCAAT ACCGAGGGGA CACTGGAGGT 1260  
 GCTAGCAGTG AGGACAGCCT GATGACCAGC TTCTGCGCAG GCCCTAAGCC TGGAGCTCCC 1320  
 45 TTCCCTAATG GACAGTGGG TGCTGGAGGC AGTGGCCTGC TCCCACTCC ACCCGCGCTC 1380  
 TGCGGGGCTC CTGCGCTGTA GTCTCCGTA CGTGTGGTGG TGGGTGAGCC CACCGAGGCC 1440  
 AGGGTGGTTC CGGGCGGGG CATCTGCTG GACCTCGCCA TCCTGGATAG TGCCTCTCTG 1500  
 CTGTCCAGG TGGCCCATC CTTGTTTATG GGCTCCATTG TCCAGCTCAG CCAGTCTGTC 1560  
 ACTGCCTATA TGGTGTCTGC CGCAGGCGCT GGTCTGGTGC CCATTACTT TGCTACACAG 1620  
 GTAGTATTGG ACAAGAGCGA CTGGGCCAAA TACTCAGCGT GA

50 Seq ID NO: 548 Protein sequence  
 Protein Accession #: NP\_149093.1

55 1 11 21 31 41 51  
 MVQRLNVSRL LRHRKAQLLL VMLLTGLEV CLAAGITYVP PLLLEVGVVEE KFMIMVLGIG 60  
 FVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120  
 ELALLILGVG LLDPCQVCP TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180  
 60 IDWDSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTEPAS GLSAPSLSPH 240  
 CCPCRARLAP RNLGALLPRL EQLCRMPRT LRLLEVAELC SWMALMTFTL FYTFVVEGL 300  
 YQGVPRAEFG TEARRHYDEG VRMGSGLGLFL QCAISLVFSL VMDRLVQRFQ TRAVYLASVA 360  
 AFPVARGATC LSHSVAVVTA SAALTGTFPS ALQILPYTLA SLYHREKQVF LPKYRGDTGG 420  
 ASSEDSLMIS FLPGPKPGAP FPNGHVAGG SGLLPFPFAL CGASACDVSV RVVVEPTEA 480  
 65 RVVPGRIGLC DLAILDSAFI LSQVAPSLFM GSIVQLSQSV TAYMVAAGL GLVRIYPATQ 540  
 VVFDKSDLAK YSA

70 Seq ID NO: 549 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1389

75 1 11 21 31 41 51  
 ATGGGCTACC AGAGGCAGGA GCGTGTATC COGCGCAGA GAGATTAGA TGACAGAGAA 60  
 ACCCTGTGTT CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGTGTC TCTTTTAAAT 120  
 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTATTCAAT GAAGCAAGCT 180  
 GGGTTTCTTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACGGA CTTTCCCTT 240  
 GTTTTATTGA TAAAGGAGG GGCCTCTCTT GGAACAGATA CCTACCAATC TTTGGTCAAT 300  
 AAAACITTCG GCTTTCCAGG GTATCTGCTC CTCTCTGTTT TTCAGTTTGT GTATCTTTT 360  
 80 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGA 420  
 ATCCAGGAGG TTGATCTCTG AAACGTGTTT ATTTGGTCGC ACTTCATTAT TGGACTTTCC 480  
 ACAGTTACTT TTACTCTGCC TTTATCTGTC TACCGAAATA TAGCAAGCT TGGAAAGGTC 540  
 TCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGAA TTGTAATGGC AAGGGCAATT 600  
 TCACCTGGTC CACACATACC AAAAACAGAA GACGCTGGG TATTTGCAA GCCCAATGCC 660  
 ATCAAGCGCG TCGGGGTTAT GTCCTTTTGA TTTATTTGCC ACCATAACTC CTTCTTAGTT 720

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TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
GTGATTTCTG TATTTATCTG TATATCTTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840
TTCACCCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTGGGA 900
AGATTTTGGT ATGGTGTGAC TGTCAATTTG ACATACCCTA TGGAAATGCTT TGTGACAAGA 960
GAGGTAAATG CCAATGTGTT TTTTGGTGGG AATCTTTTCAT CGGTTTTCCA CATTTGTGTA 1020
ACAGTGTGAG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTCGGGATA 1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
GTTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
ATGCTTCCCA TTGGTGTGCT GGTGATGGTT TTTGGATTGG TCATGGCTAT TACAAATACT 1260
CAAGACTGCA CCAATGGGCA GGAATGTTC TACTGCTTTC CTGACAATT CTCTCTCACA 1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC 1380
TTTCAATGA

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Seq ID NO: 550 Protein sequence  
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIIGSGI IGLPYSMKQA 60
GFPLGLILLF WVSYYTDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPP 120
IAMISYNIIA GDTLSKVFOR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIAKLKGV 180
SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPNA IQAVGVMSPA FICHHNSFLV 240
YSSLEETVA KWSRLHMSI VISVFICIFF ATCGYLTFTG FTQGDLPENY CRNDDLVTFG 300
RFCYGVTVIL TYMPCFVTR EVIANVFFGG NLSSVFHIVV TVMVITVATL VSLLDCLGI 360
VLELNGVLCA TPLIFIIPSA CYLKLSEEPK THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420
QDCTHGQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNISI FQ

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Seq ID NO: 551 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1284

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGGA GAGGATTGCC TTATTCAATG 60
AAGCAAGCTG GGTTCCTCTT GGAATATTG CTTTATTCTT GGGTTTCATA TGTACAGAC 120
TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
TTGGTCAATA AACTTTCGGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTC TCAGTTTTTG 240
TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGTACTTTT GAGCAAAAGT 300
TTTCAAAGAA TCCCAGGAGT TGATCCTGAA AACGTGTTTA TTGGTCGCCA CTTCAATTAT 360
GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACOGAAATAT AGCAAAGCTT 420
GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAA TGTAAATGGCA 480
AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540
CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC 600
TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
ATGTCATCAT TGATTTCTGT ATTTATCTGT ATATTCTTGT CTACATGTGG ATACTTGACA 720
TTTACTGGCT TCACCCAGGG GGACTTATTT GAAAATTAAT GCAGAAATGA TGACCTGGTA 780
ACATTTGGAA GATTTTGTTA TGGTGTCACT GTCAATTTGA CATACCCCTAT GGAATGCTTT 840
GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900
ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCAATTGCT GATTGATTGC 960
CTCGGATAGT TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCTCTCAT TTTTATCATT 1020
CCATCGACCT GTTATCTGAA ACTGTCTGAA GAAACCAAGG CACACTCCGA TAAGATTATG 1080
TCTTGTGTC TACTTCCCAT TGGTGTGCTG GTGATGGTTT TTGATTGGT CATGGCTATT 1140
ACAAATATCT AAGACTGCAC CCATGGGCAG GAAATGTCTT ACTGCTTTCC TGACAATTTC 1200
TCTCTCACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
ATTAGTATCT TTCAACTCGA GTAA

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Seq ID NO: 552 Protein sequence  
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLEFWVSYYTD FSLVLLIKGG ALSGTDYQSS 60
LVNKTFFGPPG YLLSVLQFL YPFIAMISYN ILAGDTLSKV PQRIPGVDP E NVPIGRHFII 120
GLSTVTFITLP LSLYRNIAKL GKVSLLSTGL TTLILGIVMA RAISLGPHIP KTEDAWVPAK 180
FNAIQAVGVM SPAFICHENS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240
FTGFTQGDLE ENYCRNDDLVT FGRFCYGVTV VILTYPMCEP VTREIVANVF FGNLSSVFH 300
IVTVVMVITV ATLVSLLIDC LGIVLELNGV LCATPLIPII PSACYLKLSE EPRTHSDKIM 360
SCVMLPIGAV VMVFGFVMAI TMTQDCTHGQ EMFYCFPDNF SLNTSSEHV QQTTLSTLN 420
ISIFQLE

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Seq ID NO: 553 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1203

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80

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGT TTTCCCTTGT TTTATTGATA 60
AAAGGAGGGG CCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCCGC 120
TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTPTTTGT ATCCTTTTAT AGCAATGATA 180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAGTTT TCAAGAAGAT CCAGGAGTT 240
GATCCTGAAA ACGTGTITAT TGGTCCGCAC TTCAATTATG GACTTTCCAC AGTTACCTTT 300
ACTCTGCCTT TATCCTTGTA CGAAATATA GCAAGCTTGG GAAAGGTCTC CCTCATCTCT 360
ACAGGTTTAA CAACTCTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTTT ACTGGGTCCA 420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAGC CCAATGCCAT TCAAGCGGTC 480

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GGGTTATGT CTTTGCATT TATTTGCCAC CATAACTOCT TCTTAGTTTA CAGTTCTCTA 540  
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTATCCATA TGTCATCGT GATTTCTGTA 600  
TTTATCTGTA TATCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660  
GACTTATTTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTTGGAG ATTTTGTGTAT 720  
GGTGTCACTG TCATTTTGAC ATACCCATG GAATGCTTTG TGACAAGAGA GGTAAATGCC 780  
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTCCACA TTGTTGTAA AGTGATGGTC 840  
ATCACTGTAG CCACGCTGT GTCAATTGCTG ATTGATTGCC TOGGGATAGT TCTAGAATCTC 900  
AATGGTGTGC TCTGTGCAAC TCCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960  
CTGTCTGAAG AACCAAGGAC ACACCTCGAT AAGATTATGT CTGTGTGTCAT GCTTCCCAT 1020  
GGTGTCTGGG TGATGGTTTT TGGATTGCTG ATGGCTATTA CAAATACTCA AGACTGCACC 1080  
CATGGGCAAG AAATGTTCTA CTGCTTTCCT GACAATTTCT CTCTCACAAA TACCTCAGAG 1140  
TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCACTCGAG 1200  
TAA

Seq ID NO: 554 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
| | | | |  
MGYQRQBPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFFG FPGYLLLSVL QFLYPFIAMI 60  
SYNIIAGDTL SKVQRIPIGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLLS 120  
TGLTTLILGI VMARAIISLGP HIPKTEDAWV FAKPNAIQAV GVMSPAFICH HNSFLVYSSL 180  
EPTVAKWSR LIHMSIVISV FICIFPATCG YLFTGTGFTQG DLFENYCRND DLVTGFRFCY 240  
GTVILTYPM ECFVTREVI NVPFGNLS VPHIVVTVMV ITVATLVSL IDCLGIVLEL 300  
NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGPV MAITNTQDCT 360  
RQEMFYCFP DNFSLTNTSE SHVQTTQLS TLNISIFQLE

Seq ID NO: 555 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1140

1 11 21 31 41 51  
| | | | |  
ATGGGCTACC AGAGGCAGGA GCGTGTCTC CCGCCGCGAG TCAATAAAAC TTTGGGCTTT 60  
CCAGGGATC TGCTCCTCTC TGTCTTTCAG TTTTGTATC CTTTTATAGC AATGATAAGT 120  
TACAATATA TAGCTGAGGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180  
CTGAAAACG GTTTTATGG TGCCCACTTC ATTATGGAC TTCCACAGT TACCTTTACT 240  
CTGCCCTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCCTCCCT CATCTCTACA 300  
GGTTTAAACA CTCTGATTCT TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360  
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCCGG 420  
GTTATGTCTT TTGCAATTTT TTGCCACCAT AACTCTCTCT TAGTTTACAG TTCTCTAGAA 480  
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540  
ATCTGTATAT TCTTGTCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600  
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGTT 660  
GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720  
GTGTTTTTTT GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780  
ACTGTAGCCA CCGTGTGTCT ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840  
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCAT CAGCCTGTTA TCTGAAACTG 900  
TCTGAAGAAC CAAGGACACA CTCOGATAAG ATTATGTCTT GTGTCATGCT TCCCATTGGT 960  
GCTGTGGTGA TGTGTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTCGACCCAT 1020  
GGGAGGAAA TGTCTACTG CTTCCTGAC AATTCTCTCT TCACAATAC CTCAGAGTCT 1080  
CATGTTGAGC AGACACACA ACTTCTACT TTAAATATTA GTATCTTTCA ACTGAGTAA

Seq ID NO: 556 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
| | | | |  
MGYQRQBPVI PPQVNKTFFG FGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIGV 60  
PENVPFGRHF IIGLSTVTFI LPLSLYRNI KLKVSLLIST GLTTLILGIV MARAIISLGP 120  
IPKTEDAWVF AKPNAIQAVG VMSFAPICH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180  
ICIFPATCGY LFTGTGTQGD LFNENYCRND LVTFGRFCY VTVILTYPME CFVTREVIAN 240  
VFPFGNLSV FHVIVVTVMV TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300  
SEEPRTSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLINTSES 360  
HVQTTQLST LNISIFQLE

Seq ID NO: 557 DNA sequence

Nucleic Acid Accession #: XM\_057188.1

Coding sequence: 769..4269

1 11 21 31 41 51  
| | | | |  
ATGGGATGTC CTCTCCCTCT CACTCTGGGC TTCTGTCCCA CTCTTATCTT AGTGTCACTC 60  
CTCCCCCAAG TCTGTGTCCC TCTCTCTCCC CTAATCTCTT GGGCCCTCCT TTCTGAGTTC 120  
CTGCCCTTCC CCAATTTCTT TGGTTTGTG ATCCCCCTCT GCGCCCTGCC TCAGTCAAGT 180  
CTCCCCCTGG TGTCTCTCTC CCCCCGCCCC GGACCTCTGC ACCCCCCAGG TCGTGTCCC 240  
TCTGTCCCTT TATCGGGGCC TGGGACCGCG CCTCTCCCGG CCTCCCGCTT TGGGTCTCTC 300  
AAGACTCCCC GCGCCCCAGA CCTCGCCCCG CCGCAGGCTA GCGTGGAAAG TGGAGGATCC 360  
GGTTTGTCTT GGGCGGGTCT GGAAGCAGAG CCGCGGAGG GAGCGCGCGG GCGCTGGGCT 420  
GCAGGAGGTT GCGCGGCGCG CCGCAGCATG GTGGTCCCG AGAAGGAGCA GAGCTGGATC 480  
CCCAAGATCT TCAAGAAGAA GACCTGCACG AGGTTCTATG TTGACTCCAC AGATCGGGG 540  
GATGGGGTCT CGCTCTATTG CCCAGGCTGT TCTCAAATCT CTGGGCTCAA GCAGTCTCTC 600  
TGCCCTGACC TCCCAAAGTG CTTGGATTGT GCGCAGCGCT CCTTGAAGTT TTGCTCAGAA 660  
GAGCAACTT TCTGGGAAGT AGCTGCAGGT GTTGAAGTA GCTGCAGGGG AACTAGGGGA 720

5	TTCAAGGATG	GAGCTGAAAT	GGGTGAACGG	ACAAAGTCGG	TAAACTGAAT	GGAGGATGCC	780
	TTCCGGGGCAG	CCGTGGTGAC	CGTGTGGGAC	AGCGATGCAC	ACACCACGGA	GAAGCCCAACC	840
	GATGCCCTAG	GAGAGCTGGA	CTTCACGGGG	GCCGGCCGCA	AGCACAGCAA	TTTCTCTCGG	900
	CTCTCTGACC	GAACGGATCC	AGCTGCAGTT	TATAGTCTGG	TCACACGCAC	ATGGGGCTTC	960
	CGTGCOCGA	ACCTGGTGGT	GTCAGTGCTG	GGGGGATCGG	GGGGCCCCGT	CCTCCAGACC	1020
	TGGCTGCAGG	ACCTGCTGGG	TCTGTGGGCTG	GTGCGGGCTG	CCCAGAGCAC	AGGAGCCTGG	1080
	ATTGTCACTG	GGGGTCTGCA	CACGGGCATC	GGCGGCATG	TTGGTGTGGC	TGTACGGGAC	1140
	CATCAGATGG	CCAGCACTGG	GGGCACCAAG	GTGGTGGCCA	TGGGTGTGGC	CCCCTGGGGT	1200
10	GTGGTCCGGA	ATAGAGACAC	CCTCATCAAC	CCCAAGGGCT	CGTTCCCTGC	GAGGTACCGG	1260
	TGGCGCGGTG	ACCCGAGGGA	CGGGGTCCAG	TTTCCCTTGG	ACTACAACTA	CTCGGCCTTC	1320
	TTCTCTGGTG	ACGACGGCAC	ACACGGCTGC	CTGGGGGGGG	AGAACCGCTT	CCGCTTGGCG	1380
	CTGGAGTCTC	ACATCTCACA	GCAGAAGACG	GGCGTGGGAG	GGACTGGAA	TGACATCCCT	1440
	GTCTGTCTCC	TCTGTATTGA	TGGTGTAGAG	AAGATGTTGA	CGCGAATAGA	GAACGCCACC	1500
	CAGGCTCAGC	TCCCATGTCT	CCTCGTGGCT	GGCTCAGGGG	GAGCTGCGGA	CTGCCTGGGG	1560
15	GAGACCTGCG	AAGACACTCT	GGCCCCAGGG	AGTGGGGGAG	CCAGGCAAGG	CGAAGCCCGA	1620
	GATCGAATCA	GGCGTTTCTT	TCCCAAAGGG	GACCTTGAGG	TCTCTCAGCG	CCAGGTGGAG	1680
	AGGATTATGA	CCCGGAAGGA	GCTCCTGACA	GTCTATTCTT	CTGAGGATGG	GTCTGAGGAA	1740
	TTGAGAGACA	TAGTTTGTAA	GGCCCTTGTG	AAGGCCTGTG	GGAGCTCGGA	GGCCTCAGCC	1800
20	TACCTTGGATG	AGCTGGGTTT	GGCTGTGGCT	TGGAACCGCG	TGGACATGTG	CCAGAGTGAA	1860
	CTCTTTCTGG	GGGACATCCA	ATGGCGGTCC	TTCCATCTCG	AAGCTTCCCT	CATGGAACGCC	1920
	CTGCTGAATG	ACCGGCTTGA	GTTCGTGCGC	TTGCTCATTT	CCCACGGCCT	CAGCCTGGGG	1980
	CACCTTCTGA	CCCAGATGGG	CCTGGCCCAA	CTCTACAGCG	CGGCGCCCTC	CAACTCGCTC	2040
	ATCCGCAACC	TTTTGGACCA	GGCGTCCAC	AGCGCAGGCA	CCAAAGCCCC	AGCCCCAAAA	2100
25	GGGGGAGCTG	CGGAGCTCCG	GCCCCCTGAC	GTGGGGCATG	TGCTGAGGAT	GCTGCTGGGG	2160
	AAGATGTGGG	CGCCGAGGTA	CCCCCTCGGG	GGCGCCTGGG	ACCTCACACC	AGGCCAGGGC	2220
	TTCCGGGAGA	GCAATATCTT	GCTCTCGGAC	AAGGCCACCT	CGCCGCTCTC	GCTGGATGCT	2280
	GGCCTCGGGC	AGGCCCCCTG	GAGCGACCTG	CTTCTTTGGG	CACCTGTGCT	GAACAGGGGA	2340
	CAGATGGCCA	TGTACTTCTG	GGAGATGGGT	TCCAAATGAG	TTTCTCTCAG	TCTTGGGGCC	2400
30	TGTTTGTCTG	TCCGGGTGAT	GGCACGCTCG	GAGCCTGACG	CTGAGGAGGC	AGCACGGAGG	2460
	AAAGACCTGG	CGTTCAAGTT	TGAGGGGATG	GGCGTTGACC	TCCTTGGCGA	GTGCTATCGC	2520
	AGCAGTGAGG	TGAGGGCTGC	CCGCCTCCTC	CTCCGTGCGT	GGCCGCTCTG	GGGGGATGCC	2580
	ACTTGCCTCC	AGCTGGCCAT	GCAAGCTGAC	GGCCGTGCGT	TCCTTGGCCA	GGATGGGGTA	2640
	CAGTCTCTCG	TGACACAGAA	GTGGTGGGGA	GATATGGCCA	GCACTACACC	CATCTGGGCC	2700
	CTGGTTCTCG	CCCTCTTTTG	CCCTCCACTC	ATCTACACCC	GGCTCATCAC	CTTCAGGAAA	2760
35	TCAGAAAGAG	AGCCCCACAG	GGAGGAGCTA	GAGTTTGACA	TGGATAGTGT	CATTAAATGG	2820
	GAAGGGCCTG	TCCGGAGCGG	GGACCCAGCC	GAGAAGACGC	CGCTGGGGGT	CCCGCGCCAG	2880
	TCCGGCCGTC	CGGGTGTCTG	CGGGGGCCGC	TGCGGGGGGC	GCGCGTGCTC	ACGCCGCTGG	2940
	TTCCACTTCT	GGGGCGCGCC	GGTGACCATC	TTCTATGGGA	AGTGGTCTAG	CTACCTGTCT	3000
40	TTCTGTCTCG	TTTCTCTCGG	GGTGTGCTCT	GTGGATTTC	AGCCCGCGCC	CCCGGGCTCC	3060
	CTGGAGCTGC	TGCTCTATTT	CTGGGCTTTC	ACGCTGCTGT	GCGAGGAAT	GCGCCAGGGC	3120
	CTGAGCGGAG	CGCGGGGCGG	CCTCGCCAGC	GGGGGCCCGG	GGCTGGGCA	TGCTCTACTG	3180
	AGCCAGCGCC	TGCGCCTCTA	CCTCGCCGAC	AGCTGGAACC	AGTGGGACCT	AGTGGCTCTC	3240
	ACCTGCTTCC	TCCTGGGCGT	GGGCTGCGCG	CTGACCCCGG	GTCTGTACCA	CCTGGGCGCC	3300
45	ACTGTCTCT	GCATCGACTT	CATGGTTTTC	ACGGTGGCGG	TGCTTCACAT	CTTCAAGGTC	3360
	AACAAACAGC	TGGGGCCCAA	GATCGTCATC	GTGAGCAAGA	TGATGAAGGA	CGTGTCTTTC	3420
	TTCTCTTCT	TCCTCGGCGT	GTGGCTGGTA	GCCTATGGGG	TGGCCACGGA	GGGGCTCCTG	3480
	AGGCCACGCG	CCAGTGTGCT	CCCAAGTATC	CTGCGCCCGG	TCCTTCTACG	TCCTTCTACG	3540
	CAGATCTTCC	GGCAGATTCC	CCAGGAGGAC	ATGGAAGTGG	CCCTCATGGA	GCACAGCAAC	3600
50	TGCTCGTGG	AGCCCGGCTT	CTGGGCACAC	CCTCTGGGGG	CCAGGCGGGG	CACCTGCGTC	3660
	TCCAGATGTC	CCCACTGGCT	GGTGGTGTCT	CTCTCGTCTG	CTTCTCTGCT	CGTGGCCAAC	3720
	ATCTGTCTGG	TCAACTTGCT	CATTGCCATG	TTCACTTACA	CATTGGGCAA	AGTACAGGGC	3780
	AACAGCGTGG	TCTACTGGAA	GGCGCAGCGT	TACCGCTTCA	TCCGGGAATT	CCACTCTCGG	3840
	CCCGCGCTGG	CCCGGCCCTT	TATCGTCATC	TCCCACTTGC	GCCTCTGCTC	CAGGCAATTG	3900
55	TGCAGGGGAC	CCCGGAGGCC	CCAGCGGTCC	TCCCGGGCCC	TGGAGCATTT	CCGGGTTCAC	3960
	TTTCTTAAGG	AAGCGGAGCG	GAACTGTCTA	ACGTGGGAAT	CGGTGCATAA	GGAGAACTTT	4020
	CTGCTGGCAC	GGGCTAGGGA	CAAGCGGGAG	AGCGACTCCG	AGCGTCTGAA	GCGCACGTCC	4080
	CAGAAGGTGG	ACTTGGCACT	GAAACAGCTG	GGACACATCC	GCGAGTACGA	ACAGCGCCTG	4140
	AAAGTGCTGG	AGCGGGAGGT	CCAGCAGTGT	AGCCCGGTCC	TGGGTGGGT	GGCCGAGGCC	4200
60	CTGAGCGCTG	CTGCTGTGCT	GGCCCGAGGT	GGGCGGCCAC	CCCTGACCT	GGCTGGGTCC	4260
	AAAGACTGAG	CCCTGCTGGC	GGACTTCAAG	GAGAAGCCCC	CACAGGGGAT	TTTGTCTCTA	4320
	GAGTAAGGCT	CATCTGGGCC	TGGGCCCCCG	CACCTGGTGG	CCTTGTCTCT	GAGGTGAGCC	4380
	CCATGTCCAT	CTGGGCCACT	GTGAGGACCA	CCTTGGGAG	TGTCATCTCT	ACAAACCACA	4440
	GCAATGCCGG	CTCTCTCCAG	AACCACTCCC	AGCCTGGGAG	GATCAAGGCC	TGGATCCCGG	4500
65	GCCGTATATC	ATCTGGAGGC	TGCAGGGTCC	TGGGGTAAAC	AGGGAACACA	GACCCCTCAC	4560
	CACCTACAGA	TTCTCTACAC	TGGGGAATA	AAGCCATTTC	AGAGGAAAAA	AAAAAAAATA	4620
	AAAAAAAATA	AAAAAAAATA	A				

Seq ID NO: 558 Protein sequence  
Protein Accession #: XP\_057188.1

70	1	11	21	31	41	51	
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	TWGFAPRNLV	VSVLGGSGGP	VLQTLWQDLL	RRGLVRAAQS	TGAWIVTGGL	HTGIGRHVGV	120
75	AVRDHMAST	GGTKVVMGV	APWGVVRNRD	TLINPKGSFP	ARYRMWDPE	DGVQFPLDYN	180
	YSAFFLVDDG	THGCLGGENR	FRLRLSEYIS	QKKTGVGGTG	IDIPVLLLLL	DGDEKMLTRI	240
	ENATQAQLPC	LLVAGSGGAA	DCLAETLEDT	LAPSGSGGARQ	GEARDRIIRRF	FPRGDLVLQ	300
	AQVERIMTRK	ELLITVYSSD	GSEEFETIVL	KALVKACGSS	EASAYLDELRL	LAVAMNRVDI	360
80	AQSELFRGDI	QWRSHFLEAS	LMDALLNDRP	EFVRLLSHSG	LSLGHFLTPM	RLAQLYSAAP	420
	SNSLIRNLID	QASHSAGTKA	PALKGGAEL	RPPDVGHVLR	MLLGMKCAPR	YPSGGANDPH	480
	PGQGPESMY	LLSDKATSPL	SLDAGLGQAP	WSDLLWALL	LNRAQMAMVF	WEMGSNAVSS	540
	ALGACILLRV	MARLEPDABE	AARRKDLAFK	PEGMGVLDLP	ECYRSSEVRA	ARLLLRRCPL	600
	WGDATCLQLA	MQADARAPFA	QDGVQSLLTQ	KWWDMASTT	PIWALVLAFF	CPFLIYTRLI	660
	TPRKSEEPET	RELEPDMDS	VINGEGPVGT	ADPAEKTPLG	VPRQSGRPGC	CGRCGGRRRC	720



LRRNFHFWGA PVTIFMGNV SYLLFLLLF S RVLVDFQPA PPGSLELLLY FWAFTLLCEE 780  
 LRQGLSGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840  
 HLGRTVLICID FMVPTVRLH IPTVNRQLQP KIVIVSKMK DVFFFLFLG VMLVAYGVAT 900  
 EGLLRPRDS PFSILRRVPY RPYLQIFQOI PQEDMDVALM EHSNCSSEPO FWAHPPGAQA 960  
 GTCVSOYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQGNSDLYN KAQRYELIRE 1020  
 FHSRPAALPP FIVISHLRLL LRQLCRRPRS PQSSPALEH FRVYLSKBAE RKLLTWESVH 1080  
 KENELLARAR DKRESOSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQCSRVLGW 1140  
 VAELSRSL LPPGGPPPPD LPSKD

Seq ID NO: 559 DNA sequence  
 Nucleic Acid Accession #: NM\_006853.1  
 Coding sequence: 26..874

1 11 21 31 41 51  
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 CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180  
 CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCAG CCCTGGCAGG CAGCCCTGTT 240  
 CGAGAAGAGC CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCAGATGGC TCCTGACAGC 300  
 AGCCCACTGC CTCAGCCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCAGAAGGA 360  
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCCG GCTTCAACAA 420  
 CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480  
 CTCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTCA CTGCTGGCAC 540  
 CAGCTGCCTC ATTTCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCTTCAAC 600  
 CTTGGGATGC GCCAACATCA CCATCATTTA GCACCAAGAG TGTGAGAAGC CCTACCCCGG 660  
 CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAAGAA GGGGGCAAGG ACTCTGCCA 720  
 GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCACTCTCTT CAAGGCATTA TCTCTGGGG 780  
 CCAGGATCCG TGTGCGATCA CCGAAAGGCC TGGTGTCTAC ACGAAAGTCT GCAAATATGT 840  
 GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900  
 ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCACCT GTTAATAAGA AACCTAAGC 960  
 CAAGACCTTC TACGAACATT CTTTGGGCCT CCTGGACTAC AGGAGATGCT GTCACTTAAT 1020  
 AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080  
 GACTCTGGGA ATGACAACAC CTGGTTTGT CTCTGTGTGA TCCCCAGCCC CAAAGACAGC 1140  
 TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

Seq ID NO: 560 Protein sequence  
 Protein Accession #: NP\_006844.1

1 11 21 31 41 51  
 MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60  
 AHCLKPRYIV HLGQRNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV 120  
 SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCNAYPG 180  
 NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCATIRKP GVTYTKVCKV 240  
 DWIQETMKNY

Seq ID NO: 561 DNA sequence  
 Nucleic Acid Accession #: AY046419.1  
 Coding sequence: 1..1743

1 11 21 31 41 51  
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 GAGCAGGAAA TGGTGTGAG CTCCTCTGTC ATTGAGAGCC TCCTTGCTTC ACTCACCGGA 180  
 GGGGTCTGTA TAGACAGATA TGAAGAAGG ACAGCAATCA TCTGTGATC CTGCTGCTT 240  
 GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCCTACA CGGTCTTAT AGTGGGACGC 300  
 ATTGCCATAG GGGTTTCCAT CTCCTCTCTT TCCATTGCCA CTGTGTGTTA CATGCGAGAG 360  
 ATTGCTCTCT AACACAGAAG AGGCCCTTCT GTGTCACTGA ATGAGCTGAT GATTGTATC 420  
 GGCATTCTTT CTGCCTATAT TTCAAATTAC GCATTGCCA ATGTTTCCA TGGCTGGAAG 480  
 TACATGTTTG GTCTGTGAT TCCTTGCGGA GTTTTGCAAG CAATTGCAAT GTATTTTCTT 540  
 CCTCCAAGCC CTCGGTTTCT GGTGATGAAA GGACAGAGG GAGCTGCTAG CAAGGTTCTT 600  
 GGAAGGTAA GAGCACTCTC AGATACAAC TGGGAACTCA CTGTGATCAA ATCTCTCCTG 660  
 AAAGATGAAT ATCAGTACAG TTTTGGGAT CTGTTTCGTT CAAAAGACAA CATGCGGACC 720  
 CGAATAATGA TAGGACTAAC ACTAGTATTT TTTGTACAAA TCACTGGCCA ACCAAACATA 780  
 TTGTTCTATG CATCAACTGT TTTGAAGTCA GTTGGAITTC AAAGCAATGA GGCAGCTAGC 840  
 CTCGGCTCCA CTGGGGTTGG AGTGTGCAAG GTCATTAGCA CCATCCCTGC CACTCTTCTT 900  
 GTAGACCATG TGGGAGCAAA AACATTCTCT TGCATTGGCT CCTCTGTGAT GGCAGCTTGG 960  
 TTGGTGACCA TGGGCATCGT AAATCTCAAC ATCCACATGA ACTTCACCCA TATCTGCAGA 1020  
 AGCCACAATT CTATCAACCA GTCTCTGAT GAGTCTGTGA TTTATGGACC AGGAAACCTG 1080  
 TCAACCAACA ACAATACTCT CAGAGACCAC TTCAAAGGGA TTTCTTCCCA TAGCAGAAGC 1140  
 TCACTCATGC CCTGAGAAA TGATGTGGAT AAGAGAGGGG AGACGACCTC AGCATCTCTG 1200  
 CTAATATGCTG GATTAGCCCA CACTGAATAC CAGATAGTCA CAGACCTCTG GGCAGTCCCA 1260  
 GCTTTTGA AATGGCTGTC CTTAGCCAGC TTGCTTGTAT ATGTGTGCTG TTTTCAATT 1320  
 GGTCTAGGAC CAATGCCCTG GCTGGTCTC AGCGAGATCT TTCCTGGTGG GATCAGAGGA 1380  
 CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCTCAT CTGCTGACA 1440  
 TTTTGTAGTG TAAGTATCT TATTGGCCTG CCATGGGTGT GCTTTATATA TACATCATG 1500  
 AGTCTAGCAT CCTGCTTTT TGTGTTATG TTTATACCTG AGACAAAGGG ATGCTCTTGT 1560  
 GAACAAATAT CAATGGAGCT AGCAAAAGTG AACTATGTGA AAAACAACAT TTGTTTATG 1620  
 AGTCATCACC AAGAAGAATT AGTGCCAAA CAGCTCAAA AAAGAAAACC CCAGGAGCAG 1680  
 CTCTGGAGT GTAAACAGCT GTGTGGTAGG GGCCATCCA GGCAGCTTC TCAGAGAGCC 1740  
 TAA

Seq ID NO: 562 Protein sequence  
Protein Accession #: AAL02327.1

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5      1      11      21      31      41      51
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GVLIDRYGRR TAILSSCLL GLGSLVLILS LSYTVLIVGR IAIGVISISLS SIATCVYIAB 120
IAPQHRRLGL VSLNLMIVI GILSAYISNY AFANVFHGWK YMFGLVPLG VLQAIAMYFL 180
PPSPRFLVMK QDEGAASKVL GRLRALSDTT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
10 RIMIGLTLVP FVQITGQPNL LFYASTVLKS VGFQSNAAAS LASTGVGVVK VISTIPTALL 300
VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMFTHICR SHNSINQSLD ESVIYGPGLN 360
STNNNTLRDH PKGISSHSRS SLMLPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
AFLKWLSLAS LLVYVAAPSI GLGPMPLVLV SEIPFGGIRG RAMALTSSMN WGINLLISLT 480
15 FLTVTDLIGL PWVCFIYTIM SLASLLFVVM FIPETKGCSE EQISMELAKV NYVKNNICFM 540
SHHQEELVPK QPQKRKPQEQ LLECNKLCGR GQSRQLSPET

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Seq ID NO: 563 DNA sequence  
Nucleic Acid Accession #: XM\_059466.1  
Coding sequence: 1..894

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CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTAAGAGA CCGACCCCGG GCGCCACAAG 120
25 GAGAGCTGCG AGCGCAGCCG CGCGGGCGCC GACCCCGCGG ACCAGAAGAA CCGCCTGATG 180
CGCTGTGTCG ACCTGCGCTG CGCGGACTCG CCCCCTGCGG GCGCGCGGCT GCTCCCGGGC 240
GGCCCGGGCG GCGCGAGACC CGAGTCTCTG CGCTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
GCCGAGTGCG GCGCGCCCTT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGTACTTTC 360
CTGGGCAATG ACCCGGACAT CGACACCTTC ATCTGAAAG GTATTGCGCA GCGATGCACG 420
30 GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCTTTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGTGTCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGAATCTGTT TCCTCATGAC AGGGATATTT 660
TGCACCATTT CCCTCTGTAC TTATGCGGCC AGTATCTGTT ATGATTGAA CCGGCTCCCA 720
35 AAGCTAATTT ATAGCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCCTGGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCGGTTT 840
ATTAGCGCGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

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Seq ID NO: 564 Protein sequence  
Protein Accession #: XP\_059466.1

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40      1      11      21      31      41      51
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45 PLSHLPLRDS PPLGRRLLPG GPGRADPESW RSLGLGLGLD AECGRPLFAT YSGLWRKCYF 120
LGIDRIDITL ILKGIAQCT AIKYHFSQPI RLNRNIPNLT KTIQDEWHL LHLRRITAGF 180
LGMVAVALLC GCIVATVSFF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRKIAQLK SGRDSTV

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Seq ID NO: 565 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3315

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ACCCGAGACC TGTACTCCAG CGCGTCTCGG AGCAGAGACT TGTCTTACAG TGAAGCGCAC 120
TTGGTGAATT TTATTCAAGC AAATTTTAAG AAACGAGAAT GTGTCTTCTT TACCAAAGAT 180
TCCAAGGCCA CGGAGAAATG GTGCAAGTGT GGCTATGCCC AGAGCCAGCA CATGGAAGGC 240
60 ACCCAGATCA ACCAAAGTGA GAAATGGAAC TACAAGAAAC ACACCAAGGA ATTTCTTACC 300
GAGCCTTTTG GGGATATTCA GTTTGAGACA CTGGGGAAGA AAGGGAAGTA TATACGTCTG 360
TCTCTGCGAC CGGACGCGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGAAA 420
ACACCCAAAC TGGTCAATTC TGTGACGGGG GCGGCCAAGA ACTTCGCCCT GAAGCGCGC 480
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65 ACGGGAGGCA CCCATTATGG CCTGATGAAG TACATCGGGG AGGTGGTGAG AGATAACACC 600
ATCAGCAGGA GTTCAGAGGA GAATATTGTG GGCATTGGCA TAGCAGCTTG GGGCATGGTC 660
TCCAACCGGG ACACCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTTT AGCCAGTAC 720
CTTATGGAGT ACTTCACAAG AGATCCACTG TATATCCTGG ACAACAACCA CACACATTG 780
70 CTGCTCGTGG ACAATGGCTG TCATGGACAT CCCACTGTGG AAGCAAAGCT CCGGAATCAG 840
CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
ATTGTGTGTT TTGCCCAAGG AGGTGGAATA GAGACTTTGA AAGCCATCAA TACCTCCATC 960
AAAAATAAAA TTCTTGTGT GGTGGTGGAA GGCTCGGGCC AGATCGCTGA TGTGATCGCT 1020
AGCCTGGTGG AGGTGGAGGA TGCCCTGACA TCTTCTGCGG TCAAGGAGAA GCTGGTGGCG 1080
75 TTTTACCCC GCACGCTGTC CCGGCTGCCT GAGGAGGAGA CTGAGAGTTG GATCAAAATG 1140
CTCAAGAAA TTCTCGAATG TTCTCACCTA TTAACAGTTA TTAAATGGA AGAAGCTGGG 1200
GATGAAATTG TGAGCAATGC CATCTCCTAC GCTCTATACA AAGCCTTCAG CACCACTGAG 1260
CAAGACAAGG ATAACTGGAA TGGGCAGCTG AAGCTTCTGC TGGAGTGGAA CCAGCTGGAC 1320
TTAGCCAATG ATGAGATTTT CACCAATGAC CGCGATGGG AGTCTGCTGA CCTTCAAGAA 1380
GTCAATGTTA CGGCTCTCAT AAAGGACAGA CCAAGTTTGG TCGGCTCTT TCTGGAGAA 1440
80 GGCTTGAACC TACGGAAGTT TCTCACCAT GATGCTCTCA CTGAATCTT TCCCAACCAC 1500
TTCAGCACGC TTGTGTACCG GAATCTGCAG ATCGCAAGA ATTCTATAA TGATGCCCTC 1560
CTCACGTTTG TCTGGAATC GGTGCGAATC TTCGAAGAG GCTTCCGGAA GGAAGACAGA 1620
AATGGCGGG AGAGATGGA CATAGAATC CAGCAAGTGT CTCCTATTAC TCGGCAACCC 1680
CTGCAAGCTC TCTTCATCTG GGCCATTCTT CAGAATAAGA AGGAATCTC CAAAGTCATT 1740

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5  
10  
15  
20  
25

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TACGAGACCC GGGCTGTTGA GCTGTTCACT GAGTGTACGA GCAGCGATGA AGACTTGGCA 1920  
GAACAGCTGC TGGTCTATTG CTGTGAAGCT TGGGGTGGAA GCAACTGTCT GGAGCTGGCG 1980  
GTGGAGGCCA CAGACCAGCA TTTCATCGCC CAGCCTGGGG TCCAGAAATT TCTTTCTAAG 2040  
CAATGGTATG GAGAGATTTC CCGAGACACC AAGAACTGGA AGATTATCCT GTGTCTGTTT 2100  
ATTATACCTT TGGTGGGCTG TGGCTTTGTA TCATTTAGGA AGAAACCTGT CGACAAGCAC 2160  
AAGAAGCTGC TTGGTACTA TGTGGCGTTC TTCACCTCCC CCTTCTGGGT CTCTCTCTGG 2220  
AATGTGTCTT TCTACATCGC CTTCCTCCTG CTGTTTGCTT ACGTGTCTGT CATGGATTTC 2280  
CATTGCTGTC CACACCCCCC CGAGCTGGTC CTGTACTCGC TGGTCTTTGT CCTCTCTGT 2340  
GATGAAGTGA GACAGTGGTA CGTAAATGGG GTGAATTATT TTACTGACCT GTGGAATGTG 2400  
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CAGAGGATGC TGATCGATGT GTTCTTCTTC CTGTTCTCTT TTGGGTGTG GATGGTGGCC 2640  
TTTGGCGTGG CCAGGCAAGG GATCCTTAGG CAGAATGAGC AGCGCTGGAG GTGGATATTC 2700  
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30 Seq ID NO: 566 Protein sequence  
Protein Accession #: Bos sequence

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55 Seq ID NO: 567 DNA sequence  
Nucleic Acid Accession #: NM\_006911.1  
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75 Seq ID NO: 568 Protein sequence  
Protein Accession #: NP\_008842.1

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Seq ID NO: 569 DNA sequence  
Nucleic Acid Accession #: XM\_036453.1

Coding sequence: 1..3978

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75 Seq ID NO: 570 Protein sequence  
Protein Accession #: XP\_036453.1

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20 Seq ID NO: 571 DNA sequence  
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 Coding sequence: 116..4093

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Seq ID NO: 572 Protein sequence

Protein Accession #: AAC27076.1

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Seq ID NO: 573 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1365

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GGCATAAATG GTATCAAAGA TGCAAGGAAG GTCACCTGAG GTGTGATTGG AAGTGGAGAT 120
TTTGCCAATC CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180
AGAAATCCTA AGTTTGCTTC TGAATTTTTT CCTCATGTGG TAGATGTGAC TCATCATGAA 240
GATGCTCTCA CAAAACAAAT TATAATATT GTTGCTATAC ACAGAGAACA TTATACCTCC 300
CTGTGGGACC TGAGACATCT GCTTGTGGGT AAAATCCTGA TTGATGTGAG CAATAACATG 360
AGGATAAACC AGTACCACCA ATCCAATGCT GAATATTGCG CTTCATTATT CCCGATTCT 420
TTGATTGTCA AAGGATTTAA TGTGTCTCA GCTTGGGCAC TTCAGTTAGG ACCTAAGGAT 480
GCCAGCCGCG AGGTTTATAT ATGCAGCAAC AATATTCAAG GCGACACAAC GGTATTGAA 540
CTTGCCCGCC AGTTGAATTT CATTCGCCAT GACTTGGGAT CCTATCATC AGCCAGAGAG 600
ATTGAAATTT TACCCTTACG ACTCTTTACT CTCTGGAGAG GGCAGGTGGT GGTAGCTATA 660
AGCTTGGCCA CATTTTTTTT CCTTTATGCC TTGTGACAG ATGTGATTCA TCCATATGCT 720
AGAAACCAAC AGAGTGACTT TTACAAAATT CCTATAGAGA TTGTGAATAA AACCTTACCT 780
ATAGTGTCCA TTACTTTGCT CTCCTAGTA TACCTGCGAG GTCTCTGGC AGCTGCTTAT 840
CAACTTTATT ACGGCACCAA GTATAGGAGA TTTCCACCTT GGTGGAAC CTGGTTACAG 900
TGTAAGAAAC AGCTTGGAAT ACTAAGTTT TCTTTCGCTA TGGTCCATGT TGCCTACAGC 960
CTCTGCTTAC CGATGAGAAG GTCAGAGAGA TATTGTTTC TCAACATGGC TTATCAGCAG 1020
GTTTCATGCA ATATTGAAA CTCTTGAAT GAGGAAGAAG TTTGGAGAAT TGAAATGTAT 1080
ATCTCCTTGG GCATAATGAG CCTTGGCTTA CTTTCCCTCC TGGCAGTCAC TTCTATCCCT 1140
TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTAA TTCAGTCTAC ACTTGGATAT 1200
GTGCTCTGCG TCATAAGTAC TTTCCATGTT TTAATTTATG GATGGAACG AGCTTTTGAG 1260
GAAGAGTACT ACAGATTTTA TACACCAOCA AACTTTGTTT TTGCTCTGTG TTTGCCCTCA 1320
ATTGTAATTC TGGATCTTTT GCAGCTTTCG AGATACCCAG ACTGA

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Seq ID NO: 574 Protein sequence

Protein Accession #: Eos sequence

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|      |      |      |      |      |
MESISMGGSP KSLSETCLPN GINGIKDARK VTGVIGSGD PAKSLTIRLI RCGYHVIGS 60
RNPKEASEFP PHVVDVTHHE DALTKTNII PVAIHREHYTS LMDLRHLLVG KILIDVSNM 120
RINQYPSNA EYLAFLPPDS LIVKGFNVVS AWALQGLPKD ASRQVYICSN NIQARQOVIE 180
LARQLNFIPI DLGSLSSARE IENLPLRLFT LWRGPVVVAI SLATFFFLYS FVRDVHPYA 240
RNQSDPYKI PIEIVNKLTP IVAITLLSLV YLAGLLAAAY QLYYGTKYRR PFWLETNLQ 300
CRKQLQLLSP PFAMVHVAYS LCLPMRERSE YLFLANMAYQH VHANIENSWN EREVWRIEM 360
ISFGIMSLGL LSLAVTSIP SVSNALNWR EFSFIQSTLGY VALLISTFHV LIYGWKRAPE 420
EZYRYFTTPP NFVLALVLPS IVILDLLQLC RYPD

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Seq ID NO: 575 DNA sequence  
Nucleic Acid Accession #: NM\_001873.1  
Coding sequence: 3..1721

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GTGGCCCCAG	TGCGCGGGCT	GACACTCATT	CAGCCGGGGA	AGGTGAGGCG	AGTAGAGGCT	180
GGTGCGGAAC	TTGCCGCCCC	CAGCAGCGCC	GGCGGGCTAA	GCCCAGGGCC	GGGCAGACAA	240
AAGAGGCGCG	CGCGTAGGA	AGGCACGGCC	GGCGCGGCG	GAGCGCAGCG	ATGGCCGGGC	300
GAGGGGCGAG	CGCGTGTCTG	GCTCTGTGCG	GGGCACTGGC	TGCTCTGGGG	TGGCTCCTGG	360
GCGCCGAAGC	CCAGGAGCCC	GGGGCGCCCG	CGGCGGGCAT	GAGGCGGCGC	CGGCGGCTGC	420
AGCAAGAGGA	CGGCATCTCC	TTCCAGTACC	ACCGCTACCC	CGAGCTGCGC	GAGGCGCTCG	480
TGTCCTGTGT	GCTGCAGTGC	ACCGCCATCA	GCAGGATTTA	CACGGTGGGG	CGCAGCTTCG	540
AGGGCCGGGA	GCTCTGTGTC	ATCGAGCTGT	CGACAAACCC	TGGCGTCCAT	GAGCCTGGTG	600
AGCCTGAATT	TAAATACATT	GGGAATATGC	ATGGGAATGA	GGCTGTTGGA	CGAGAACTGC	660
TCATTTTCTT	GCCTCAGTAC	CTATGCAACG	AATACCAAG	GGGGAACGAG	ACAATTGTCA	720
ACCTGATCCA	CAGTACCGCG	ATTACATCA	TGCCTTCCCT	GAACCCAGAT	GGCTTTGAGA	780
AGGCAGCGTC	TCAGCTCGGT	GAACCTAAGG	ACTGGTTTGT	GGTTCGAAGC	AATGCCCCAGG	840
GAATAGATCT	GAACCGGAAC	TTTCCAGACC	TGGATAGGAT	AGTGTACGTG	AATGAGAAAG	900
AAGGTGGTCC	AAATAATCAT	CTGTTGAAAA	ATATGAAGAA	AATTGTGGAT	CAAAACACAA	960
AGCTTGCTCC	TGAGACCAAG	GCTGTCTATC	ATTGGAATTAT	GGATATTCCT	TTTGTGCTTT	1020
CTGCCAATCT	CCATGGAGGA	GACCTTGTGG	CCAATTATCC	ATATGATGAG	ACGCGGAGTG	1080
GTAGTGTCTA	CGAATACAGC	TCCTCCCCAG	ATGACGCCAT	TTTCCAAAGC	TTGGCCCGGG	1140
CATACCTCTC	TTTCAACCCG	GCCATGTCTG	ACCCCAATCG	GCCACCATGT	CGCAAGAATG	1200
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GAGGGATGCA	AGACTTCAAT	TACCTTAGCA	GCAACTGTTT	TGAGATCACC	GTGGAGCTTA	1320
GCTGTGAGAA	GTTCACCACT	GAAGAGACTC	TGAAGACCTA	CTGGGAGGAT	AACAAAAAAT	1380
CCCTCATTAG	CTACCTTGAG	CAGATACACC	GAGGAGTTAA	AGGATTGTTC	CGAGACCTTC	1440
AAGGTAACCC	AATTGCGAAT	GCCACCATCT	CCGTGGAAGG	AATAGACCAC	GATGTTACAT	1500
CGCAAAAGGA	TGGTGATTAC	TGGAGATTGC	TTATACCTGG	AACTATATAA	CTTACAGCCT	1560
CAGCTCCAGG	CTATCTGGCA	ATAACAAAGA	AAGTGGCAGT	TCCTTACAGC	CCTGCTGCTG	1620
GGGTTGATTT	TGAACCTGGG	TCATTTTCTG	AAAGGAAAGA	AGAGGAGAAG	GAAGAATTGA	1680
TGGAATGTGT	GAAAAATGAT	TCAGAAACTT	TAAATTTTAA	AAAAGGCTTC	TAGTTAGCTG	1740
CTTTAAATCT	ATCTATATAA	TGTAGTATGA	TGTAATGTGG	TCITTTTCTT	AGATTTTGAG	1800
CAGTTAATAC	TAAACATTGA	TTTATTTTCT	AATCATTTAA	ATATTATCA	ACTTTCCTTA	1860
AAATAAATAG	CCCTTAGGTG	AAAAATATAA	GAACCTTGATA	TATTTCAATC	TCTTATATAG	1920
TATTCATTTT	CCTACCTATA	TTACACAAAA	AAGTATAGAA	AAGATTAAAG	TAATTTTGCC	1980
ATCCTAGGCT	TAAATGCAAT	ATTCCTGGTA	TTATTTACAA	TGCAGAAATT	TTTGAGTAAT	2040
TCTAGCTTTC	AAAAATTAGT	GAAGTTCTTT	TACTGTAAAT	GGTGACAATG	TCACATAATG	2100
AATGCTATTG	AAAAGGTTAA	CAGATACAGC	TCGGAGTTGT	GAGCACTCTA	CTGCAAGACT	2160
TAAATAGTTC	AGTATAAAAT	GTGCTTTTTT	TCTTGTGCTG	ACTAATCTATA	AGCATGATCT	2220
TGTTAATGTT	TTTTTGTATG	GAAGAAAAAG	TACATGTTTA	CAAAGAGGTT	TTATGAAAAA	2280
AATAAAAAAT	GACTTCTTGC	TTGTACATAT	AGGAGCAATA	CTATTATATT	ATGTAGTCCG	2340
TTAACACTAC	TTAAAAGTTT	AGGGTTTTCT	CTTGGTTGTA	GAGTGGCCCA	GAATTGCATT	2400
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Seq ID NO: 576 Protein sequence  
Protein Accession #: NP\_001864.1

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MAGRGGSALL	ALCGALAAAG	WLLGABAEQEP	GAPAAQMRER	RRLQEDGIS	FEYHRYPELR	60
EALVSVWLQC	TAISRYITVG	RSFEGRELLV	IELSDNPGVH	EPGEPEPKYI	GNMHGNEAVG	120
RELLIFLAQY	LCNEYQKQNE	TIVNLIHSTR	IHIMPSLNPD	GPEKAASQPG	ELKDWPFVGRS	180
NAQIDILNEN	FDDLDIRIVV	NEKEGGFNNH	LLKNMKKIVD	QNTKLAPETK	AVIHWIMDIP	240
FVLSANLHGG	DLVANYFYDE	TRSGSAHEYS	SSPDDAIFQS	LARAYSSFPN	AMSDFNRPFC	300
RKNDSDSSPV	DGTTNGGAWY	SVPGGMQDFN	YLSNCFBIT	VELSCEKFPF	EETLKYTWED	360
NKNSLISYLE	QIHRGVKGFV	RDLQGNPIAN	ATISVEGIDH	DVTSARDGDY	WRLLIPGNYK	420
LTASAPGYLA	ITKKVAVPYS	PAAGVDFELE	SPSERKEEBK	EELMEWKMM	SETLAF	

Seq ID NO: 577 DNA sequence  
Nucleic Acid Accession #: E05 sequence  
Coding sequence: 1..933

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TTGACACAGA	GTGATGAGAA	GGAGTGCCCC	AAGGCTAAGT	CGAAATGTGG	CCGACCTTTC	120
TTCCCTCTGT	CCAGCGGCAT	CCATTGCATC	ATTGGTCTGT	TCCGTGCAAA	TGGGTTTGGG	180
GACTGTCCCG	ATGGCAGCGA	TGAAGAGAAC	TGCACAGCAA	ACCCCTCTGT	TTGCTCCACC	240
GCCCGCTACC	ACTGCAAGAA	CGGCTCTGT	ATTGACAAGA	GCTTCATCTG	CGATGGACAG	300
AATAACTGTC	AAGACAACAG	TGATGAGGAA	AGCTGTGAAA	GTTCCTCAAG	ACCCGGCAGT	360
GGGCAAGTGT	TTGTGACTTC	AGAGAACCAG	CTTGTGTATT	ACCCAGCATG	CACCTATGCC	420
ATCATCGGCA	GCTCCGTCAT	TTTTGTGCTG	GTGGTGGCCC	TGCTGGCACT	GGTCTTGAC	480
CACCAAGCGA	AGCGGAACAA	CCTCATGACG	CTGCCCCTGC	ACCGGCTGCA	GCACCCCTGT	540
CTGCTGTCCC	GCTCGGTGGT	CCTGGACCA	CCCCACCACT	GCAACGTCAC	CTACAACTGC	600
AATAATGGCA	TCCAGTATGT	GGCCAGCCAG	GCGGAGCAGA	ATGCGTCCGA	AGTAGGCTCC	660
CACCCCTCCT	ACTCCGAGGC	CTTGCTGGAC	CAGAGGCGCT	OGTGGTATGA	CCTTCTCTCA	720
CGGCCCTACT	CTTCTGACAC	GGAATCTCTG	AAACCAAGCG	ACCTGCCCCC	CTACCGCTCC	780
CGGTCCGAGA	GTGCCAGGCA	TGCCAGCTCC	CAGGCAGCCA	GCAGCCTCCT	GAGCGTGGAA	840
GACACACGCC	ACAGCCCGGG	GCAGCCTGCG	CCCCAGGAGG	GCACTGCTGA	GCCAGGGGAC	900

TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence  
 Protein Accession #: Eos sequence

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1	11	21	31	41	51	
MCSNGRCIPG	AWQCDGLPDC	FDKSDKESCP	KAKSKCGPTF	PPCASGIHCI	IGRFRONGPE	60
DCPDGSDEEN	CTANPLLCT	ARYHCKNGLC	IDKSFICDGO	NNQDNDSE	SCSSQEPGS	120
GQVFVTSNQ	LVYVPSITYA	IIGSSVIFVL	VVALLALVLH	HQRJRNLM	LPVHRLQHPV	180
LLSRLVLDH	PHNCVNTNV	NNGIQYVASQ	AEQNASEVGS	PPSYSEALLD	QRPAYDLP	240
PPYSSDTESL	NQADLPYRS	RSGSANSASS	QAASSLLSVE	DTSHSPGQPG	PQEGTAEPRD	300
SEPSQGTTEE						

Seq ID NO: 579 DNA sequence  
 Nucleic Acid Accession #: AF179274.1  
 Coding sequence: 1..1125

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TGGCTGCTGCT	TGCTGCCCGT	CATGCTACTC	ATCGTAGCCC	GCCCGGTGAA	GCTCGCTGCT	120
TTCCCTACCT	CCTTAAGTGA	CTGCCAAAGC	CCCAACGGCT	GGAATTGTCT	TGGTTATGAT	180
GACAGAGAAA	ATGATCTCTT	CCTCTGTGAC	ACCAACACCT	GTAATTTTGA	TGGGGAATGT	240
TTAAGAATTG	GAGACACTGT	GACTTGOGTC	TGTCAGTTCA	AGTGCAACAA	TGACTATGTG	300
CCTGTGTGTG	GCTCCAATGG	GGAGAGCTAC	CAGAATGAGT	GTTACCTGCG	ACAGGCTGCA	360
TGCAACACAG	AGAGTGAGAT	ACTTGTGGTG	TCAGAAGGAT	CATGTGCCAC	AGATGCAGGA	420
TCAGATCTGT	GAGATGGAGT	CCATGAAGGC	TCGAGAGAAA	CTAGTCAAAA	GGAGCATCC	480
ACCTGTGATA	TTTGCCAGTT	TGGTGCAGAA	TGTGAAGAG	ATGCCGAGGA	TGCTCGGTGT	540
GTGTGTAATA	TTGACTGTTC	TCAAACCAAC	TTCAATCCCC	TCTGCGCTTC	TGATGGGAAA	600
TCTTATGATA	ATGCATGCCA	AATCAAAGAA	GCATCGTGTC	AGAAACAGGA	GAAAATTGAA	660
GTCAATGTCTT	TGGTGTGATG	TCAAGATAAC	ACAACTACAA	CTACTAAGTC	TGAAGATGGG	720
CATTATGC	GAACAGATTA	TGCAGAGAAT	GCTAACAAAT	TAGAAGAAAG	TGCCAGAGAA	780
CACACATAC	CTGTGCGGGA	ACATTACAAT	GGCTTCTGCA	TGCATGGGAA	GTGTGAGCAT	840
TCTATCAATA	TGCAGGAGCC	ATCTTGACAG	TGTGATGCTG	GTTATACCTG	ACAACACTGT	900
GAAAAAAGG	ACTACAGTGT	TCTATACGTT	GTTCCCGGTC	CTGTACGATT	TCAGTATGTC	960
TTAATGCGAG	CTGTGATTGG	AACAATTCAG	ATTGCTGTCA	TCTGTGTGGT	GGTCCTCTGC	1020
ATCACAAGGA	AATGCCCCAG	AAGCAACAGA	ATTCACAGAC	AGAAGCAAAA	TACAGGGCAC	1080
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Seq ID NO: 580 Protein sequence  
 Protein Accession #: NP\_057276.2

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DRENDLFLCD	TNTCKFDGEC	LRIGDTVTVC	QQFKCNNDYV	PVCGSNGESY	QNECYLRQAA	120
CRQGSILV	SEGSCTADAG	SGSGDGVHEG	SGETSQKETS	TCDICQFGAE	CEDEADVWNC	180
VCMIDCSQTN	FNPLCASDGG	SYDNACQIKE	ASQCKQEKIE	VMSLGRQDN	TTTTTKSEDD	240
HYARTDYAEN	ANKLEESARE	HHIPCPPEHYN	GFCMHGKCEH	SINMQEPSCR	CDAGYTGQHC	300
EKKDYSVLV	VPGPVRFQV	LIAAVIGTIQ	IAVICVVVLC	ITRKCPRSNR	IHRQKQNTGH	360
YSSDNTTRAS	TRLI					

Seq ID NO: 581 DNA sequence  
 Nucleic Acid Accession #: S78203.1  
 Coding sequence: 1..2190

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AACATATCCAC	TGAGCATTTG	CTTCATTGTG	GTGAATGAAT	TCTGCGAGCG	CTTTTCCTAT	180
TATGGAATGA	AAGCTGTGCT	GATCCTGTAT	TTCTGTATT	TCTGCACTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCCTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCTCGGGA	300
GCAGCCATTG	CTGACTCGTG	GTTGGGAAAA	TTCAAGACAA	TCATCTATCT	CTCCTTGGTG	360
TATGTGCTTG	GCCATGTGAT	CAGTCTCTTG	GGTGCCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TCCTATCATT	GATCGGCTTG	AGTCTAATAG	CTTTGGGGAC	AGGAGGCATC	480
AAACCCGTGT	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCAG	GGAGCTTGAT	TTCTACATTT	600
ATCACACCCA	TGCTGAGAGG	AGATGTGCAA	TGTTTTGGAG	AAGACTGCTA	TGCATTGGCT	660
TTTGGAGTTG	CAGGACTGCT	CATGTTAATT	GCACTTGTGT	TGTTTGCAAT	GGGAAGCAAA	720
ATATACAAAT	AACCAACCCC	TGAAGGAAAC	ATAGTGGCTC	AAGTTTTCAA	ATGTATCTGG	780
TTTGTCTATT	CCAATCGTTT	CAAGAACCGT	TCTGGAGACA	TTCCAAGCG	ACAGCACTGG	840
CTAGACTGGG	CAGCTGAGAA	ATATCCAAG	CAGCTCATT	TGGATGTAAA	GGCACTGACC	900
AGGGTACTAT	TCCTTTATAT	CCCATTGCCC	ATGTTCTGGG	CTCTTTTGG	TCAGCAGGGT	960
TCAGATGGA	CTTTGCAAGC	CATCAGGATG	AATAGGAATT	TGGGGTTTTT	TGTGCTTCAG	1020
CCGACACAGA	TGCAGGTTCT	AAATCCCTTT	CTGGTTCTTA	TCTTCATCCC	GTGTGTTGAC	1080
TTTGTCTATT	ATGCTCTGGT	CTCCAAGTGT	GGAATTAAT	TCTCATCACT	TAGGAAAAATG	1140
GCTGTTGTTA	TGATCCTAGC	GTGCTGGGCA	TTTGCAAGTT	CGGCAGCTGT	AGAGATAAAA	1200
ATAAATGAAA	TGGCCCCAGC	CCAGTCAGGT	CCCCAGGAGG	TTTTCCTACA	AGTCTTGAAT	1260
CTGCGAGATA	ATGAGGTGAA	GGTGACAGTG	GTGGGAAATG	AAACAATTC	TCTGTTGATA	1320
GAGTCCATCA	AATCCTTTCA	GAAAAACCCA	CACATTTCCA	AACTGCACCT	GAAAAACAAA	1380
AGCCAGGATT	TTCACTTCCA	OCTGAAATAT	CACAATTTGT	CTCTCTACAC	TGAGCATTTCT	1440
GTGCAGGAGA	AGAACTGGTA	CAGTCTTGTC	ATTGTTGAAG	ATGGGAACAG	TATCTCCAGC	1500



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15 Seq ID NO: 582 Protein sequence  
 Protein Accession #: AAB34388.1

1 11 21 31 41 51  
 20 MNPFQKNBSK ETLFSFVSIE EVFPRPPSP KKPSPITCGS NYPLSIAPIV VNEFCERFSY 60  
 YGMKAVLILY FLYPLHWNED TSTSIYHAPS SLCYPTPILG AALADSWLKG FKTIYLSLV 120  
 YVLGHVILSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFQGD QFEKHAER 180  
 TRYFSVFEYLS INAGSLISTP ITPMLRGDVQ CPGEDCYALA FGVPGLLMVI ALVVVFAMGSK 240  
 IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKQHW LDWAAEKYPK QLIMDVKALT 300  
 25 RVLFYIPLP MFWALLDQGG SRWTLQAIRN NRNLGFFVLQ PDQMQLNPP LVLIFLPLFD 360  
 FVIYRLVSKC GINFSSLRKM AVGMILACLA PAVAAAVEIK INEMAPAQSG PQEVLQVLN 420  
 LADDEVKVTY VGNENSLLI ESIKSPQKTP HYSKLHLKTK SQDFHFLKY HNLSTLYEHS 480  
 VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDLSLVNG 540  
 EDYGVSAIRT VQRGEYPAWH CRTEDKNFSL NLGLLDPGAA YLFVITNTN OQLQAWKIED 600  
 IPANKMSIAW QLPGYALVTA GEVMSFVTGL EFSYSQAPSS MKSVLQAALW LTIAVGNIIV 660  
 30 LVVAQFSGELV QWAEFILFSC LLLVICLIFS IMGYTYPVK TEDMRGPADK HIPHTQGNMI 720  
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35 Seq ID NO: 583 DNA sequence  
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 Coding sequence: 184..1263

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 ACAGAGGGAA CCTACTCTG GAAACTGTCA GTCCCGAGGC ACTGGGGAGG GCTGAGGCCG 180  
 ACCATGCCCA GCGTGTGCT GCTGTTCACG GCTGTCTCTG TGTCCAGCTG GGCTCAGCTT 240  
 CTGACAGAGC CCAACTCTCT GTGGTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG 300  
 45 TTTATCATCG GTGCCAGCC CGTGTGCACT CAGCTTCCCG GGCTCTCCCC TGGCCAGAGG 360  
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 70 GGAACGGCTC CTCCCTAAA ATGAGAAGTC CAAGGTATC TCTGGCCAG TGACACAGA 1860  
 GAGATCTGCA CTTCCCGGAC TTCAGGCTG CTTTCCAGC GAGAATTCTT CATCCTCCAC 1920  
 GGTTCACATG CTCTCACTG AAGAGGAAAG GGGGCCATT GACCTGACAT GTCAGGAAG 1980  
 CCTAAACTG AATGTTTGG CTTGGCTGC AGAAGCCAGG GTGCATGACC AGGCTGCGTG 2040  
 GACGTTATAC TGTCTTCCCC CACCCCGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100  
 75 CTCCACCGAG GGAGGCTCA CAAACCAAG GACGCTGCA CGGCTCAGGC TGGCGGGCCC 2160  
 GCGGTGCTCA TCATCTCTGC CCCAGGTGTA CGGTTTCTCT CTGACATTAA ATGCCCTTCA 2220  
 TGGAAAAAAA AAAAAGAAAA AAAAAAAAAA AA

80 Seq ID NO: 584 Protein sequence  
 Protein Accession #: NP\_116031.1

1 11 21 31 41 51  
 MPSLLLLFTA ALLSSNAQLL TDANSWWSLA LNFVQRPENF IIGAQPVCQS LPGLSPGQRK 60  
 LCQLYQEHMA YIGEGAKTGI KECQHQFRQR RWNCSADNA SVFGRVMQIG SRETAFTHAV 120

SAAGVVAIS RACREBELST CGCSRTARPK DLPRDWLWGG CGDNVEYGYR FAKEFVDARE 180  
 REKNPAKGE EQGRVLMNLQ NNEAGRRAVY KMADVACKCH GVSQSCSLKT CWLQLAEPRK 240  
 VGDRLKEKYD SAAAMRVTRK GRLELVNSRF TQPTPEDLVY VDPSPDYCLR NESTGSLGTQ 300  
 GRLCNKTSSE MDGCELMCOG RGVNQPKSVQ VERCHCKPHW CCFVRCKKCT EIVDQYICK

Seq ID NO: 585 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1479

1 11 21 31 41 51  
 ATGGCTTTGA ACTCAGGGTC ACCACCAGCT ATTGGACCTT ACTATGAAA CCATGGATAC 60  
 CAACCGGAAA ACCCCTATCC GGCACAGCCC ACTGTGGTCC CCACTGTCTA CGAGGTGCAT 120  
 COGGCTCAOT ACTACCGTCC CCCCGTCCOC CAGTAAGCCC CGAGGGTCTT GACGCGAGCT 180  
 TCCAACCCCG TCGTCTGCAC GCAGCCCAAA TCCCCTATCC GGACAGTGTG CACCTCAAAG 240  
 ACTAAGAAAG CACTGTGCAT CACCTTGACC CTGGGGACCT TCCTCGTGGG AGCTGCGCTG 300  
 GCGCTGGCC TACTCTGGAA GTTCTAGGGC AGCAAGTGCT CCAACTCTGG GATAGAGTGC 360  
 GACTCTCAG GTACTCTGAT CAACCCCTCT AACTGGTGTG ATGGCGTGTG ACTCTGCCCC 420  
 GGCGGGGAGG ACGAGAATCG GTGTGTTCGC CTCTACGGAC CAAACTTCAT CCTTCAGGTG 480  
 TACTCATCTC AGAGGAAGTC CTGGCACCTT GTGTGCCAAG ACGACTGGA CGAGAACTAC 540  
 GGCGGGGCGG CCTGCAGGGA CATGGGCTAT AAGAATAATT TTTACTCTAG CCAAGGAATA 600  
 GTGGATGACA GCGGATCCAC CAGCTTTATG AAATGAACA CAAGTGCCGG CAATGTCTGAT 660  
 ATCTATAAAA AACTGTACCA CAGTGATGCC TGTTCCTCAA AAGCAGTGGT TTCTTTACGC 720  
 TGTATAGCCT GCGGGGTCAA CTTGAATCA AGCCGCCAGA GCAGGATCGT GGGCGGCGAG 780  
 AGCGCGCTCC CGGGGGCCTG GCGCTGGCAG GTCAAGCTGC ACGTCCAGAA CGTCCACGTG 840  
 TGGGAGGCT CCATCATCAC CCCGAGTGG ATCGTGACAG CGGCCACTG CGTGGAAAAA 900  
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 TTCTATGGAG CCGGATACCA AGTAGAAAA GTGATTCTCT ATCCAAATTA TGACTCCAAG 1020  
 ACCAAGAAAC ATGACATTGC GCTGATGAAG CTGCAGAAAG CTCTGACTTT CAAAGACCTA 1080  
 GTGAACACAG TGTGTCTGCC CAACCCAGGC ATGATGCTGC AGCCAGAAAC GCTCTGCTGG 1140  
 ATTTCCGGGT GGGGGGCCAC CGAGGAGAAA GGAAGACCT CAGAAGTGTG GAACGCTGCC 1200  
 AAGGTGCTTC TCATTGAGAC ACAGAGATGC AACAGCAGAT ATGTCTATGA CAACCTGATC 1260  
 ACACCGCCA TGATCTGTGC CGGCTTCTG CAGGGGAACG TCGATTCTTG CCAGGGTGAC 1320  
 AGTGAAGGCG CTCGTGTCACT TCGAAGAAC AATATCTGGT GGCTGATAGG GGATACAAGC 1380  
 TGGGGTTCTG GCTGTGCCAA AGCTTACAGA CCAGGAGTGT ACGGGAATGT GATGGTATTC 1440  
 ACGGACTGGA TTTATGACA AATGAGGGCA GACGGCTAA

Seq ID NO: 586 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYTPSPVP QYAPRVLTQA 60  
 SNPVVCTQPK SPGGTCTSK TKKALCITLT LGTFLVGAAL AAGLLWFKMG SKCSNSGIEC 120  
 DSSGCTCINFS NWCDGVSHCF GGEDENRCVR LYGENFILQV YSSQRKSWHP VQDDWNNENY 180  
 GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240  
 CIACGVNLNS SRQSRVGGG SALPGAHPWQ VSLHVQNVHV CGGSIIITPEW IVTAAHCVEK 300  
 PLANPWHMTA FAGILRQSPM FYGAGYQVER VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360  
 VKPVCLPNFG MMLQPEQLCW ISGWGATEER GKTSEVLNAA KVLIIETQRC NSRYVYDNL 420  
 TPAICAGFL QGNVDSQGD SGGPLVTSKN NIWMLIGDTS WSGGCAKAYR PGVYGNVMVF 480  
 TDHIYRQMA DG

Seq ID NO: 587 DNA sequence  
 Nucleic Acid Accession #: NM\_005656.1  
 Coding sequence: 57..1535

1 11 21 31 41 51  
 GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGATAAC AGCAAGATGG 60  
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 CGGAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180  
 CTCACTACTA CCGGTCCCCC GTGCCCCAGT ACGCCCGAG GGTCTGAGC CAGGCTTCCA 240  
 ACCCGCTCGT CTGCAAGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAGACTA 300  
 AGAAAGCACT GTGCATCAAC TTGACCTTGG GGACCTTCTT CGTGGGAGCT GCGCTGGCCG 360  
 CTGGCTTACT CTGGAAGTTC ATGGGCGAGCA AGTGTCTCAA CTCTGGGATA GAGTGGGACT 420  
 CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG GGTGTACAC TGCCCCCGCG 480  
 GGGAGGACGA GAATCGGTGT GTTGGCTCTT ACGGACCAAA CTTATCCTT CAGATGTACT 540  
 CATCTCAGAG GAAGTCTCGG CACCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600  
 GGGCGGCTTG CAGGACATG GGCTATAAGA ATAATTTTTA CTCTAGCCAA GGAATAGTGG 660  
 ATGACAGCGG ATCCACCGAG TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720  
 ATAAAAAAT GTACCAACAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT 780  
 TAGCCTGGGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGG GGTGAGAGCG 840  
 CGCTCCCGGG GGCCTGGCCC TGSCAGGTCA GCCTGCACGT CCAGAACGTC CACGTGTGCG 900  
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC 960  
 TTAACATACC ATGGCAATTG ACGGCATTG CGGGGATTIT GAGACAATCT TTCTATGTTCT 1020  
 ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAGACCA 1080  
 AGAACAAATGA CATTGGCTGT ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA 1140  
 AACCAGTGTG TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200  
 COGGTGGGG GGCCACCGAG GAGAAAGGGA AGACCTCAGA AGTGTGAAAC GCTGCCAAGG 1260  
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320  
 CAGCCATGAT CTGTGCCGCG TTCTTGCAAG GGAACGTCGA TTTCTGCCAG GGTGACAGTG 1380  
 GAGGCGCTCT GGTCACTTGG AACCAATAA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440  
 GTTCTGGCTG TGCCAAAGCT TACAGACCA GAGTGTACGG GAATGTGATG GTATTACGG 1500  
 ACTGGATTTA TGACAAATG AAGGCAAGC GCTAATCCAC ATGGTCTTGG TCCTTGAGCT 1560

5 CGTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCC TGCAATGATT ACTCTTAGAG 1620  
 ATGATTGAGA GGTCACTTCA TTTTATTAA ACASTGAAC TGTCTGGCTT TGGCACTCTC 1680  
 TGCCATACGT TGCAAGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTGT 1740  
 COGCAAGGGG TGATGGCCGG CTGGTTGTGG GCATGGCGG TCAATTGTGG AAGGAAGAGG 1800  
 GTTGGAGGCT GCCCCATTG AGATCTTCTT GCTGAGTCT TCCAGGGGG CAATTTTGGG 1860  
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GATGACTTG AGATGAAAA GGAGAGACAT 1920  
 GGAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGTGTAGTG 1980  
 TCCCCAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040  
 10 GATGGTGGCG AGAAATAAAG GGACCAAGCC TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100  
 AAGGGGAACA GAAACATTTT TGTTCCTATG GGGTGAGAAT ATAGACAGTG CCCTTGGTGC 2160  
 GAGGGAAGCA ATTGAAAAG AACTTGCCTT GAGCACTCCT GGTGCAAGTC TCCACCTGCA 2220  
 CATTTGGTGG GGTCTCTGGG AGGGAGACTC AGCCTTCTCT CTCATCCTCC CTGACCCCTG 2280  
 TCCTAGCACC CTGGAGAGTG AATGCCCTT GGTCCCTGGC AGGGGCGCAA GTTTGGCACC 2340  
 15 ATGTCCGGCT CTTCAGGCTT GATAGTCAAT GGAATTTAG GTCCATGGGG GAAATCAAGG 2400  
 ATGCTCAGTT TAAGGTACAC TGTTCCTATG TTATGTTTCT ACACATTGAT GGTGTGACC 2460  
 CTGAGTTCAA AGCCATCTT

Seq ID NO: 588 Protein sequence  
Protein Accession #: NP\_005647.1

20 1 11 21 31 41 51  
 MALNSGSPFA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60  
 25 SNPVVCTQPK SPSTGVTCTSK TKKALCITLT LGTFLVGAAL AAGLLWRFMG SKCSNSGIEC 120  
 DSSGTCINFS NWCAGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VQDDWNNENY 180  
 GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240  
 CLACGVNLNS SRQSRIVGGE SALPGAWFWQ VSLHVQNVHV CGGSIIPTPEW IVTAACHVEK 300  
 PLNNPWNWTA FAGLLRQSFM FYGAGYQVQK VISHPNYDSK TKNDIALMK LQKPLTFNDL 360  
 30 VKFVCLNPNP MMLQPEQLCH ISGWGATEEK GKTSEVLNAA KVLIIETQRC NSRYVYDNL 420  
 TPAMICAGPL QGNVDSQGD SGGPLVTSNN NIWWLIGDTS WSGCAKAYR PGVYGNVMVF 480  
 TDWYRQMKKA NG

Seq ID NO: 589 DNA sequence  
Nucleic Acid Accession #: NM\_001935.1  
Coding sequence: 1..2301

35 1 11 21 31 41 51  
 40 ATGAAGACAC CGTGAAGAT TCTTCTGGGA CTGCTGGGTG CTGCTGCGCT TGTCACCATC 60  
 ATCACCGTGC CCGTGGTTCT GCTGAACAAA GGCACAGATG ATGCTACAGC TGACAGTCGC 120  
 AAAACTTACA CTCTAACTGA TTAATCTAAA AATACTTATA GACTGAAGTT ATACTCCTTA 180  
 AGATGGATTT CAGATCATGA ATATCTCTAC AAACAAGRAA ATAATATCTT GSTATTCAAT 240  
 GCTGAATATG GAAACAGCTC AGTTTTCTTG GAGAACAGTA CATTTGATGA GTTTGGACAT 300  
 45 TCTATCAATG ATTATTCAT ATCTCCTGAT GGGCAGTTTA TTCTCTTAGA ATACAACATC 360  
 GTGAAGCAAT GGAGGCAATC CTACACAGCT TCATATGACA TTTATGATTT AAATAAAAGG 420  
 CAGCTGATTA CAGAAGAGAG GATTCCAAAC AACACACAGT GGGTCACATG GTCAACCATG 480  
 GGTCAATAAT TGGCATATGT TTGGAACAAT GACATTTATG TTAATAATGA ACCAAATTTA 540  
 CCAAGTTACA GAATCACATG GACGGGGAAA GAAGATATAA TATATAATGG AATAACTGAC 600  
 TGGGTTTATG AAGAGGAAGT CTTCAGTGCC TACTCTGCTC TGTGGTGGTC TCCAAACGGC 660  
 50 ACTTTTTTAT TTTGCTATTT CCRAATAGAT AAAAAAGACT GCACATTAT TACAAAAGGC 720  
 TACTCTGATG AGTCACTGCA GTACCCAAAG ACTGTACGGG TTCCATATCC AAAGGCAGGA 780  
 GCTGTGAATC CAACTGTAAA GTTCTTTGTT GTAAATACAG ACTCTCTCAG CTCAGTCACC 840  
 AATGCAACTT CATACAAAT CACTGCTCCT GCTTCTATGT TGATAGGGGA TCACACTTGT 900  
 TGTGATGTGA CATGGGCAAC ACAAGAAAGA ATTCTTTTGC AGTGGCTCAG GAGGATTCAG 960  
 55 AACTATTCGG TCATGGATAT TTGTGACTAT GATGAATCCA GTGGAAGATG GAACCTGCTTA 1020  
 GTGGCAAGGC AACACATTGA AATGAGTACT ACTGGCTGGG TTGGAAGATT TAGGCCCTTA 1080  
 GAACCTCATT TTACCTTTGA TGGTAATAGC TTCTACAAGA TCATCAGCAA TGAAGAAGGT 1140  
 TACAGACACA TTTGCTATTT CCRAATAGAT AAAAAAGACT GCACATTAT TACAAAAGGC 1200  
 ACCTGGGAAG TCATCGGGAT AGAAGCTCTA ACCAGTATTT ATCTATACTA CATTAGTAAT 1260  
 60 GAATATAAAG GAATGCCAGG AGGAAGGAAT CTTTATAAAA TCCAACTTAG TGACTATACA 1320  
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 TTCAGTAAGG AGGCGAAGTA TTATCAGCTG AGATGTTTCG GTCCTGGTCT GCCCCTCTAT 1440  
 ACTCTACACA GCAGCGTGAA TGATAAAGGG CTGAGAGTCC TGGGAAGCAA TTCAGCTTTG 1500  
 GATAAAATGC TGCAGAAATG CCAGATGCCC TCCAAAAAAC TGGACTTCAT TATTTTGAAT 1560  
 65 GAAACAAAAT TTTGGTATCA GATGATCTTG CCTCCTCATT TTGATAAATC CAAGAAATAT 1620  
 CCTCTACTAT TAGATGTGTA TGCAAGGCCA TGTAGTCAAA AAGCAGACAC TGTCTTCAGA 1680  
 CTGAACCTGG CCACTTAACCT TGCAAGCACA GAAAAACATTA TAGTAGCTAG CTTTGATGGC 1740  
 AGAGGAAGTG GTTACCAAGG AGATAAGATC ATGCATGCAA TCAACAGAAG ACTGGGAACA 1800  
 70 TTTGAAGTTG AAGATCAAT TGAAGCAGCC AGACAATTTT CAAAAATGGG ATTTGTGGAC 1860  
 AACAAAGCAA TTGCAATTTG GGGCTGGTCA TATGGAGGT ACSTAACTCT AATGGTCTG 1920  
 GGATCGGGAA GTGGCGTGT TCAAGTGTGA ATAGCCGTGG CGCCTGTATC CCGGTGGGAG 1980  
 TACTATGACT CAGTGATCAC AGAACGTTAC ATGGGTCTCC CAATCCAGA AGACAAACCT 2040  
 GACCATTACA GAATTTCAAC AGTCATGAGC AGAGCTGAAA ATTTTAAACA AGTTGAGTAC 2100  
 75 CTCTTATATC ATGGAACAGC AGATGATAAC GTTCACITTC AGCAGTCAGC TCAGATCTCC 2160  
 AAAGCCCTGG TCGATGTTGG AGTGGATTTT CAGGCAATGT GGTATACTGA TGAAGACCAT 2220  
 GGAATAGCTA GCAGCACAGC ACACCAACAT ATATATACCC ACATGAGCCA TCTCATAAAA 2280  
 CAATGTTTCT CTTTACCTTA G

Seq ID NO: 590 Protein sequence  
Protein Accession #: NP\_001926.1

80 1 11 21 31 41 51  
 MKTPWKILLG LLGAAALVTI ITVPVLLNKK GTDDATADSR KTYTLTDYLR NTRYRLKLYSL 60

5 RWISDHEYL KQENNILVFN AEYGNSSVFL ENSTFDEFHG SINDYSISPD GQFILLEINY 120  
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVWTSFV GHKLAYVWNN DIYVVKIEPNL 180  
 PSYRITWTGK EDIYNGITD WYEEVEVPSA YSALNWSFNG TFLAYAQFND TEVPLIEYSF 240  
 YSDESLLQYPK TVRVPYPKAG AVNPTVKFPV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300  
 CDTVWATQER ISLQWLRRIO NYSVMDICDY DBSSGRWNCL VARQHIEMST TGVVGRFRPS 360  
 EPHTLDGNS FYKIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420  
 EYKMPGGGRN LYKIQLSDDY KVTCLSCBLN PERCQYYSVS FSKKAKYYQL RCGSPGLPLY 480  
 TLHSSVNDKG LRVLEDNSAL DRMLQNVQMP SKKLDPIILN ETXFWYQML PPHFDKSKKY 540  
 10 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RSGSVQGDKI MHAINRLGT 600  
 FEVEDQIEAA RQFSKMGFVD NKRIAIWGS YGGYVTSMLV GSGSVFVKCG IAVAPVSRWE 660  
 YDSVYTERY MGLPTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQSAQIS 720  
 KALVDVGVD FQAMWYTDDEH GIASSTAHQH IYTHMSHFIL QCFSLP

15 Seq ID NO: 591 DNA sequence  
 Nucleic Acid Accession #: NM\_016077.1  
 Coding sequence: 128..667

20 1 11 21 31 41 51  
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 CGCGATAGAA AGTGTTCGC TTGCCAGAA GAAGGGGAAG CGCGAGTGA GAAAGGAGGT 120  
 ACTGTAGATG CCTCCAAAT CCTGGTTAT GGAATATTG GCTCATCCA GTACACTCGG 180  
 CTGGCTGTT GGAGTTGCTT GTGGCATGTG CTGGGCTGG AGCCTTCGAG TATGCTTTGG 240  
 25 GATGCTCCCC AAAAGCAGA CGAGCAGAC ACACACAGT ACTGAAAGTG AAGCAGCAT 300  
 CTTGGGAGAC AGCGGGAGT ACAAGATGAT TCTTGTGTT CGAAATGACT TAAAGATGGG 360  
 AAAAGGGAAA GTGGCTGCC AGTGCTCTCA TGCTGCTGTT TCAGCTTACA AGCAGATTCA 420  
 AAGAAGAAAT CTGAATAATG TCAACAATG GGAATACTGT GGCACGCCA AGGTGGTGGT 480  
 CAAAGCTCCT GATGAAGAAA CCCTGATTGC ATTATTGGCC CATGCAAAAA TGCTGGGACT 540  
 GACTGTAAAT TTAATTCAAG ATGCTGGAGC TACTCAGATT GCACCAAGCT CTCAACTGT 600  
 30 CTTAGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAACT 660  
 TTACTAGGTG GACTTTGATA TGACACAAAC CCCTCCATCA CAAGTGTGTT AAGCCTGTCA 720  
 GATTTCAACA ACAAAAGCTG AATTTCTTCA CCCAATTAA ATGTTCTTGA GATGAAAAA 780  
 AAACCTATTCC CATGTTCTA AAAAA

35 Seq ID NO: 592 Protein sequence  
 Protein Accession #: NP\_057161.1

40 1 11 21 31 41 51  
 | | | | | |  
 MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60  
 DSGEYKMLLV VRNDLKMKGK KVAACQSHAA VSAYKQIQRR NPEMLKQWEY CGQPKVWVKA 120  
 PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPAPADLID KVTGHLKLY

45 Seq ID NO: 593 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1896

50 1 11 21 31 41 51  
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 GCTCCGCGCG CCGCGCCGAG CAGAGCCGAG TCCGTCTCCG GCGCTGGGCC CGAACCCGAG 120  
 CGCGAGTCCG GCGCCCGGCC GCGCCCGGGG CCGCGGAACA CCACCCGGTT TGGGCTGGG 180  
 GCGCGGGGCG GCAGCGGCGC CTCCAGCTCC AACAGCAGTG GCGACGCCCT GGTGACCCGC 240  
 55 ATTTCATCC TCCCTCGGGA CCTACCCACC CTCAGGCAG CCGTGATCGT GCGGTTGCGC 300  
 TTTACACACC TCCCTATGCG CTGCGCTGCT CTGCGGCTCT TCAGGTGCGG AAAGAGGTTA 360  
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGGCCCA 420  
 CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TGACATCAA ATACAGAGTG 480  
 TCCCTGCCCG CTGCACGTAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCTT 540  
 60 GTGCCGCCAC CCTTCATCCT CGACATGAC CTTCCAGCAA GATGCACTGG AAGGCTGAT 600  
 GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAGTTGG 660  
 TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGGCT CCGAGGTGTT 720  
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGGGTGTC AGGCACTGTC 780  
 TCAGACTGTC ACTGGCAAGC TGGTTTCCAC GTACCACAA TGGAGTTGCT TCTGCCACCC 840  
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 65 CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTAAGCA GAAACACCCG GGCTCCATCT 960  
 GCCAGGTGCT TGGCACTGGT CTGGCAGAAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020  
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 AGTACCTGG GCTTGGATGT TTTCTGTGTT GCGCGCCAGC GGGGCACCTT TTGTGAAGAC 1140  
 70 AGAGCAGTGA CTAAGGTTCT CCAGGGTAGC TCTTCTCCA AACAGCTGCG CTGGAAGCCA 1200  
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTC TCCGTGAGC 1260  
 ACCCATCTCT TCAGGTTGGC TCGTTGAGT GCGCGGGGAC AAGCCAGCCT GAGCGGGAGG 1320  
 AGGGTGTTC GCGGTGCGCG GCACTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380  
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 75 ATCTGTCTCC CCGTCTGTGC CGTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500  
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 AAAAGAGGGC GAGACTTGGA ATTGACAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620  
 GCGAACCTGC AGACAATTCG AGATACCCAA GGCCAGGAAG GCCACGTGGA GGATGTCACT 1680  
 CACCTCTGAG GAGACTTTGA TGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG 1740  
 80 GATGGCAGAT GCCAGAAGAT GGTCTGTATG TCTGAGGAAG GGCACCTTAG TTTGACAGGA 1800  
 TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCTT 1860  
 TCCCCCGCAC AGCCCTGTTT TCTGTCCAGG CCTGTA

Seq ID NO: 594 Protein sequence  
 Protein Accession #: FGENESH predicted

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1      11      21      31      41      51
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5  MRVAPLPAPL LPLLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNITRFGSG 60
AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAFAP FTTLIIACLL LRVFRSGKRL 120
KRTRKYDIIT TPAERVEMAP LNEEDEDDED STVPDIKYRV SLPAALRRQL PGQQTLLTVP 180
VPPPFILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHPEKVPPT STPHGFRQLQ 300
10 LNLMEKLDS ALRRNTRAPS ARCLPLVLAE MAAAESDLFN PWWHFSATGS PIKTLTYQTM 360
STLGLDVPFG AGQRGTFCEP RAVTKVLQGS SFSKQLRWKP ALESGFPHL RLLRECPPLS 420
THPVRLARSD ARGQASLTGR RVFRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHAHGFV KRGPSGQLTR HTCPGWGITH 540
ANLQTIPTDQ QGEGPREDVT HPGGDLDGVA NFYLEEBGFQ DGRQCQKMLM SEEGPPSLTG 600
15 CERLTGSHHF SSSKSWNSFL SPRQPLFLSR P

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Seq ID NO: 595 DNA sequence  
Nucleic Acid Accession #: NM\_021614.1  
Coding sequence: 1..1740

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CGCGGAGAAC TGACAGAGAT GGACTCAGAG GCGCAGCCCC TGACGCCCCC CGCGCTCTGT 120
25 GGAGGAGGTG GCGGCGCGTC CTCCCGTCT GCAGCGCGTG CGCGCGCGCG CGCTGTTCOG 180
TCCTCAGCCC CGAGATCGT GGTGTCTAAG CCGAGCACA ACACTCCAA CAACCTGGCG 240
CTCTATGGAA CCGCGCGCG AGGCAGCACT GGAGGAGCG GCGGCGGTGG CCGGAGCGGG 300
CAGGCGAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360
CTGGGCCACC GGGCGGCCCT GTTCGAAAAG CGCAGCGCG TCAGCGACTA CGCGCTCATC 420
30 TTGCGCTTCT TCGGCATCGT GGTCTATGTC ATCGAGACCG AGCTGTCTGT GGGCGCCTAC 480
GACAAGCGGT CGCTGTATTC CTTAGCTCTG AATGCCTTA TCAGTCTCTC CAGCATCATC 540
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GGAGCAGATG ACTGGAGAT AGCCATGACT TATGAGCGTA TTTCTTCAT CTGCTGGAA 660
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Seq ID NO: 596 Protein sequence  
Protein Accession #: NP\_067627.1

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Nucleic Acid Accession #: NM\_016029.1  
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Protein Accession #: NP\_000784.2

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Protein Accession #: NP\_005224.1

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	MDCQLSILL	LSCSVLDSFG	ELIPQPSNEV	NLLDSKTIQG	ELGWISYPSH	GWEESIGVDE	60
50	HYTPRTYQV	CNMDHRSQNN	WLRINWVFRN	SAQKIYVELK	FTLRDCNSIP	LVLGTCKETP	120
	NLYYMESDDD	HGVKPREHQF	TKIDTIAADE	SFTQMDLGRD	ILKLNTEIRE	VGPVNRKGFY	180
	LAFQDVQACV	ALVSRVRYFK	KCPFTVQMLA	MFPDTPVMDS	QSLVEVRGSC	VNNSKEEDPP	240
	RMVCSLEGSE	LVPISGKCSN	AGYEERGPMC	QACRPGPYKA	LDGNMKCAKC	PPHSSTQEDG	300
	SMNCRGNNY	FRADKPPSM	ACTRPPSSPR	NVISININETS	VILDWSWPLD	TGGRKDVTFN	360
55	IICKKCGWNI	KQCEPCSPNV	RFLPRQFGLT	NTTVTVDLL	AETNYTPEID	AVNGVSELSS	420
	PPRQNAVSI	TTNQAAPSFV	LTIKKDRTSR	NSISLSHQEP	EHFNGIILDY	BVKYKQEQEQ	480
	ETSYTILRLR	GTNVTSSSLK	PDTIYVFOIR	ARTAAGVGTN	SRKFEPETSP	DSFISIGESS	540
	QVVMIAISAA	VAIILLTVVI	VYLIGRFQCY	KSKHGADEKR	LHFGAGHLKL	PGLRTYVDFH	600
	TYEDPTQAVH	EPFAKELDATN	ISIDKVVAG	EPGEVCSGRL	KLPSEKKEISV	AIKTLKVGYT	660
60	EKQRRDFLGE	ASIMGQFDHP	NIIRLEGVVT	KSKPVMIVTE	YMENGSLDSF	LKHKDAQPTV	720
	IQLVGMLRGI	ASGMKYLSDM	GYVHRDLAAR	NILINSNLVC	KVSDPGLSRV	LEDDPEAAAT	780
	TRGKTIPIRW	TSPEAIAYRK	PTSASDVMSY	GIVLNEVMSY	GERPYWEMSN	QDVIKAVDEG	840
	YRLPPPMDCP	AALYQLMLDC	WQKDRNNRPK	FEQIVSILDK	LIRNPGSLKI	ITSAARPSN	900
	LLLDQSNVDI	STFRITGDWL	NGVRTAHCKE	IFTGVEYSSC	DTIAKISTDD	MKIVGVTVVG	960
65	PQKIISSIK	ALETQSKNGF	VPV				

Seq ID NO: 603 DNA sequence

Nucleic Acid Accession #: NM\_005727.1

Coding sequence: 122..847

70	1	11	21	31	41	51	
	GCCAGGGGTC	CCTCTGCGCT	CCCACTCAGT	GGCAACACCC	GGGAGCTGTT	TTGTCTCTTG	60
	TGGAGCCTCA	GCAGTTCCTT	CTTTCAGAAC	TCACCTGCCA	GAGCCCTGAA	CAGGAGCCAC	120
75	CATGCACTGC	TTACGCTTCA	TTAAGACCAT	GATGATCTCT	TTCAATTGCG	TCACTTTTCT	180
	GTGTGTGTGA	GCCCTGTTGG	CAGTGGGCAT	CTGGGTGTCA	ATCGATGGGG	CATCCTTTCT	240
	GAAGATCTTC	GGGCGACTGT	CGTCCAGTGC	CATGCAGTTT	GTCAAGCTGG	GCTACTTCTT	300
	CATCGCAGCC	GGCGTTGTGG	TCTTTGCTCT	TGGTTTCTCG	GGCTGCTATG	GTGCTAAGAC	360
	TGAGAGCAAG	TGTGCGCTCG	TGACGTTCTT	CTTCATCTCT	CTCCTCATCT	TCATTGCTGA	420
80	GGTTGCAGCT	GCTGTGGTGG	CCTTGGTGTA	CACCAACATG	GCTGAGCACT	TCTGACGTT	480
	GCTGTGTAGT	CCTGCCATCA	AGAAAGATTA	TGGTTCCGAG	GAAGACTTCA	CTCAAGTGTG	540
	GAACACCAAC	ATGAAAGGGC	TCAAGTGCTG	TGGCTTCACC	AACTATACGG	ATTTTGAGGA	600
	CTCACCCATC	TTCAAAGAGA	ACAGTGCCTT	TCCCCCATTC	TGTTGCAATG	ACAACGTCAC	660
	CAACACAGCC	AATGAAACCT	GCACCAAGCA	AAAGGCTCAC	GACCAAAAAG	TAGAGGGTTG	720
	CTTCAATCAG	CTTTTGTATG	ACATCCGAAC	TAATGCAGTG	ACCGTGGGTG	GTGTGGCAGC	780



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TGAATTGGG GGCCTCGAGC TGGCTGCCAT GATTGTGTCC ATGTATCTGT ACTGCAATCT 840
ACAAATAGTC CACTTCTGCC TCTGCCACTA CTGCTGCCAC ATGGGAAGTG TGAAGAGGCA 900
CCCTGGCAAG CAGCAGTGAT TGGGGGAGGG GACAGGATCT AACAAATGCA CTTGGGCGAG 960
AATGGACCTG CCCTTCTGTC TCCAGACTTG GGGCTAGATA GGGACCACTC CTTTATAGCG 1020
ATGCGCTGACT TTCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080
GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAAACC CTTGATATGC CCCCTAGGCC 1140
TAGTGGTGAT CCCAGTGCT TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200
AAGTGAAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAAAC 1260
TGTTACAATG TTAATAAAA

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Seq ID NO: 604 Protein sequence  
Protein Accession #: NP\_005718.1

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1 11 21 31 41 51
| | | | |
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IAAGVVVFAL GFLGCGYART ESKCALVTFF FILLIPIAE VAAAVVALVY TMAEHFLTL 120
LVVPAIKRDY GSGEDFTQVW NITMKGLKCC GFTNYTDFED SPYFKENSAP PPFCCNDNVT 180
NTANETCTEQ KAHDQRKVEGC FNQLLYDIRT NAVTVGGVAA GIGGLELAAM IVSMYLYCNL 240
Q

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Seq ID NO: 605 DNA sequence  
Nucleic Acid Accession #: NM\_000729.2  
Coding sequence:

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1 11 21 31 41 51
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AGCCATGAAC AGGGGGGTGT GCCTGTGGGT GCTGATGGCG GTACTGGCGG CTGGCGCCCT 120
GAGCGACGCG GTGCTCCCGC CAGATCCCGC GGGCTCCGGG CTGACGCGGG CAGAGGAGGC 180
GCCCGGTAGG CAGCTGAGGG TATGCGCAGG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240
CGCCCTGCTG GCACGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAG GAATGTCCAT 300
CGTTAAGAAC CTCGACAAAC TGGACCCGAG CCACAGGATA AGTGACCGGG ACTACATGGG 360
CTGGATGGAT TTTGGGCGTC GCAGTGCAGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420
GCCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACAA 480
TCACACTCAT AACTCATTTG CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540
TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACACGCT CACCAGAGT 600
TGTGCAAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660
TATGCTATTA AAGTGATTTC ATTCTGCC

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Seq ID NO: 606 Protein sequence  
Protein Accession #: NP\_000720.1

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50

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1 11 21 31 41 51
| | | | |
MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEBAP RRQLRVSRQT DGESRAHLGA 60
LLARYIQQAR KAPSGRMSIV KNLQNLDPFH RISDRDYMGW MDFGRRSABE VEYPS

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Seq ID NO: 607 DNA sequence  
Nucleic Acid Accession #: NM\_001423.1  
Coding sequence: 219..692

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1 11 21 31 41 51
| | | | |
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CAGGGCTGGT GCCAGCACTT GCCACTCAGA GGCCTCTGT CGCTGGGACC CTTCAGAACT 180
CTCTTTGCTC ACAAGTTACC AAAAAAAAAA GAGCCACAT GTTGGTATTG CTGGCTGGTA 240
TCTTTGTGTT CCACATCGCT ACTGTTATTA TGCTATTGTT TAGCACCATT GCCAATGTCT 300
GGTTGGTTTC CAATACGGTA GATGCATCAG TAGGTCTTTG GAAAACTGT ACCAACATTA 360
GCTGCAGTGA CAGCTGTCTA TATGCCAGTG AAGATGCCCT CAGACAGTG CAGGCTTCA 420
TGATTCTCTC TATCATCTTC TGTGTCTTGG CCCTCCTGGT CTTCTGTGTC CAGCTCTTCA 480
CCATGGAGAA GGGAAACCGG TTCTTCTCTT CAGGGGCCAC CACACTGGTG TGCTGGCTGT 540
GCATTCTTGT GGGGGTGTCC ATCTACACTA GTCAATTATG GAATCGTGAT GGAAACGAGT 600
ATCACCAAGG CTATTCTTAC ATCCTGGGCT GGATCTGCTT CTGCTTCAGC TTCACTATCG 660
GCGTCTCTTA TCTGCTCTG AGAAAGAAAT AAGGCCGAGC GAGTTCATGG GGATCTGGGG 720
GGTGGGGAGG AGGAAGCCGT TGAATCTGGG AGGGAAGTGG AGGTGCTGT ACAGGAAAAA 780
CCGAGATAGG GGAGGGGGGA GGGGGAAGCA AAGGGGGGAG GTCAAATCCC AAACCATTAC 840
TGAGGGGAT CTCTACTGCC AAGCCCTGCG CCTGGGGAGA AAGTAGTTGG CTAGTACTTT 900
GATGCTCCCT TGATGGGGTC CAGAGAGCCT CCTGCAGCC ACCAGACTTG GCCTCCAGCT 960
GTTCTTAGTG ACACACACTG TCTGGGGCCC CATCAGCTGC CACAACACCA GCCCCACTTC 1020
TGGGTGATGC ACTGAGGTCC ACAGACCTAC TGCACTGAGT TAAATAGCG GTACAGTTTC 1080
TGGCAAGAGC AGATACTGTC TTTGTGCTGA ATACGCTAAG CCTGGAAGCG ATCCTGCCCT 1140
TCTGACCCAA AGCAAAACAT CACATTCCAG TCTGAAGTGC CTAAGTGGGG GCTTTGGCCT 1200
GTGAGCCATT GTCCCTCTTT GGAACAGATA TTTAGCTCTG TGGAAATTCG TGACAAAATG 1260
GGAGGAGGAA AGAGAGTTTG TAAGGTCAAT CTGGTGGGTT AGCTAAACCA AGAAGGAGAC 1320
CTTTTCACAA TGGAAACCTT GGGGATGGT CAGAGCCAGC TOGAGACCTC ACACACGGCT 1380
GTCCCTCATG GAGACCTCAT GCCATGGTCT TTGCTAGGCC TCTTGTCTGA AGCCAGGCA 1440
GCTCTTCTGG AGTTCTCTTA AAGTCACTAG TGAACAATTC GGTGTTAAA GTACCAACA 1500
AAGTATGGGA TCCAGGGGC AGTCTTGCA CAGTGCCATG TTAGGGTTAT GTTTTATGGA 1560
TTCCCTCAA TGCAGTCAGT GTTCTTTTFA AGTATACAA AGGAGAGAGA TGGACATGGC 1620
TCATTGTAGC ACAAATCTAT TACTCTTCTT CTAACATTTT TGAGGAAGTT TGTCTAATT 1680
ATCAATATTG AGGATCAGGG CTCCTAGGCT CAGTGGTAGC TCTGGCTTAG ACACCACTG 1740
GAGTGATCAC CTCCTGGGGA CCCTGCCTAT CCCACTTAC AGGTGAGGCA TGGCAATCT 1800

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GGAGCTGAT TAAACACAC ATAAACCAAA ACCAAACAAC AGGCCCTTGG GTGAAAGGTG 1860
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GCATTTCCCG GAAATACGA AAATCCCATG AGATAAATAA AAATATAGGT GATGGGCAGA 1980
TCTTTTCTTT AAAATAAAAA AGCAAAAACCT CTTGTGGTAC CTAGTCAGAT GGTAGACGAG 2040
CTGTCTGCTG COGCAGGAGC ACCTCTATAC AGGACTTAGA AGTAGTATGT TATTCCTGGT 2100
TAAGCAGGCA TTGCTTTGCC CTGGAGCAGC TATTTAAGC CATCTCAGAT TCTGTCTAAA 2160
GGGGTTTTTT GGAAGACGT TTTCTTTATC GCCCTGAGAA GATCTACCCC AGGGAGAATC 2220
TGAGACATCT TGCCCTACTT TCTTTATTAG CTTTCTCCTC ATCCATTTCCT TTTATACCTT 2280
TCCTTTTGGG GGATTTGTTA TGCCATGATT TTTGGTATTT ATGTAAAAGG ATTATTACTA 2340
ATTCTATTTC TCTATGTTTA TTCTAGTTAA GGAAATGTTG AGGGCAAGCC ACCAAATTAC 2400
CTAGGCTGAG GTTAGAGAGA TTGGCCAGCA AAAACTGTGG GAAGATGAAC TTTGTCAATTA 2460
TGATTTCATT ATCACATGAT TATAGAAGGC TGTCTTAGTG CAAAAACAT ACTTACATT 2520
CAGACATATC CAAAGGGAAT ACTCACATTT TGTAAAGAAG TTGAACATAG ACTGGAGTAA 2580
ACCATGTATT CCCTTATCTT TACTTTTTTT TCTGTGACAT TTATGTCTCA TGTAAATTGC 2640
ATTACTCTGG TGGATTGTTT TAGTACTGTA TTGGGCTTCT TCGTTAATAG ATTATTTCAT 2700
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TCTGATTCC CTCAAAAA AAAA

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20 Seq ID NO: 608 Protein sequence  
Protein Accession #: NP\_001414.1

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1 11 21 31 41 51
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LKTQVAFMIL SIIFCVIALI VFVFQLFTME KGNRPFLSGA TTLVCHLCLIL VGVSIIYTSY 120
ANRDGTQYHH GSYILGWIC FCFSPFIIGVL YLVLRKK

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30 Seq ID NO: 609 DNA sequence  
Nucleic Acid Accession #: NM\_004961.2  
Coding sequence: 55..1575

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1 11 21 31 41 51
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TCCAAAGTTC TTCCAGTCTC CTAGGCAATC TTATTGATCC TCCAGTCGAG GGTGAGGGA 120
CCTCAGACTG AATCAAGAA TGAAGCCTCT TCCCGTGATG TTGTCTATGG CCCCAGGCC 180
CAGCCTCTGG AAAATCAGCT CCTCTCTGAG GAAACAAAGT CAACTGAGAC TGAGACTGGG 240
AGCAGAGTTG GCAACTGCC AGAAGCCTCT CGCATCTCTG AACTATCTCT GAGTAATTAT 300
GACCACAAAC TGCGCCCTGG CATTTGGAGAG AAGCCCACTG TGGTCACTGT TGAGATCGCC 360
GTCAACAGCG TTGGTCCCTC CTCTATCCCT GACATGGAAT ACACCATTTA CATCATCTTC 420
TCCCAAGACT GGTAGGAAGA ACGCCTCTGT TACAACGACA CCTTTGAGTC TCTTGTCTGT 480
AATGGCAATG TGGTAGGACA GCTATGGATC CCGGACACCT TTTTATAGAA TTCTAAGAGG 540
ACCCACGAGC ATGAGATCAC CATGCCCAAC CAGATGGTCC GCATCTACAA GGATGGCAAG 600
GTGTTGTACA CAATTAGGAT GACCATTGAT GCCGGATGCT CACTCCACAT GCTCAGATT 660
CCAATGGATT CTCATCTTTG CCTCTATCTT TTCTCTAGCT TTTCTATCC TGAGAAATGAG 720
ATGATCTACA AGTGGGAAAA TTTCAGCTT GAAATCAATG AGAAGAACTC CTGGAAGCTC 780
TTCCAGTTTG ATTTTACAGG AGTGAGCAAC AAAACTGAAA TAATCACAAC CCCAGTTGGT 840
GACTTCAATG TCATGACGAT TTTCTTCAAT GTGAGCAGGC GGTTTGGCTA TGTGCTCTTT 900
CAAAACTATG TCCTTCTCTC CGTGACCACG ATGCTCTCTC GGGTTTCCCT TTGGATCAAG 960
ACAGAGTCTG CTCCAGCCCG GACCTCTCTA GGGATCAACT CTGTTCTGAC CATGACCAAG 1020
TTGGGCACTT TTCTCTGTAA GAATTTCCCG CGTGTCTCTT ATATCACAGC CTTGGATTTC 1080
TATATGCCCA TCTGCTTCTG CTCTCTGCTC TGGCTCTCTG TGGAGTTTGC TGTGCTCAAC 1140
TTCTGATCT ACACCCAGAG AAAAGCCCAT GCTTCTCTTA AACTCCGCCA TCCTCGTATC 1200
AATAGCCGTG CCAATGCCCG TACCCGTGCA CGTTCGCCAG CCTGTGCCCG CCAACATCAG 1260
GAAGCTTTTG TGTGCCAGAT TGTCAACACT GAGGGAAGTG ATGGAGAGGA GCGCCCGTCT 1320
TGCTCAGCCC AGCAGCCCCC TAGCCAGGT AGCCCTGAGG GTCCCCGCGC CTTCTGTCTC 1380
AAGCTGGCCT GCTGTGAGTG GTGCAAGCGT TTTAAGAAGT ACTTCTGCAT GGTCCCCGAT 1440
TGTGAGGGCA GTACCTGGCA GCAGGGCCCG CTCTGCATCC ATGTCTACCG CTGGATAAC 1500
TACTCGAGAG TTGTTTTCOC AGTGACTTTC TTCTTCTTCA ATGTGCTCTA CTGGCTTGT 1560
TGCTTTAATC TGTAGGTACC CTTGTTTACC CTGTGGGGCA ACCTCTCCAG TTCCCGAGGA 1620
GGTCCAGGCC CCTTGCCPAG GGAGTTGGGG GAAAGCAGCA GCAGCAGCAG GAGCGACTAG 1680
AGTTTTTCTC GCCCCATTCC CCAACAGAA GCTTGCAGAG GGTTTGTCTT TGCTGCCCT 1740
CTCCCTACC TTGCCCATTC ACTGAGTCTT CTCAGCAGAC CATTTCAAAT TATTAATAAA 1800
TGGGCCACCT CCTCTTCTT CAAGGAGCAT CCGTGATGCT CAGTGTCAA AACCAAGCC 1860
ACTTAGTGAT CAGTCCCTA AAACCATGCC TAAGTACAGG CGATTAGCT ATCTTCCAAC 1920
AATGCTGACC ACCAGACAAT TACTGCATTT TTCCAGAAGC CCACTATTGC CTTTGTAGTG 1980
CTTTGGCCCC AGTCTTGGCC TCAGCCCTCA AGTGCAAGCA CTAGTTGCTT GCCTATACCT 2040
GGCACCCTCAT TAAGATGCTG GGCAGCAGTA TAACAGGAGG AAGAGATCCC TCTCCTTTGG 2100
TCAGATTATT ATGTTCTCAG TTCTCTCTCC CTGTACCCCC TTTCTCTGCA GATAGATAGA 2160
CACTGGCAAT ATCCCTTTAG GAAGAGGGGG GGCAGCAGAG AGAGCCTATT TGGGACAGCA 2220
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ACTTTCCAG TGACTTCCCC TAGCCCTGAC CCAGGCACTA GGCCCTGGTG ACTTCTGGG 2460
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CACTGTATTA CCGCGGGCAG TCTAACATC ACAATCAATC AATCAAAATC CCTTAAATTT 2640
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TGTTGGGGGG TGATAGGGT GGGGTCTCCA TCTACTTTT GTCACCATCA TCTGAAATGG 3120  
GGAAATATGT AAATAAATAT ATCAGCAAAG CAAAAGAAA AAAAAAAA

Seq ID NO: 610 Protein sequence  
Protein Accession #: NP\_004952.1

5  
1 11 21 31 41 51  
10 MLKRVLPVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60  
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IFSQTWYDER LCYNDTFESL VLANGVVSQ L WIPDTFFRNS KRTHHEBITM PNQMVRIYKD 180  
GKVLTYTIRM IDAGCSLHML RFPMDSHSCP LSPSSFSYPE NEMIIKWENP KLEINBKNSW 240  
KLFQDFDTGV SNKTEIITP VGDPMVMTIF FNVSRRFYV AFQNTYVSSV TTMLSWSVFW 300  
IKTESAPART SLGITSVLTM TTLGTFPSRKN FPRVSYITAL DFYIAICFVF CFCALLEFAV 360  
15 LNFLIYNQTK AHASPKLRHP RINSRAZHART RARSRACARQ HQBAFVQCIV TTEGSDGEER 420  
PSCSAQPPPS PGSPBGPRLS CSKLACCCEWC KRFFKYFCMV PDCBGSWQQ GRLCIHVYRL 480  
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Seq ID NO: 611 DNA sequence  
Nucleic Acid Accession #: NM\_021984.1  
Coding sequence: 572..1753

25 1 11 21 31 41 51  
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CAGAGAAGTG CTCAATCAT AAGTGACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180  
GGTAAAGAA AGCCAAATCA AGGACCGGAA TGTGAGCAGS ACCTCAGAAG CCCCTTTGT 240  
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30 TCAGAGTGAA TCAAGAAATG AAGCCTCTTC CGTGATGTT GTCTATGGCC CCCAGCCCCA 360  
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420  
CAGAGTTGGC AAATGCGCAG AAGCCTCTCG CATCTGAAC ACTATCCTGA GTAATTATGA 480  
CCACAACTG CGCCTGGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTTG AGATCTCCGT 540  
35 CAACAGCCTT GGTCTCTCT CTATCTAGA CATGGAATAC ACCATTGACA TCATCTTCTC 600  
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CTGTTATACC CGGGGCACT TAACCATCAC AATCAATCAA TCAATTTCC TTAATTTGT 2820  
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CTTCTAGACC ACATGATAGG GCTAGACAGC TCAGTTTACC ATGATTCTCT TCTGTCACT 3060  
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CCTGAGGTGC TCAGACTGCC CCAAGATCA AATCTCTCT GCGTGTAGTA ACCAGTGGG 3180  
ATGAATTTGG ACATGCCCA ATGCTCTAT ATGCTAAGTG AAATCTGCTG CTGTAATTG 3240  
80 TTGGGGGGTG GATAGGTGG GGTCTCCATC TACTTTTGT CACCATCATC TGAATGGGG 3300  
AAATATGTAA ATAAATATAT CAGCAAAGC

Seq ID NO: 612 Protein sequence  
Protein Accession #: NP\_068819.1

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1      11      21      31      41      51
MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFPRNSKRT HEHEITMPNQ 60
5 MVIYIKDKRV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSPYENEM IYKWNFKLE 120
INEKNSWKLF QLDPTGVSNK TEIITTPVGD FMVMTIFPNV SRRFGYVAFQ NYVPSSVTM 180
LSWVSFWIKT ESAPARTSLG ITSULTMTTL GTFPSRKNFPR VSYITALDFY IAICFVFCFC 240
ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVITE 300
GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVDFC EGSTWQQARL 360
10 CIHVYRLDNY SRVVPVTFPF FNVLYWLVC LNL

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Seq ID NO: 613 DNA sequence  
Nucleic Acid Accession #: NM\_021987.1  
Coding sequence: 572..1657

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TCCAAAGTTC TTCCAGTCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120
CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180
20 GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTGT 240
CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300
TCAGACTGAA TCAAAGAATG AAGCCTCTTC CGTGATGTT GTCTATGGCC CCCAGCCCCA 360
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420
CAGAGTTGGC AAACCTGCCAG AAGCCTCTCG CATCTGAAC ACTATCTGA GTAATTATGA 480
25 CCACAACTG CGCCTGGCA TTGGAGAGAA GCCACTGTG GTCACTGTG AGATCTCCGT 540
CAACAGCCTT GGTCTCTCT CTATCTAGA CATGGAATAC ACCATTGACA TCATCTTCTC 600
CCAGACCTGG AATTCTAAGA GGACCCACGA GCATGAGATC ACCATGCCCA ACCAGATGGT 660
CCGCACTCAC AAGGATGGCA AGGTGTTGTA CACAATTAGG ATGACCATG ATGCCGGATG 720
CTCACTCTAC ATGCTCAGAT TTCCAATGGA TTCTCACTCT TGCCCTCTAT CTTTCTCTAG 780
30 CTTTTCTTAT CCTGAGAATG AGATGATCTA CAAGTGGGAA AATTTCAGC TTGAAATCAA 840
TGAGAAGAAC TCCTGGAAGC TCTTCCAGTT TGATTTTACA GGAGTGAGCA ACAAACCTGA 900
AATAATCACA ACCCCAGTTG GTGACTTCAT GGTGATGACG ATTTCTTCA ATGTGAGCAG 960
CGCGTTTGGC TATGTTGCC TTCAAACCTA TGTCCCTTCT TCCGTGACCA CGATGCTCTC 1020
CTGGGTTTCC TTTTGGATCA AGACAGAGTC TGCTCCAGCC CGGACCTCTC TAGGGATCAC 1080
35 CTCTGTTCTG ACCATGACCA CGTTGGGCAC CTTTCTCGT AAGAATTTCC CGCGTGTCTC 1140
CTATATCACA GCCTTGGATT TCTATATGCG CATCTGCTTC GTCTTCTGCT TCTGCGCTCT 1200
GTTGGAGTTT GCTGTGCTCA ACTTCTGAT CTACAACCAG ACAAAGCCC ATGCTTCTCC 1260
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CCTGGCTGTA GTAACCCAGT GGAATGAATT TGGACATGCC CCAATGCTTC TATATGCTAA 3120
70 GTGAAATCTG TGTCTGTAAT TTGTTGGGGG GTGGATAGGG TGGGGTCTCC ATCTACTTTT 3180
TGTCAACATC ATCTGAAATG GGGAAATATG TAAATAAATA TATCAGCAA GC

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Seq ID NO: 614 Protein sequence  
Protein Accession #: NP\_068822.1

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VMTIFPNVSR RFGYVAFQNY VPSSVTMLLS WVSFWIKTES APARTSLGIT SVLMTTLTGT 180
PSRKNFPRVS YITALDFYIA ICFVFCFAL LEFAVLNPLI YNQTKAHASP KLRHPRINSR 240
AHARTRARSR ACARQHQAEP VCQIVTTESG DGEERPSCSA QPPSPGSPSE GPRSLCSKLA 300
CEWCKRFRK YFCMVDFCEG STWQQRLCI HVYRLDNYSR VVFPVTFPPF NVLYWLVLN 360
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Seq ID NO: 615 DNA sequence  
Nucleic Acid Accession #: NM\_021990.1  
Coding sequence: 1309..2490

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CAGAGAAAGT CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180
GTGTAAGAA AGCCAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTTGT 240
CACTGCCTCC CAGCAAAAGC AGCACTATCC GGACTTCTAA CACCATCGGT GAGTTTCATA 300
CCTTGGCAGA TGGCCTTTAA CATTTTGTGT TAATTCAATT ATTCTTACTA ATCTTCTTCT 360
TTTTCTTGGC TGTGGTGCAT GGCTGTGGAG CTCAGGGTGG ACTCCTGTGT GGCAGCCAGT 420
TCTGGATGG CTGTCTGTGG GTGGAGGACT CCTGCCCTTC CTGTTTAGAC ACCCACAAG 480
GCTGCTCTTT AGCCTCCTTC CCTTCATCCC CTTCCTCTGC CCCAGTGCAC ACGAGTATTA 540
CACAAACCAAC AAAACCGCAA AATATCCCA CAATTTCTGT GTCTCTCTGT GGAGAGGCCG 600
CTCTGGCTTT CCTCTCAGC CCTGGCCCTC TGCTGTCTCC TCACCTCTGG TTGGTGTCTG 660
TCAGGCTGAC TAGAGGCCAA GCGGACCAAC ACTAGGCAAA CGGGCCAGC GCTCAGACAT 720
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GAGACTGAGA CTGGGAGCAG AGTTGGCAAA CTGCCAGAAG CCTCTGCTAT CCTGAACACT 1200
ATCCTGAGTA TTATGACCA CAAACTGCGC CCTGGCATTG GAGAGAAGCC CACTGTGCTC 1260
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GATTGGAGCT TCATGATAGC CTTGTGACAT CTTTAGGGCA GGATTTCTAT CCCCATTTTG 3660
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Seq ID NO: 616 Protein sequence  
Protein Accession #: NP\_068830.1

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MVIYKDKGV LYTIKRTIDA GCSLHMLRFP MDSHSCPLSF SSFSPYENEM IYKWNFKLE 120
INEKSNWKLQ QFDFTGVSNK TBIITFPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSVVTM 180
LSNVSVWIKT ESAPARTSLG ITSVLTMVTL GTFSRQNFPR VSYITALDPY IAICFVPCFC 240

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ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQB AFVQIVTTE 300  
 GSDGGERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPCD EGSTWQQGRL 360  
 CIHVYRLDNY SRVVPVTFP FPNVLYWLVC LNL

5

Seq ID NO: 617 DNA sequence  
 Nucleic Acid Accession #: NM\_004864.1  
 Coding sequence: 26..952

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 15 ATTCCGAGAG TTGGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGG CCAACCAGAG 240  
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 AGTGGGGCTG GGTACGGCG GGCACCTGCA CTGCGTATC TCTGGGCGG CCCTTCCOGA 360  
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 20 ATCTTCGTCC GCACGGCCCC AGCTGGAGTT GCACTTGGG CGCAAGCCG CCAGGGGGCG 600  
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 25 CTGCTGCGTG CCGCGCAGCT ACAATCCCAT GGTGCTCATT CAAAGACCG ACACCGGGGT 900  
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 AAAA

35

Seq ID NO: 618 Protein sequence  
 Protein Accession #: NP\_004855.1

40 1 11 21 31 41 51  
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 EDLLRLRLAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLEASRL 120  
 45 HRLFLRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSARPLQL 180  
 ELHLRPQAA RRRRARARNG DDCLPLGPRC CRLHTVRASL EDLGWADWVL SPREVQVTMC 240  
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 LAKDCHCI

45

Seq ID NO: 619 DNA sequence  
 Nucleic Acid Accession #: NM\_003979.2  
 Coding sequence: 254..1357

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 55 CTGCGCTGCT GCGCTCTTGC GCGCGGGAAG CAGCACCAG TTCAAGGCA ACGCTTGGC 240  
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5  
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CTCATCTGC ACCCAACCT CTGTAATAG ATTTACGCA TTTACGGCTG CATTCTGTAA 2340  
GTGGGCATGG TCTCTAATG GAGGAGTGT CATTGTATAA TAAGTTATTC ACCTGAGTAT 2400  
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10 Seq ID NO: 620 Protein sequence  
Protein Accession #: NP\_003970.1

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1 11 21 31 41 51  
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KLVGRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTMNRT NVNVFSELSA PRNEDFVLL 180  
LTYVLFMLAL TFLMSSFTEC GSFTGWRRHG AHIYLTMLLS IAIWVANITL LMLPDFDRRW 240  
DDTLSSALA ANGVVFLAY VSPFVLLTK QRNPMDYFVE DAFCKPQLVK KSYGVENRAY 300  
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20 Seq ID NO: 621 DNA sequence  
Nucleic Acid Accession #: NM\_002423.2  
Coding sequence: 48..851

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30 ATGACTCAGA AACAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAGAAAT 240  
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CCAGATGTGG AGTGCCAGAT GTTGCAAGAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360  
CTTCCAAAGT GGTCACTTAC AGGATGCTAT CATATACTCG AGACTTACCG CATATTACAG 420  
35 TGGATCGATT AGTGCAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTC 480  
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ACTCTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCCTTGGG CCTGGGACAG 600  
GTCTCGGAGG AGATGCTCAC TCGATGAGG ATGAAAGCTG GACGGATGGT AGCAGTCTAG 660  
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40 CCTCTGATCC TAATGCACTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780  
AACTTTCCCA GGATGATATT AAAGGCATT AGAACTATA TGGAAAGAGA AGTAATTC 840  
GAAAGAAATA GAACTCTCAG GCAGAACATC CATTCAATCA TCAATTGGAT TGTATATCAT 900  
TGTGTCATA CAGAAATGTA TAAGCACTGT TCCTCCACTC CATTAGCAA TTATGTCAAC 960  
CTTTTATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTTGGT AAACCTCTTT 1020  
45 ATGGTGTGAC TGTGCTTAT TCCATCTATG AGCTTTGTCA GTGCGGTAG ATGTCAATAA 1080  
ATGTTACATA CACAAATAAA TAAATGTTT ATTCATGGT AAATTTA

Seq ID NO: 622 Protein sequence  
Protein Accession #: NP\_002414.1

50  
1 11 21 31 41 51  
MRLTVLCAVC LLPGLALPL PQEAGGMSL QWRQAQDYLK RFLYDSETK NANSLEAKLK 60  
EMQKFFGLPI TGMILNSRVIE IMQKPRGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120  
PHITVDRLS KALNMWKEI PLHFRKVVWG TADIMIGPAR GAHGDYPPD GPGNTLAHAF 180  
55 APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGED 240  
PQNFILSQDD IKGIQKLYGK RSNRKK

60 Seq ID NO: 623 DNA sequence  
Nucleic Acid Accession #: NM\_031457.1  
Coding sequence: 204..956

65  
1 11 21 31 41 51  
AAACAGGAAA TAAATACGAA TGAAACTGAG CTCTAAGCAG CATGTAACCT GGCCTGCATC 60  
CAGGAAATAG AGGACTTGG ATCCTTCTAA CCCTACCACC CAACTGGCCC CAGTACATTC 120  
ATTCTCTCAG GAAAAAATC AAGGTCCCCA CAGCAAAGAA AAGGAATAGG ATCAAGAGAT 180  
ACGTGGCTGC TGSCAGAGCA AGCATGAATT CGATGACTTC AGCAGTTCCG GTGGCCAAAT 240  
CTGTGTTGGT GGTGGCACCC CACAATGGTT ATCCTGTGAC CCCAGGAAT ATGTCTCACG 300  
70 TGCCCTCTGA TCCAAACAGC CAGCGCAAG TCCACCTAGT TCCTGGGAAC CCACTAGTT 360  
TGGTGTGAAA TGTGAATGG GAGCTGTGC AGAAGCTCT GAAAGAGGC AAAACCTTGG 420  
GGGOCATCCA GATCATCAT GGCCTGGCTC ACATGGCCCT GCGCTCCATC ATGGCGACGG 480  
TTCTCGTAGG GGAATACCTG TCTATTTCAT TCTACGGAGG CTTTCCCTTC TGGGGAGGCT 540  
TGTGTTTTAT CATTTGAGGA TCTCTCTCG TGGCAGCAGA AAATCAGCCA TATTCTTATT 600  
75 GCTCTGCTGC TGSCAGTTTG GCTTGAACA TGCTCAGTGC AATCTGCTCT GCAGTTGGAG 660  
TCATACTCTT CATCAGAT CTAAGTATTC CCCACCCATA TGCCCTACCC GACTATTATC 720  
CTTACGCTG GGGTGTGAAC CCTGGAATGG CGATTCTGG CGTGTCTGCT GTCTTCTGCC 780  
TCTTGAGTT TGGCATCGCA TGCGCATCTT CCCACTTGG CTGCCAGTTG GTCTGCTGTC 840  
AATCAAGCAA TGTGAGTGT ATCTATCCAA ACATCTATGC AGCAAAACCA GTGATCACCC 900  
80 CAGAACCGGT GACTCACA CCAAGTTATT CCAGTGAGT CCAAGCAAAT AAGTAAGGCT 960  
ACAGATTCTG GAAGCATCTT TCACTGGGAC CAAAGAAAGT CCTCTCCCT TCTTGGGCTT 1020  
CCATAACCCA GTTCTGCTCT GTTCTGACAG CTGAGGAAAC GTCTCTCCA CTGTTTGTAC 1080  
TCTCACCTTC ATTCTTCAAT TCAGTCTAGG AAACCATGCT GTTCTCTAT CAAGAAGAAG 1140  
ACAGAGATT TAAACAGATG TTAACCAAGA GGGACTCCCT AGGGCAGATG CATCAGCACA 1200  
TATGTGGGCA TCCAGCTCT GGGGCTTGG CACACACACA TTGTTGTCT CTGCTGCATG 1260

TGAGCTTGTG GGTTAGAGGA ACAAATATCT AGACATTCAA TCTTACTCT TTCAATTGTG 1320  
CATTCAITTA ATAAATAGAT ACTGAGCATT CAAAAA AAAAAA

Seq ID NO: 624 Protein sequence  
Protein Accession #: NP\_113645.1

5  
1 11 21 31 41 51  
MNSMTSAVPV ANSVLVVAPH NGYPVTPGIM SHVPLYPNSQ PQVHLVPGNP PSLVSNVNGQ 60  
10 PVQKALKEGK TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISFYGGFFPW GGLWFIISGS 120  
LSVAAENQFY SYCLLSGSLG LNIVSAICSA VGVILFITDL SIPHPYAYPD YYPYANGVNP 180  
GMAISGVLLV FCLLEPGIAC ASSHFGCQLV CCQSSNVSVI YPNIIAANPV ITPEPVTSP 240  
SYSSEIQANK

15  
Seq ID NO: 625 DNA sequence  
Nucleic Acid Accession #: NM\_005221.3  
Coding sequence: 1..870

20 1 11 21 31 41 51  
ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60  
TCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT 120  
TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCGCAGCG CTACTGCTCT 180  
25 CTTACCTCGG CTTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCAOGGCGTG 240  
AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCGC ACTATAGCTA CGCTAGCTCC 300  
TACCACCACT ACGGGGCGGC CTACAACCCG GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360  
GAAGTGCACG AGCCGAGGT GAGAATGGTG AATGGCAAC CAAGAAGAGT TCGTAAACCC 420  
AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480  
TACCTCGCTG TGGCGGAACG CGCGAGCTG GCGCCTCGC TGGGATTGAC ACAACACAG 540  
30 GTGAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG 600  
ATGCCCCCGG AGCAGCTCC CAGCTCCAGC GACCAATGG CGTGTAACTC GCCCGAGTCT 660  
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCAC 720  
CCTCGACCT CCAACCACTC CCCAGCGTCC AGCTACCTGG AGAAGCTCTG ATCTGGTAC 780  
35 ACAAGTGCAG CCAGCTCAAT CAATCCAC CTGCGCGCGC CGGCTCCTT ACAGCACCCG 840  
CTGCGCTGG CCTCGGGAC ACTCTATTAG

Seq ID NO: 626 Protein sequence  
Protein Accession #: NP\_005212.1

40 1 11 21 31 41 51  
MTGVFDRRPV SIRSGDFQAP FQSAAMHHP SQESPTLPES SATSDYYSF TGGAPHGYS 60  
PTASASYGKAL NPYYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120  
45 EVTEPEVRMV NGKPKKVRKP RTIYSSPQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180  
VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQSSS RSLSHHPFAH 240  
PPTSNQSPAS SYLENSASWY TSAASSINSH LPPFGSLQHP LALASGILY

Seq ID NO: 627 DNA sequence  
Nucleic Acid Accession #: NM\_014420  
Coding sequence: 118..792

50 1 11 21 31 41 51  
GCACGAGAGA CGACGTGCTG AGCTGCCAGC TTAGTGGAAG CTCTGCTCTG GGTGGAGAGC 60  
AGCCTCGCTT TGGTGAAGCA CAGTGTCTGG ACCCTCCAGG AGCCCCGGGA TTGAAGGATG 120  
GTGGGGGCGG TCGTGTCTGG GCTGAGCTGG CTCTGCTCTC CCCTGGGAGC TCTGGTCTG 180  
GACTTCAACA ACATCAGGAG CTCTGCTGAC CTGCATGGGG CCCGGAAGGG CTCACAGTGC 240  
CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCCTCC AGCCCCGCGA TGAGAAGCCG 300  
TTCTGTGCTA CATGTCTGTG GTTGGCGAGG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT 360  
60 GGGACACTCT GTGTGAACGA TGTTTGTACT ACGATGGAAG ATGCAACCCC AATATTAGAA 420  
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAACTGGGCA CCCAGTCCAG 480  
GAAAACCAAC CCAAAAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG 540  
GGAGAAAGTT GTCTGAGAAC TTTTACTGT GGCCCTGGAC TTGTCTGTGC TGTCTATTT 600  
TGGACGAAA TTTGTAAAGC AGTCTTTTG GAGGACAGG TCTGCTCCAG AAGAGGGCAT 660  
65 AAAGACACTG CTCAGCTCC AGAAATCTTC CAGGTTGGC ACTGTGGCCC TGGACTACTG 720  
TGTGGAAGCC AATTGACCAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA 780  
GAAAAGCTAT AAATATTTC AATAAAGAA GAATCCACAT TGCAAAAAA AAAAAAATA 840  
A

70  
Seq ID NO: 628 Protein sequence  
Protein Accession #: NP\_055235

75 1 11 21 31 41 51  
MVAALLGLS WLCSPLGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR KFCLOPRDEK 60  
PFCATCRGLR RRCQRDAMCC PGTLCVNDVC TTMEDATPIL ERQLDEQDGT HAEGTGHFV 120  
QENQPKRKPS IKKSQGRKGQ EGESCLRTFD CGPGLCCARH FMTKICKPVL LEGQVCSRRG 180  
HKDTAQAPFI FQRCDCGPGI LCRSLTSNR QHARLRVCQK IEKL

80  
Seq ID NO: 629 DNA sequence  
Nucleic Acid Accession #: NM\_002448.1  
Coding sequence: 241..1134

1 11 21 31 41 51



Seq ID NO: 630 Protein sequence  
Protein Accession #: NP\_002439.1

Seq ID NO: 631 DNA sequence  
Nucleic Acid Accession #: NM\_002557.1  
Coding sequence: 13..2049

1192

CTCTTTTCCA TTAATAAAC TGTAAACACA AGAACCCA

Seq ID NO: 632 Protein sequence

Protein Accession #: NP\_002548.1

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1	11	21	31	41	51	
MMKLLLVVGL	VLVLKHHHGA	AHKLVCYPTN	WAHSRPGPAS	ILPHDLDPFL	CTHLIPAFAS	60
MNNNQIVAKD	LQDEKILYPE	FNKLKERNRE	LKTLISIGGW	NFGTSRFTTM	LSTFANREKF	120
IASVISLLRT	HDPDGLDLFF	LYPGLRGSPM	HDRWTFLELI	EELLFAFRKE	ALLTMRPRL	180
LSAASGVPH	IVQTSVDVRF	LGRLLDPIV	LSYDLHGSWE	RFTGHNSPLF	SLPEDPKSSA	240
YAMNYWRKLG	APSEKLIMGI	PTYGRTFRLL	KASKNGLQAR	AIGPASPGKY	TKQEGFLAYF	300
EICSFVWGAK	KHWIDYQYVP	YANKGKEWVG	YDNAISFSYK	AWFIRREHFG	GAMVNTLDMO	360
DVRGTFCGTG	PFPLVYVLND	ILVRAEFSST	SLPQFWLSSA	VNSSSTDPER	LAVTTAWTTD	420
SKILPFGGEA	GVTEIHGKCE	NMTITPRGIT	VTPTKETVSL	GKHTVALGEK	TEITGAMTMT	480
SVGHQSMTPG	EKALTPVGHQ	SVTTGQKTLT	SVGYQSVTPG	EKTLTPVGHQ	SVTPVSHQSV	540
SPGGTMTMPV	HFQTEFLRQN	TVAPRRKAVA	REKVTVPSPN	ISVTFEGQTM	PLRGENLTSE	600
VGTHPRMGNL	GLQMEANENM	MLSSSPVIQL	PEQTPLAFDN	RFVPIYGNHS	SVNSVTPTQS	660
PLSLKKEIPE	NSAVDEEA					

Seq ID NO: 633 DNA sequence

Nucleic Acid Accession #: NM\_003885.1

Coding sequence: 98..1021

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1	11	21	31	41	51	
AAACTCAGAA	TTTTGCGGG	CTCGGTGAGC	GGTTTTATCC	CTCCGGCCGG	CAGGCTGGGC	60
GCAGGGGGCG	AGCCCCCGCC	CGGCGCGCAG	CAGCACCATG	GGCACGGTGC	TGTCCTCTGC	120
TCCAGCTACT	CGGAAGGCCA	CGCTGTTTGA	GGATGGCGCG	GCCACCGTGG	GCCACTATAC	180
GGCGGTACAG	AACAGCAAGA	ACGCCAAGGA	CAAGAACCTG	AAGCGCCACT	CCATCATCTC	240
CGTGCTGCTT	TGGAAGAGAA	TCGTGGCCGT	GTGGGCCAAG	AAGAAGAACT	CCAAGAAGGT	300
GCAGCCTAAC	AGCAGCTACC	AGAACAACAT	CACGCACCTC	AACAATGAGA	ACCTGAAGAA	360
GTCGCTGTGG	TGCGCCAACC	TGTCCACATT	GCCTCAGCCC	CCACCGGCCC	AGCGCGCTGC	420
ACCCCGCGCC	AGCCAGCTCT	CGGGTTCCCA	GACCGGGGGC	TCTCTCTCAG	TCAAGAAAGC	480
CCCTCACCTT	CCGCTCACCT	CCGCAGGGAC	GCCCAACCGG	GTCTCTGTCC	AGGCGTCCAC	540
CAGTGAGCTG	CTTCGCTGCC	TGGGTGAGTT	TCTCTGCGCG	CGGTGCTACC	GCCTGAAGCA	600
CCTGTCCCCC	ACGGACCCCG	TGCTCTGGCT	GCGCAGCGTG	GACCGCTCGC	TGCTTCTGCA	660
GGGCTGGCAG	GACCAAGGGT	TCATCACGCC	GGCCAACGTG	GTCTTCTCTT	ACATGCTCTG	720
CAGGGATGTT	ATCTCTCTCG	AGGTGGGGCTC	GGATCACGAG	CTCCAGGCCG	TCCTGTCTGAC	780
ATGCCGTGAC	CTCTCTACT	CCTACATGGG	CAACGAGATC	TCCTACCCCG	TCAAGCCCTT	840
CCTGGTGAGG	AGCTGCAAGG	AGGCCTTTTG	GGACCGTTGC	CTCTCTGTCA	TCAACCTCAT	900
GAGCTCAAAG	ATGCTGCAGA	TAAATGCGGA	CCCACTACT	TTCACACAGG	TCTTCTCCGA	960
CCTGAAGAAC	GAGAGCGGCC	AGGAGGACAA	GAAGCGGCTC	CTCCTAGGCC	TGGATCGGTG	1020
AGCACTGTAG	CCTGCGTCAT	GGCTCAAGGA	TTCAATGCAT	TTTTAAGAAT	TTATTATTAA	1080
ATCAGTTTGT	TGTACAG					

Seq ID NO: 634 Protein sequence

Protein Accession #: NP\_003876.1

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1	11	21	31	41	51	
MGTVLSLSPS	YRKATLFEDG	AATVGHYTA	QNSQNAKDRN	LKRHSIISVL	PWKRIVAVSA	60
KKQNSKKVQP	NSSYQNNITH	LNENLKKSL	SCANLSTPAQ	PPPAQPPAPP	ASQLSGSQTG	120
GSSSVKKAPH	PAVTSAGTPK	RVIVQASTSE	LLRCLGEFLC	RRCYRLKHL	PTDPLVWLRS	180
VDRSLLLQGW	QDQGFITPAN	VVFLYMLCRD	VISSEVGS DH	ELQAVLLTCL	YLSYSYMGNE	240
ISYPLKPFIV	ESCKEAFWDR	CLSVINLMSS	KMLQINADPH	YFTQVPSDLK	NESGQEDKKR	300
LLGLGLDR						

TABLE 79A:

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence identification number linking information in Table 79A to sequences in Table 80			
10	Pkey	ExAccn	UnigenelD	Unigene Title	Seq ID No.
15	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
20	443646	AI085198	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
	409556	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	Seq ID No. C8 & C224
	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
	421582	AI910275	Hs.350470	trefoil factor 1 (breast cancer, estrogen	Seq ID No. C10 & C226
25	411789	AF245505	Hs.72157	Adfican	Seq ID No. C11 & C227
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
30	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
	432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
35	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
	409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C23 & C238
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C24 & C239
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
40	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No. C26 & C241
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	Seq ID No. C27 & C242
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
	415214	AI445236	Hs.125124	EphB2	Seq ID No. C30 & C245
45	443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
	410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
	411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
50	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C38 & C253
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
55	437935	AW939591	Hs.6940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
	422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	Seq ID No. C44 & C259
	437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
60	408243	Y00787	Hs.624	interleukin 8	Seq ID No. C46 & C261
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
	439738	BE246502	Hs.9598	serma domain, immunoglobulin domain (Ig),	Seq ID No. C48 & C263
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
65	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazarus	Seq ID No. C51 & C266
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
	413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
	443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
70	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
	442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
	450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
75	416955	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
	442275	AW449467	Hs.54795	Homo sapiens secretoglobulin, family 3A, m	Seq ID No. C62 & C277
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C63 & C278
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C64 & C279
	453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
80	421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
	421563	NM_006433	Hs.105806	granulysin	Seq ID No. C68 & C283
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
	414991	C17898		Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
	419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-RNA synthetas	Seq ID No. C71 & C286
	424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287

	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	AJ393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
	410407	X56839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
5	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
10	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
	431846	BE019924	Hs.271580	uroplakin 18	Seq ID No. C82 & C297
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No. C84 & C299
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
15	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
20	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
35	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalini	Seq ID No. C106 & C321
	440659	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
45	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
	426761	AJ015709	Hs.172089	PORIMIN Pro-oncogene receptor inducing me	Seq ID No. C120 & C335
50	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfamily	Seq ID No. C121 & C336
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	Seq ID No. C125 & C340
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
	428513	BE220806	Hs.184697	plaxin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
60	432874	W94322	Hs.279651	melanoma inhibitory activity	Seq ID No. C131 & C346
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
65	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
70	432596	AJ224741	Hs.278461	matrilin 3	Seq ID No. C141 & C356
	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protel	Seq ID No. C146 & C361
75	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gastrin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefol factor 3 (intestinal)	Seq ID No. C150 & C365
80	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
	426227	U57058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

5	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	Seq ID No. C156 & C371
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
	413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	Seq ID No. C160 & C375
	436729	BE621807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
	451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
10	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
	421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
15	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholestergic	Seq ID No. C172 & C387
	439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
20	411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
	412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	Seq ID No. C176 & C391
	419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
25	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
	421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
	433336	AF017988	Hs.31386	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
	436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
30	410258	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No. C184 & C399
	416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
	437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
	421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
35	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
	410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	Seq ID No. C191 & C406
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	Seq ID No. C192 & C407
	418576	AW968159	Hs.302740	Epithelial calcium channel 2, CaT-like A	Seq ID No. C193 & C408
40	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C194 & C409
	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C195 & C410
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
45	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
	430144	AF732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
	408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
50	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
	425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
	432800	BE391046	Hs.278962	AIM-1 protein	Seq ID No. C207 & C422
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
55	424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
	434293	NM_004445	Hs.3796	EphB6	Seq ID No. C212 & C427
	427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
60	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
	422424	AI186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
	432378	AI493046	Hs.146133	ESTs	Seq ID No. C432 & C433
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

## 65 TABLE 798

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

## 70

Pkey CAT Number Accession

414991 1785136\_1 D78831 C17898 D78863

## 75 TABLE 79C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

## 80

Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

Pkey Ref Strand NL\_position

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404682	9797231	Minus	40977-41150
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281

Table 80:

Seq ID NO: C1 DNA Sequence  
Nucleic Acid Accession #: NM\_005814  
Coding sequence: 345..1304

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	AGTAGGTGAC	ACATGAGCCC	AGCCCCAGCT	CACCTGCCAA	TCCAGCTGAG	GAGCTCACCT	180
	GCCAAATCCAG	CTGAGGCTGG	GCAGAGGTGG	GTGAGAAGAG	GGAAAATTGC	AGGGACCTCC	240
	AGTTGGGCCA	GGCCAGAAGC	TGCTGTAGCT	TTAACCAGAC	AGCTCAGACC	TGCTGGAGG	300
15	CTGCCAGTGA	CAGGTTAGGT	TTAGGGCAGA	GAAGAAGCAA	GACCATGGTG	GGGAAGATGT	360
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	CTCCGCAGGA	CGTTCCTCGG	GCTTCGCAGG	GAAAGAGTGT	CACCTGCCCC	TGCACCTACC	480
	ACACTTCCAC	CTCCAGTCGA	GAGGGACTTA	TTCATGGGGA	TAAGCTCCTC	CTCACTCATA	540
	CGGAAAGGGT	GGTCATCTGG	COGTTTTCAA	ACAAAACTA	CATCCATGGT	GAGCTTTATA	600
20	AGAATCGGCT	CAGCATATCC	AACAATGCTG	AGCAGTCCGA	TGCCTCCATC	ACCAATTGATC	660
	AGCTGACCAT	GGCTGACAAC	GGCACCTACG	AGTGTTCTGT	CTCGCTGATG	TCAGACCTGG	720
	AGGGCAACAC	CAAGTCACGT	GTCGCCCTGT	TGGTCCCTCG	GCCACCTGCC	AAACCAAGAT	780
	GCGGCATCGA	GGGAGAGACC	ATAATTGGGA	ACAACATCCA	GCTGACCTGC	CAATCAAAGG	840
	AGGGCTCACG	AACCCCTCAG	TACAGCTGGA	AGAGGTACAA	CATCCTGAAT	CAGGAGCAGC	900
25	CCCTGGCCGA	CCAGGCTCCA	GCTCAGCCTG	TCTCCCTGAA	GAATATCTCC	ACAGACACAT	960
	CGGGTTACTA	CATCTGTACC	TCCAGCAATG	AGGAGGGGAC	GCAGTTCTGC	AACATCACGG	1020
	TGGCCGTGAG	ATCTCCCTCC	ATGAACGTGG	CCCTGTATGT	GGGCATCGCG	GTGGCGGTGG	1080
	TGCGACCCCT	CATTATCATT	GGCATCATCA	TCTACTGCTG	CTGCTGCCGA	GGGAAGGACG	1140
	ACAACACTGA	AGACAAGGAG	GATGCAAGGC	CGAACCGGGA	AGCCTATGAG	GAGCCACCAG	1200
30	AGCAGCTAAG	AGAACTTTCC	AGAGAGAGGG	AGGAGGAGGA	TGACTACAGG	CAAGAAGAGC	1260
	AGAGGAGCAC	TGGGCGTGAA	TCCCCGAGCC	ACCTCGACCA	GTGACAGGCC	AGCAGCAGAG	1320
	GGCGGCGGAG	GAAGGGTTAG	GGGTTCAATC	TCCCGCTTCC	TGGCCTCCCT	TCTCCTTTCT	1380
	AAGCCCTGTT	CTCCTGTCCC	TCCATCCGAG	ACATGTATGG	GGACATTTCT	TCCCCAGTGT	1440
	CAGCTGTGGG	GAACATGGCT	GGCCTGGTAA	GGGGGTCCCT	GTGCTGATCC	TGCTGACCTC	1500
35	ACTGTCTGTT	GAAGTAACCC	CTCCTGGCTG	TGACACCTGG	TGCGGGCCTG	GCCCTCACTC	1560
	AAGACCAGGC	TGCAGCCTCC	ACTTCCCTCG	TAGTTGGCAG	GAGCTCCTGG	AAGCACAGCG	1620
	CTGAGCATGG	GGGCTCCCA	CTCAGAACTC	TCCAGGGAGG	CGATGCCAGC	CTTGGGGGGT	1680
	GGGGGCTGTC	CTGCTCACTC	GTGTGCCAG	CACCTGGAGG	GGCACCAGGT	GGAGGGTTTG	1740
	CATCCACAC	ATCTTTCTTG	AATGAATGAA	AGAATAAGTG	AGTATGCTTG	GGCCCTGCAT	1800
40	TGGCCTGGCC	TCCAGCTCCC	ACTCCCTTTC	CAACCTCACT	TCCCGTAGCT	GCCAGTATGT	1860
	TCCAAACCCCT	CCTGGGAAGG	CCACCTCCCA	CTCCTGCTGC	ACAGGCCCTG	GGGAGCTTTT	1920
	GCCCAACAC	TTTCCATCTC	TGCCTGTCAA	TATGTAAGCT	GTCCCTCCAG	GCCCATCTCA	1980
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45	TGTATTAGAG	CGCCAGCTCC	TGCGGGCAGG	GCCCTGGGCT	CATGGCTTTT	GCTTTCCCTG	2160
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	TCCACCCCAA	ACCCAGTAT	TCAITTCAGT	AGTTAAACAC	GAATTGATTT	AAAGTGAACA	2340
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	CAGGCAGCGT	TAGGGCTGCT	TAGGTCTCAT	GGACCACTGG	CTGGTCTCAC	CCAACCTGCAG	2640
	TTTACTATTG	CTATCTTTTC	TGGATGATCA	GAATAATAAT	TCCATAAATC	TATTGTCTAC	2700
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	AAATGCITTC	AGTAATAATA	AAATTGTGGG	TGG			2793

Seq ID NO: C2 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3150

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60	ATGGGGAGCC	GGAGCCGAGA	GTCCCTCTCT	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
65	CGCCGACCCC	CGCTSSGTCC	GCTGCTGTGG	CTGCTSSTGC	CGCCGCCACC	CAGGGTCGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTAA	CGGCGCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACCAGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCCCT	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTGG	ACAGCAAAGG	CTCTGGGCTC	360
70	CTGGAGTCCT	CACCTGCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCCCTTGCA	420
	TGGTTGCGGG	CAACAGTTCC	AGCCCATGGC	TCTTCCATCT	TGGCATGCGC	TCCACTGTAC	480
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	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	600
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75	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGTCTGCCAC	TCAGGAGCAG	720
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	TTCAAGTGGT	ATGACACAGA	AGACTTTGTT	GCTGGTGTGC	CCAAAGGGAA	CCTCACTTAC	900
80	GGCTATGTCA	CCATCCTTAA	TGGCTCAGAC	ATTCCGATCC	TCTACAACTT	CTCAGGGGAA	960
	CAGATGGCCT	CCTACTTTGG	CTATGCAGTG	GCCGCCACAG	ACGTCAATGG	GGACGGGCTG	1020
	GATGACTTGC	TGGTGGGGGG	ACCCCTGCTC	ATGGATGCGA	CCCTGACGGG	GCGGCCCTAG	1080
	GAGGTGGCCA	GCTGCTACGT	CTACCTGCAG	CACCCAGCGG	GCAATAGAGC	CACGCCACCC	1140
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10  
15  
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ATCATCATCC TAGCCATCCT GTTGGGCTTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
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Seq ID NO: C3 DNA Sequence

Nucleic Acid Accession #: NM\_002421.2

Coding sequence: 1..1410

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GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300
GTCTCAGTGT AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360
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GATGAATATA AAGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
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Seq ID NO: C4 DNA Sequence

Nucleic Acid Accession #: E08 sequence

Coding sequence: 1..1410

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TACACGCCAG ATTGGCCAAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420
TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGCATCATG 480
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Seq ID NO: C5 DNA Sequence  
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 Coding sequence: 1..1506

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Seq ID NO: C6 DNA Sequence  
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 Coding sequence: 112..3624

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Seq ID NO: C7 DNA Sequence

Nucleic Acid Accession #: NM\_002192

Coding sequence: 86..1366

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Seq ID NO: C8 DNA Sequence  
Nucleic Acid Accession #: NM\_000955.1  
Coding sequence: 26..2299

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Seq ID NO: C9 DNA Sequence  
Nucleic Acid Accession #: XM\_057014  
Coding sequence: 143..874

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Seq ID NO: C12 DNA Sequence  
Nucleic Acid Accession #: AK001903  
Coding sequence: none

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	GTACCGGAAC	CTGCAGAAAC	AGTGTGAGAA	ATTAAGTCCT	GGTTCACTGC	GCAGTAGCAA	180
	AGATGGTCAA	GGCCATGGAA	AAAGCAGAAA	TTTACCAAGA	AAGCTGATAC	CCATGTATAG	240
40	TTCCCACTCA	TCTCAAAATAC	ATCTGCTATC	TTTTTAAGCT	AAGTCCTAGA	CATATCGGGG	300
	ATAACATGGG	GGTTGATTAG	TGACCACAGT	TATCAGAAGC	AGAGAAATGT	AATTCATAT	360
	TTTTATTGAA	ACTTATTCCA	TATTTTAATT	GGATATTGAG	TGATTGGGTT	ATCAAAACAC	420
	CACAAACTTT	AATTTTGTGA	AATTTATATG	GCTTTGAAAT	AGAAGTATAA	GTGTCTACCA	480
	TTTTTTGATA	ACATTGAAAG	ATAGTATTTT	ACCATCTTTA	ATCATCTTGG	AAAATACAAG	540
45	TCCTGTGAAC	AACCACTCTT	TCACCTAGCA	GCATGAGGCC	AAAAGTAAAG	GCTTTAAATT	600
	ATAACATATG	GGATTCTTAG	TAGTATGTTT	TTTTCTTGAA	ACTCAGTGGC	TCTATCTAAC	660
	CTTACTATCT	CCTCACTCTT	TCTCTAAGAC	TAAACTCTAG	GCTCTTAAAA	ATCTGCCCAC	720
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	CTTTCTAATT	TTTTTTTCTC	CATTGTGGGA	TTGGACTTTA	AGAGGTGACT	CTAAAAAAAC	1020
	AGAGAACAAA	TATGTCTCAG	TTGTATTAAAG	CACGGACCCA	TATTATCATA	TTCACTTAAA	1080
55	AAAATGATT	CCTGTGCACC	TTTTGGCAAC	TTCTCTTTTC	AATGTAGGGA	AAAACTTAGT	1140
	CACCTGAAA	ACCCACAAAA	TAAATAAAAC	TTGTAGATGT	GGGCAGAAAG	TTTGGGGGTG	1200
	GACATTGTAT	GTGTTTAAAT	TAAACCTCTG	ATCACTGAGA	AGCTGTGTGA	TGGGTCTAGAG	1260
	AAAATGAATG	CTTAGAAGCT	GTTCACTCT	TCAAGAGCAG	AAGCAAAACA	CATGCTCTCAG	1320
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	AGGGTTTAC	CCCTCATTTA	AATGCTTTGA	AAAACAGTGC	ATTGACAATG	GGTTGATATT	1440
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	AAAACTTTTT	ATGTTCTGTG	GTTGATGTTG	TTTGTGTTT	TGTTTCTATT	TTGTTGGTTT	1560
	TTTACTTTGT	TTTTTGTGTT	GTTTGTGTTT	GTTTGTGATA	CTACATGCAG	TTCTTTAACC	1620
	AATGCTGTGT	TGGCTAATGT	AATTAAAGTT	GTTAATTTAT	ATGAGTGCAT	TTCAACTATG	1680
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65	TTTAAAGAGA	TAAACAGTTG	ATATGTTTTC	ATGTGTTTAT	AGCAGAAGTT	ATTTATTTCT	1800
	ATGGCATTC	AGCGGATATT	TTGGTGTGTT	CGAGGCATGC	AGTCAATATT	TTGTACAGTT	1860
	AGTGGACAGT	ATTCAGCAAC	GCCTGATAGC	TTCTTTGGCC	TTATGTTAAA	TAAAGAGACC	1920
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Seq ID NO: C13 Protein Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..5001

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	CAGTCTGTGC	TTGTGTCCTG	GGTGGATCCT	GTCTCTGAAA	AACAGAAGAA	AGTTGTTGCA	180
80	TCAAGACAGT	ACACCGTGGC	CTATOGAGAG	AAGGGGGAAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGGCGTGT	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAATTT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAATGGA	GTACGTCAGT	CTTCCAAAAG	360
	ACACCAAGAT	CTGCCCTTAC	CACAGCTCCT	GAAACCTTGA	ACGCTCTGGC	AGTCAATGGC	420
	AAACCTACAG	TTGTGCTGTC	ATCTTGGGAT	GCGCTACCAAG	AGACTGAGGG	GAAAGTGAAA	480
	GTCTGCTGTC	TGGACACAGG	ACTGTTTTCA	GTTTCTCTCT	TCCAACCATC	TGCCAAATCA	540

	TTTCAGAATA	CATTCTTTCA	TAGCCCCCG	CTCTCAAACC	ATTTGGAGCA	AAGTCCCTCA	600
	CCTATCCTGG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCCTGGG	GAAOGCTATC	660
	TTTTCAAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATTG	720
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	ATOGATATCC	AAACCAAAAC	AGTTAATAAA	GATOCACAAC	TGGAAGGGAG	TGTTTTTGA	840
	CCATGTTTTT	TTTTCTACTT	CCTCACATTT	ATGCTGGATA	TTGGOGGCTT	TTCTTTCATT	900
	ATGTGCTATG	AAGAOCANNN	TGTTTCTTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	GCAGAACACG	GAGGACAATG	GGAAACCCGA	AAAACCTGAG	1020
10	CCCTTCTCAC	CTTCTCCAG	AGCTCCAGCT	TCCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAATAAT	ATTGGCTAAT	1140
	GGTGGGGGCG	CCCCAAAACC	CCAGCTTCCG	GCCAAGAAAG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTTCCCGGG	AGGACTCGCC	CATGTCAACC	1260
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	GTAGATAAGC	CTGCTTTTTC	CCTGGCCACG	CAGCCCGGCC	CAGGGGCGCC	CCCTCGGCT	1440
	TGGGCTCTCT	CTGCCACCA	CGCTTCCACC	CAGGCACTCT	CTCATCTGTC	TTCCCTGCTT	1500
	GCCAGCTTGA	ATGACAACGA	CTTGTGGAC	TCAGACGAAG	ATGACGCGGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGGCGCTTT	CGCCAGCCCG	CGGCCAGCCC	TGTCCCCAG	CCGCCAGTCC	1620
20	CCGTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGCAACCCG	GCGCAAAGCC	AGCCTGCGCG	1680
	GGCGGAGGGA	CCCCCATTC	AGGGGCGCGA	GAGGAAGATT	CCAGTGCTCT	AGCCCCACCC	1740
	TCAGACCTTT	CTCCACCCCA	TGGGGGATCA	TCTCGCTGTC	TGCCCAACCA	GCCACACCTG	1800
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25	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGGCGA	TAGGGAAGAC	1980
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35	TTCCCTGTCT	GTCTCCCGC	AGCAOCCGTA	CAGCAGCATC	CCAGTGTTC	CAGAAGGATG	2580
	ACACCCGCGC	GGGCCCCAGA	ACAGCAGCCC	CCTCTCCCG	TGCCACGCTC	CCAGCACCCAC	2640
	CCGGGACCCC	AGAGCAGAGA	CGCGGGTGGG	TCACTTCCCG	AGCCACGGCT	CTCACTGACC	2700
	CAGGCGGGCG	GGCCCGGCCC	CAGTCCGAG	GGCGCTCCCG	ACTCTCTCTC	GGACCCCTAC	2760
	ACGGCGAGCT	CCGAGGGATC	GCTCCCGACG	GCCCTCCAGA	ACCAGGACGA	GGATGCCGAG	2820
40	GGCAGCTACG	ACGACGACAG	CACAGAAGTC	GAGGCCACAG	ATGTGCGGGC	CCCGCGGCAC	2880
	GCCGCGCGCG	CCAAGGAGGC	AGCTGCGTCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCG	2940
	ACAGGCGCAG	GGGACGGTGG	GGACCAACAG	TCCAGCGCG	GACATGCGCG	CTCCCCCGCC	3000
	AGGCCCGAGC	GACCCGGCGG	CCCCAGTCC	CGCGCCCGGG	TCCCGACGAG	GGCAGCGCGC	3060
	GGGAAGTGGG	AGCTCTCTCT	CAAGCGGCC	CTGTCTCTCA	AGTCCACGCA	GTGCTCTCA	3120
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	GTCTCTTCCC	GACCGCCGCG	TGCGAGCGCT	GCCACCGTGA	GCCCGCTCGC	GGGCAACCCAC	3420
50	CCCTGGCGCG	GGTACACCCAC	GCGCGCCCCV	CCTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
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	GGTAGTAATG	GAAACCCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
	GTGTGGAGCC	TTGATGCTGG	GTTAGTATTG	AATGCAGAA	GAAGGTACCT	CCAAGATTCA	3720
55	CATGGAATTC	CTCTTGGGAT	TAAACTAGGA	GGAGATGGTC	GAACCAATTG	AGATCTGGAA	3780
	GGGACCCCGC	TGGTGAAGTC	TGACGGCCTC	CCACTCTTTG	GGCAGGGGGC	ACATGGGACA	3840
	CCTCTGGGCA	AGGCGCCAGA	TAAAGCCAA	TTGAGTCTTG	GAGGAAGGCC	GCTGGTGGGC	3900
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	ACGAGCCGCC	TGCTTACCC	TACAAACCCG	AGGCCCAACA	CTGCCACCAC	CATGCAGCCC	4020
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	ACCAACCCCA	AACCAACCA	TCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAAACGGAC	4200
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	GATGAGTTCT	CAGGCTTGGG	GACTGACACT	GCAGTAOCTA	CGGAAGAGGC	CTACGTTATA	4320
65	TATGATGAAG	ATTATGAATT	TGAGACGCTA	AGGCCACCAA	CCACCACTGA	GCCTTCGACC	4380
	ACTGCTACCA	CACGAGGGGT	GATCCAGAG	GAAGGCGCCA	TCAGTTCTCT	TCCTGAAGAA	4440
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	GATGAAATCA	TCCCAATGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCGCG	4620
70	AACATCACCG	TGGTGGCCGT	GGAAGGTTGC	CACTCAATTTG	TCATTTGTTGA	TTGGGACAAA	4680
	GCCACCCGAG	GAGATTGGT	CACAGGTTAT	TTGGTTTACA	GTGCATCCTA	TGAAGATTTC	4740
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	TTGGAGACAG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
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80	AGTATGCTCA	GGAGGCTGTC	AGGTTTGGGA	ACATCGGCTT	CGGAACCCCG	TACTACTATG	5280
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	CATTCTGGTC	ATCTCAGTCT	GGAACTCAGT	CCCACTTCTT	GGCCTGGACA	ATGAACAGGA	5520
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Seq ID NO: C14 DNA Sequence  
Nucleic Acid Accession #: NM\_003014  
Coding sequence: 238..1278

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Seq ID NO: C15 DNA Sequence  
Nucleic Acid Accession #: NM\_005940  
Coding sequence: 23..1489

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TCTGCGCGCG	GACGTCCACC	ACCTCCATGC	CGAGAGGAGG	GGGCCACAGC	CCTGGCATGC	180
AGCCCTGCCC	AGTAGCCCGG	CACCTGCCCC	TGCCAGCGAG	GAAGCCCCCC	GGCCTGCCAG	240
CAGCCTCAGG	CCTCCCCGCT	GTGGCGTGCC	CGACCCATCT	GATGGGCTGA	GTGCCCGCAA	300
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CGACTATGAT	GAGACCTGGA	CTATCGGGGA	TGACCCAGGC	ACAGACCTGC	TGCAGGTGGC	660
AGCCCATGAA	TTTGGCCACG	TGCTGGGGCT	GCAGCACACA	ACAGCAGCCA	AGGCCCTGAT	720
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TCAACACCTA	TATGCGCCAGC	CCTGGGCCAC	TGTCACTCCC	AGGACCCCTG	CCCTGGGCCC	840
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 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGGTCTCGT 1440  
 10 GGGTCCCTGAC TTCTTTGGCT GTGCCGAGCC TGCCAACTAT TTCTCTGAC CATGGCTTGG 1500  
 ATGCCCTCAG GGGTGTGAC CCTGCCCAGG CCAAGATAT CAGGCTAGAG ACCCATGGCC 1560  
 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGCTCTCTGC AGGGGGATGG 1620  
 GGTGGGGTAC AACCACCATG ACAACTGCCG GGAGGGCCAC GCAGGTCTGT GTCCACTGCC 1680  
 AGGACTGTCT TCAGACTGGG CAGGAGGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740  
 15 GGGACCCGCT ATCGAAGTCC TGGCAAACT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800  
 GTAGCAACAT GGCAGGACTG GGGGAACTGG AGTGTCTTGC CTGTATCCCT GTTGTGAGGT 1860  
 TCCTTCCAGG GGCCTGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920  
 TGAGCAACTG GGCCTGAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTTGC 1980  
 ATCTGTCTGC CTCTGGCTG ACAATCCTGG AAATCTGTTC TCCAGAAATC AGGCCAAAAA 2040  
 20 GTTCACAGTC AAATGGGGAG GGGTATCTCT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100  
 CAACATACCT CAATCTGTGC CAGGCGCGGA TCCTCCTGAA GCCCTTTTGC CAGCACTGCT 2160  
 ATCCTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTCTTTC TTCTTTTTTT 2220  
 TTTTAAACT GAGGATTGTC ATTAAACACA GTTGTTTTCT 2260

25 Seq ID NO: C16 DNA Sequence  
 Nucleic Acid Accession #: NM\_024022  
 Coding sequence: 202..1563

30 1 11 21 31 41 51  
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 ACCGGGCACC GGAACGGCTCG GGTACTTTTG TTCTTAATTA GGTTCATGCC GTGTGAGCCA 60  
 GGAAGGGGCT GTGTTTATAG GAAGCCAGTA ACATCTGTGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCCGATGTC 180  
 35 AGAGGTCCTG AAATAGTCA CAGTGGGGAA AATGATCCCG CTGCTGTGTA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCCTGTTC ACCAGATGCA 300  
 GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTCTTCC AATCATGCTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGATCCCA CTTCGATGTC 420  
 TCAGGGAAGT ACAGATGTGC CTCACTCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 40 GGAATCTCGG ATGTCAAAGA CCGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAG CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACCCAATATG TGCCCTGTGCC CAACCTGGGT TCCCAAGCTA TGTGAGTTCA 660  
 GATAAECTCA GAGTGAAGTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CACCTGACAA GGTGACTGCA TTACAACACT CAGTATATGT GAGGAGGGA 780  
 45 TGTGCTCTG GCCAGTGGT TACCTTGACG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AAGGGTACCA CCTGTGCGGG GGCTCTGTCA TCAAGCCCTC GTGGATCATC 960  
 ACTGTGACAC ACTGTGTTTA TGAATGTGAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTGG TGGAGAAGAT TGTCTACCAC 1080  
 50 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATGCCCC TTATGAAGCT GGCCGGGGCCA 1140  
 CTCAGSTTCA ATGAAATGAT CCAGCCTGTG TGCCCTGCCA ACTCTGAAGA GAACTTCCCC 1200  
 GATGGAAAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGG TGAAGCCTCC 1260  
 CCTGTCTGCA ACCACGGGCG CGTCCCTTTC ATTTCCAACA AGATCTGCAA CCACAGGGAC 1320  
 GTGTACGGTG GCATCATCTC CCGCTCCATG CTCTGGCGGG GCTACCTGAC GGGTGGCGTG 1380  
 55 GACAGCTGCC AGGGGGACAG CGGGGGGCCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG 1440  
 TTAGTGGGAG CGACAGGCTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGGTGTAC 1500  
 ACCCGTTGCA CCTCCTTCTC GGACTGGATC CACGAGCAGA TGGAGAGAGA CTTAAAAACC 1560  
 TGAAGAGGAA GGGGACAAAT AGCCACCTGA GTTCTGAGG TGATGAAGAC AGCCCGATCC 1620  
 TCCCTGGAC TCCCGGTAG GAACCTGCAC ACAGAGCAGC ACCCTTGGAG CTCTGAGTTC 1680  
 60 CGGCACCAAT AGCAGGCGCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740  
 GCTGCTTTT GTTTTGTGTT TTTTGTAGGT GGAATCTGCG TCTGTGCCCC AGGCTGGAGT 1800  
 GCAAGTGGGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG 1860  
 CCTCAGCTTC CCACTAGACT GGGACACAG GTGCCGCCA CCACACCCAA CTAATTTTTC 1920  
 TATTTTATG AGAGACAGGG TTTCAACATG TTGGCCAGGC TGCTCTCAAA CCGCTGACCT 1980  
 65 CAAATGATGT GCTGTCTTCA GCCTCCACA GTGCTGGGAT TACAGGCATG GGCCACCAAG 2040  
 CCTAGCCTCA CGCTCCTTTC TGATCTTAC TAAGAACAAA AGAAGCAGCA ACTTGCAAGG 2100  
 GCGGCTTTC CCACTGGTCC ATCTGGTTT CTCTCCAGGG GTCTTGCAAA ATTCTGAGC 2160  
 AGATAAGCAG TTATGTGACC TCAAGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220  
 CCAGCCCGA AGTGACAGAC TGCAGTCACT GCAAGTTTTC ATCTTAGGG ACCAGAACCA 2280  
 70 AACCCACCT TTCTACTTCC AAGACTTATT TTCATGATG GGGAGGTTAA TCTAGGAATG 2340  
 ACTCGTTTAA GGCCTATTT CATGATTTCT TTGTAGCATT TGGTGCTTGA CGTATTATTC 2400  
 TCCTTTGATT CCAATAATA TGTTCCTTTC CCTCAAAAAA AAAAAAATAA AAAAAAATAA 2460  
 AAAAA 2465

75 Seq ID NO: C17 DNA Sequence  
 Nucleic Acid Accession #: NM\_003220  
 Coding sequence: 63..1376

80 1 11 21 31 41 51  
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 GAATTCCGGC TCTCTGGGTG AGAGACCGAG AGGGGCATAT CGGTTACGCG CGATCCATGA 60  
 AAATGCTTTG GAAATTGACG GATAATATCA AGTACAGGGA CTGCGAGGAC CGTCAAGACG 120  
 GCACAGCAA CGGAGCGGCA CGGTTGCCCC AGCTGGGCAC TGTAGGTCAA TCTCCCTACA 180  
 CGAGCGCCCC GCGCTGTGCC CACACCCCCA ATGCGGACTT CCAGCCCCCA TACTTCCCCC 240  
 CACCTTACCA GCCTATCTAC CCCAGTGGC AAGATCCTTA CTCCACGTC AACGACCCCT 300

5 ACAGCCTGAA CCCCCGAC GCCCAGCCGC AGCCGAGCA CCCAGGCTGG CCGGCCAGA 360  
 GGCAGAGCCA GGAGTCTGGG CTCCTGCACA CGCACCGGG GCTGCCTCAC CAGCTGTGG 420  
 GCCTGGATCC TCGCAGGGAC TACAGCGGC ACAGGAGCT CCGCAGCGC CCACAGCGC 480  
 TCAGCTCAG ACTCGGAGAC CTCTCGATCC ACTCCTTACC TCAOGCCATC GAGGAGGTCC 540  
 CGCATGTAGA AGACCGGGT ATTAACATCC CAGATCAAAC TGTAAATTAAG AAAGGCCCG 600  
 TGTCCCTGTC CAAGTCCAAAC AGCAATGCCG TCTCCGCCAT CCTATTAAAC AAGGACAAAC 660  
 TCTTCGGCGG CGTGGTGAAC CCAACGAAG TCTCTGTTC AGTTCGGGT CGCTCTGCG 720  
 TCCTCAGCTC CACCTCGAAG TACAAGSTCA CGGTGGCGGA AGTGCAGCGG CGGCTCTCAC 780  
 10 CACCCGAGTG TCTCAACGCG TCGCTGCTGG GCGGAGTGCT CCGGAGGGCG AAGTCTAAAA 840  
 ATGGAGGAAG ATCTTTAAGA GAAAAACTGG ACAAATAGG ATTAATCTG CCGTGCAGGA 900  
 GAGGTAAAGC TGCCAAAGTT ACCCTGCTCA CATCACTAGT AGAGGGAGAA GCTGTCCACC 960  
 TAGCCAGGGA CTTTGGGTAC GTGTGCGAAA CCGAATTTC TGCCAAAGCA GTAGCTGAAT 1020  
 TTCTCAACCG ACAACATTCC GATCCCAATG AGCAAGTGAC AAGAAAAAAC ATGCTCCTGG 1080  
 CTACAAACCA GATATGCAAA GAGTTCACCG ACCTGCTGGC TCAGGACCGA TCTCCCTGG 1140  
 15 GGAATCTACG GCGCAACCCC ATCTGGAGC CGGCATCCA GAGCTGCTTG ACCCACTTCA 1200  
 ACCTCATCTC CCAAGGCTTC GGCAGCCCG CGGTGTGTGC CGGCTCAAG GCGCTGCAGA 1260  
 ACTATCTCAC CGAGGCCCTC AAGGCCATGG ACAAATGTA CCTCAGCAAC AACCCCAACA 1320  
 CCACACGCGC AAGCAAGGCC AAAAGCAGTG ACAAAGAGGA GAAGCACAGA AAGTGAGGCT 1380  
 CTCCTCCCGC CCGCCCTCTC CCAAGCCTCA CCAAGCCCGC GCGCGCCAC CCTCCGGCGG 1440  
 20 GTGACAGCTC CGGAGCTCAG AACCTTCTCT GCTGCTGCTA CTGCTGCTGC TGCTGCGGCC 1500  
 GCGCGCGCGC CCGTGCCTCT TGGGTCCCGC CAGTCTCCCG GAGTCTCCCT CTCAGCTGTC 1560  
 AGTGGGCGAG CCTCTCCGAC TCTGCACCGC CCTCGACCTC CCCACCGCT CCCACACCCC 1620  
 TGTGCCCCCG GAATTC 1636

25 Seq ID NO: C18 DNA Sequence  
 Nucleic Acid Accession #: NM\_002988  
 Coding sequence: 71..340

30 1 11 21 31 41 51  
 | | | | |  
 CCGGCACGAG AGGAGTTGTG AGTTTCCAAG CCCAGCTCA CTCTGACCAC TTCTCTGCGT 60  
 GCGCAGCATC ATGAAGGGCC TTGCAGCTGC CCTCCTTGTC CTGCTCTGCA CCATGGCCCT 120  
 CTGCTCCTGT GCACAAGTTG GTACCAACAA AGAGCTCTGC TGCTCTGCT ATACCTCTCTG 180  
 GCAGATCCCA CAAAAGTTCA TAGTTGACTA TTCTGAAACC AGCCCCAGT GCCCAAGCC 240  
 35 AGGTGTATC CTCTAACCA AGAGAGCGCG GCAGATCTGT GCTGACCCCA ATAAGAAGTG 300  
 GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCTGA GGGGCTGGA AGCTGCGAGG 360  
 GCGCAGTGA CTGTGTGGGC CAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420  
 CCACCCCTGA GGCACCTCT TCTAAGAGTC CCACTGCTA TGCCAGGCA CATTAACATA 480  
 40 CTTTAATCTT AGTTTATGCA TCAATTTCA TTTTGAATT GATTTCTATT GTTGAGCTGC 540  
 ATTATGAAT TAGTATTTTC TCTGACATCT CATGACATG TCTTTATCAT CCTTCCCTCT 600  
 TTCCCTTCAA CTCTTCGTC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTCTCTCA 660  
 CAGACATTTG GCCATATGTA TCAATGACA AATCTTTATT GAATGTTTTT GCTCAGCACC 720  
 45 ACCTTTTAAT ATATTGGCAG TACTTATTAT ATAAAGGTA AACAGCATT CTCATCTGTA 780  
 AAAAAAAAAA AAAAAAAAAA AAA 803

Seq ID NO: C19 DNA Sequence  
 Nucleic Acid Accession #: NM\_004063  
 Coding sequence: 121..2619

50 1 11 21 31 41 51  
 | | | | |  
 AGGGAGTGT CCGGGGGGAG ATACTCCAGT CGTAGCAAGA GTCTCGACCA CTGAATGGAA 60  
 GAAAAGGACT TTAAACACCC ATTTTGTGAC TTACAGAAAG GAATTTGAAT AAAGAAAACT 120  
 55 ATGATACTTC AGGCCCATCT TCACTCCCTG TGCTCTCTTA TGCTTTATTT GGCAACTGGA 180  
 TATGCGCAAG AGGGGAAGTT TAGTGGACCC CTGAAACCCA TGACATTTTC TATTATGAA 240  
 GGCCAGAAC CGAGTCAAT TATATTCCAG TTAAAGGCCA ATCTCTCTGC TGTGACTTTT 300  
 GAACTAATCT GGGAGACAGA CAACATATTT GTGATAGAAC GGGAGGGACT TCTGTATTAC 360  
 AACAGAGCCT TGGACAGGGA AACAGATCT ACTCACATC TCCAGGTTGC AGCCCTGGAC 420  
 60 GCTAATGGAA TTATAGTGA GGGTCCAGTC CCTATCACCA TAGAAGTGAA GGACATCAAC 480  
 GACAATGAC CCAAGTTTCT CCACTCAAAG TACGAAGGCT CAGTAAGGCA GAACTCTCGC 540  
 CCAGGAAAGC CCTTCTTGTA TGTCAATGCC ACAGAAGTGG ATGATCCGGC CACTCCCAAT 600  
 GGCAGCTTTT ATTACAGAT TGTCTCCAG CTCTCCATGA TCAACATGT CATGTACTTT 660  
 CAGATCAACA ACAAACCGGG AGCCATCTCT CTTACCCGAG AGGGATCTCA GGAATTGAAT 720  
 65 CCTGCTAAGA ATCTTCTTA TAATCTGGTG ATCTCAGTGA AGGACATGGG AGGCCAGAGT 780  
 GAGAATTCCT TCACTGATAC CACATCTGTG GATATCATAG TGACAGAGAA TATTTGAAA 840  
 GCACCAAAAC CTGTGGAGAT GGTGGAAAAC TCAACTGATC CTCACCCAT CAAATCACT 900  
 CAGGTGGGT GGAATGATCC CGGTGCACAA TATTCCTTAG TTGACAAAG GAAGCTGCCA 960  
 AGATTCCCAT TTCAATTGA CCAGGAAGGA GATATTTACG TGACTCAGCC CTTGAGCGA 1020  
 70 GAAGAAAAGG ATGCATATGT TTTTATGCA GTTGCAAGG ATGAGTACGG AAAACCACTT 1080  
 TCATATCCCG TGGAAATTTA TGTAAAAGTT AAAGATATTA ATGATAATCC ACCTACATGT 1140  
 CCGTACCAG TAACGTATT TGAGGTCCAG GAGAATGAAC GACTGGGTAA CAGTACGGG 1200  
 ACCCTTACTG CACATGACAG GGATGAAGAA AATACTGCCA ACAGTTTCT AACTACAGG 1260  
 ATTGTGGAGC AAATCCCAA ACTTCCCATG GATGGACTCT TCTAATCCA AACCTATGCT 1320  
 75 GGAATGTTAC AGTATGCTTA ACAGTCTCTG AAGAAGCAAG ATACTCTCA GTACAACTTA 1380  
 ACGATAGAGG TGTCTGACAA AGATTTCAG ACCCTTTGTT TTGTGCAAT CAACGTATT 1440  
 GATATCAATG ATCAGATCCC CATCTTGAA AAATCAGATT ATGGAAACCT GACTCTTGCT 1500  
 GAAGACACAA ACATTGGGTC CACCATCTTA ACCATCCAGG CCAGTATGTC TGATGAGCCA 1560  
 80 TTTACTGGGA GTTCTAAAT TCTGTATCAT ATCAATAAGG GAGACAGTGA GGGAGCCTG 1620  
 GGGTGTGACA CAGATCCCA TACCAACACC GGATATGTCA TAATTAATAA GCTCTTGAT 1680  
 TTTGAAACAG CAGCTGTTTC CAACATTGTG TTCAAGCAG AAAATCCTGA GCCTCTAGTG 1740  
 TTTGGTGTGA AGTACAATGC AAGTCTTTT GCCAAGTTCA CGCTTATTGT GACAGATGTG 1800  
 AATGAAGCAC CTCATATTTT CCAACACGTA TTCCAAGCGA AAGTCAGTGA GGATGTAGCT 1860  
 ATAGGCACTA AAGTGGGCAA TGTGACTGCC AAGGATCCAG AAGGTCTGGA CATAAGCTAT 1920  
 TCACTGAGG GAGACACAAG AGGTGGCTT AAAATTGACC AGTGAAGTGA TGAGATCTTT 1980

5 AGTGTGGCTC CATTGGACAG AGAAGCCGGA AGTCCATATC GGGTACAAGT GGTGGCCACA 2040  
 GAAGTAGGGG GGTCTTCCTT GAGCTCTGTG TCAGAGTTCC ACCTGATCCT TATGGATGTG 2100  
 AATGACAACC CTCGCCAGCT AGCCAAGGAC TACACGGGCT TGTCTCTCTG CCATCCCCTC 2160  
 AGTGCACCTG GAAGTCTCAT TTTGAGGCT ACTGATGATG ATCAGCACTT ATTTCCGGGT 2220  
 CCCCATTTTA CATTTTCCCT CGGCAGTGGG AGCTTACAAA ACGACTGGGA AGTTTCCAAA 2280  
 ATCAATGGTA CTCATGCCCG ACTGCTTACC AGGCACACAG AGTTTGAGGA GAGGGAGTAT 2340  
 GTCGTCTTGA TCCGCATCAA TGATGGGGGT CGGCCACCCCT TGGAAAGGCAT TGTTCCTTTA 2400  
 CCAGTTACAT TCTGCAGTTG TGTGGAAGGA AGTTGTTTCC GGCCAGCAGG TCACCAGACT 2460  
 10 GGGATACCCA CTGTGGGCAT GGCAGTTGGT ATACTGCTGA CCACCTTCTT GGTGATTGGT 2520  
 ATAATTTTGA CAGTTGTGTT TATCCGCATA AAGAAGGATA AAGGCCAAGA TAATGTTGAA 2580  
 AGTGCTCAAG CATCTGAAGT CAAACCTCTG AGAAGCTGAA TTTGAAAAGG AATGTTTGAA 2640  
 TTTATATAGC AAGTGTCTAT TCAGCAACAA CCATCTCATC CTATTACTTT TCATCTAAGC 2700  
 TGCATTATAA TTTTTTAAAC AGATATTOCC TCTGTCTCTT TAATATTGTC TAAATATTTT 2760  
 TTTTGTGAGG TGGAGTCTTG CTCTGTGCGC CAGGCTGGAG TACAGTGGTG TGATCCCAGC 2820  
 15 TCACGTCAAC TCCGCCCTCC TGGGTTTACA TGATTCCTCT GCCTCAGCTT CCTAAGTAGC 2880  
 TGGGTTTACA GGCACCCACC ACCATGCCCA GCTAATTTT GTATTTTAA TAGAGACGGG 2940  
 GTTTCGCCAT TTGGCCAGCG TGGTCTTGAA CTCTGACGT CAACTGATCT GCCTGCCTTG 3000  
 GTCTCCCAAT ACAGGCATGA ACCACTGCAC CCACCTACTT AGATATTTCA TGTGCTATAG 3060  
 20 ACATTAGAGA GATTTTTCAT TTTTCCATGA CATTTTCTCT CTCTGCAAT GGCTTAGCTA 3120  
 CTGTGTGTTT TCCTTTTGGG GGCAAGACAG ACTCATTAAA TATTCTGTAC ATTTTCTTCT 3180  
 TATCAAGGAG ATATATCAGT GTTGTCTCAT AGAAGTGCCT GGATTCATT TATGTTTTTT 3240  
 CTGATTCATC CTTGTGTGCC CTTCTCTCTT GACTCTTTG GTATTTCACT GAATTTCAAA 3300  
 CATTGTGTCG AGAAGAAAAA CGTGAGGACT CAGGAAAAAT AAATAAATAA AAGAACAGCC 3360  
 25 TTTTCCCTTA GTATTAAACAG AAATGTTTCT GTGTCAATTA CCATCTTTAA TCAATGTGAC 3420  
 ATGTTGCTCT TTGGCTGAAA TTCTTCAACT TGGAAATGAC ACAGACCCAC AGAAGGTGTT 3480  
 CAAACACAAC CTACTCTGCA AACCTTGGTA AAGGAACCAG TCAGCTGGCC AGATTTCCTC 3540  
 ACTACCTGCC ATGCATACAT GCTGCGCATG TTTTCTTCAT TCGTATGTTA GTAAAGTTTT 3600  
 30 GGTATTATTA TATTTAATAT GTGGAAGAAA ACAAGACATG AAAAGAGTGG TGACAAATCA 3660  
 AGAATAAACA CTGGTTGTAG TCAGTTTGTG TTGTTAA 3697

Seq ID NO: C20 DNA Sequence

Nucleic Acid Accession #: NM\_004443

Coding sequence: 28..3024

35 1 11 21 31 41 51  
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 GGCTGGGCTC CTAGAGCTGC CACGGCCATG GCCAGAGGCC GCCCGCGCGC GCGCGCGTGC 60  
 CCGCGCGCGG GGTCTCTGCC GCTGCTCCCT CCGCTGCTGC TGCTGCGCGT GCTGCTGCTG 120  
 40 CCGCGCGGCT GCGCGCGGCT GGAAGAGACC CTCATGGACA CAAATGGGT AACATCTGAG 180  
 TTGGCGTGGG CATCTCATCC AGAAAGTGGG TGGGAAGAGG TGAGTGGCTA CGATGAGGCC 240  
 ATGAATCCCA TCAGCACATA CCAGGTGTGT AATGTGCGCG AGTCAAGCCA GAACAACCTG 300  
 CTTCGCACGG GGTTCATCTG GCGCGGGGAT GTGCAGCGGG TCTACGTGGA GCTCAAGTTC 360  
 45 ACTGTGCGTG ACTGCAACAG CATCCCAAC ATCCCGGCT CCTGCAAGGA GACCTTCAAC 420  
 CTCTTCTACT ACGAGCTGA CAGCGATGTG GCCTCAGCCT CCTCCCGCTT CTGGATGGAG 480  
 AACCCTTACG TGAAGTGGG ACCATTGCA CCGATGAGA GCTTCTCGCG CTGGATGCC 540  
 GGCCGTGTCA ACACCAAGGT GCGCAGCTTT GGGCCACTTT CCAAGGCTGG CTTCTACCTG 600  
 GCCTTCCAGG ACCAGGGGCG CTGCATGTGC CTCATCTCG TGCGCGCTT CTACAAGAG 660  
 50 TGTGATCCA CACCGCAGG CTTGCACTC TTCCCGAGA CCTCACTGG GCGGAGGCC 720  
 ACCTGCTGG TCAATTGCTCC TGGCACCTGC ATCCCTAAG CCGTGGAGT GTGCGTGCCA 780  
 CTCAGCTCT ACTGCAACGG CGATGGGGAG TGGATGGTGC CTGTGGTGC CTGCACTGT 840  
 GCCACCGGCC ATGAGCCAGC TGCCAAAGAG TCCCACTGCC GCCCTGTCC CCCTGGGAGC 900  
 TACAAGGCGA ACCAGGGAGA GGGGCCCTGC CTCCTATGTC CCCCACACAG CCGTACCACC 960  
 55 TCCCGAGCG CACGATCTG CACTGCCAC AATAACTTCT ACGTGCAGA CTCGACTCT 1020  
 GCGSACAGT CCGTATACCAC CGTGCCATCT CCACCCGAG GTGTGATCTC CAATGTGAAT 1080  
 GAAACCTCAC TGAATCTCGA GTGGAGTGA ACCCGGAGC TGGGTGGCG GGATGACCTC 1140  
 CTGTACAATG TCACTGCAAA GAAGTGCCAT GGGCTGGAG GGGCTCAGC CTGCTCAOGC 1200  
 60 TGTGATGACA AGTGGAGTGT TGTGCTCGG CAGCTGGGCC TGACGAGCG CCGGCTCCAC 1260  
 ATCAGCCATC TGTGTGCCCA CACGCGCTAC ACCTTTGAGG TGCAGGCGGT CAAOGTGTG 1320  
 TCGGGCAAGA GCCCTCTGCC GCCTCGTTAT GCGGCGGTGA ATATCACCC AAACACAGCT 1380  
 GCCCGTCTG AAGTGCCAC ACTACGCTG CACAGCAGCT CAGGCGAGC CCTCACCTTA 1440  
 TCCCTGGGAC CCGCAGAGCG GCCCAACGGA GTCATCTGG ACTACGAGT GAACTACTTT 1500  
 GAGAAGAGCG AGGCGATGCG CTCACAGTG ACCAGCCAGA TGAACCTCGT GCAGCTGGAC 1560  
 65 GGGCTTCGCG CTGACGCGCG CTATGTGGTC CAGGTCCGTG CCCGCACAGT AGCTGGCTAT 1620  
 GGGCAGTACA GCGCGCTGCG CGAGTTTGAAG ACCACAAGTG AGAGAGGCTC TGGGGCCAG 1680  
 CAGCTCCAGG AGCAGCTTCC CCTCATCTG GGTCTCGCTA CAGCTGGGCT TGTCTTGTG 1740  
 GTGGCTGTG TGTGATGCG TATGCTCTGC CTCAGGAAG AGCGACAGG CTCTGATTG 1800  
 GAGTACAGG AGAAGCTGCA GCAGTACATT GCTCCTGAA TGAAGTTTA TATTGACCTT 1860  
 70 TTTACTACG AGGACCTTAA TGAGGCTGTT CGGGAGTTG CCAAGGAGAT CGAGTGTCC 1920  
 TGGTCAAGA TCGAGGAGT GATCGGAGCT GGGGAATTT GGGGAAGTGT CCGTGGTGA 1980  
 CTGAACACAG CTGGCGCGCG AGAGGTGTTT GTGGCCATCA AGACGCTGAA GGTGGGCTAC 2040  
 ACCGAGAGGC AGCGCGGGA CTCTCTAAGC GAGGCTTCCA TCATGGGTCA GTTTGATCAC 2100  
 CCCAATATAA TCCGGCTGGA GGGCGTGGTC ACCAAAAGTC GGCAGTTAT GATCCTCACT 2160  
 75 GAGTTTCAAG AAAACTGCGC CTGGAAGTCC TTCTCTCGGC TCAACGATG GCAGTTCAAG 2220  
 GTCATCCAGC TGTGTGGCAT GTTGGGGGCG ATTGCTCGCG GCATGAAGTA CCTGTCCAG 2280  
 ATGAACATAG TGCAACGCGA CCTGGCTGCT CGCAACATCC TTGTCAACAG CAACCTGGTC 2340  
 TGCAAGTCT CAGACTTTGG CCTCTCCGCG TTCTGAGG AGACCCCTC CGATCCTACC 2400  
 80 TACACCACT CCCTGGGCGG GAAGATCCCC ATCCGCTGGA CTGCCCCAGA GGCCATAGCC 2460  
 TATGGAAGT TCACTTCTGC TAGTGATGTC TGGAGCTAG GAATTGTCT GTGGGAGGTC 2520  
 ATGAGCTATG GAGAGGAGCC CTACTGGGAC ATGAGCAACC AGGATGTCT CAATGCGGTG 2580  
 GAGCAGGATT ACCGGCTGCC ACCACCATG GACTGTCCCA CAGCACTGCA CCAGCTCATG 2640  
 CTGAGCTGCT GGTGCGGGA CCGGAACCTC AGGCCCAAT TCTCCAGAT TGTCAATACC 2700  
 CTGGACAGC TCATCCGCAA TGCTGCCAGC CTCAGGTCA TTGCCAGCG TCAGTCTGGC 2760  
 ATGTACAGC CCCTCTGGA CCGCAOAGTC CCAGATTACA CAACCTTCAC GACAGTTGGT 2820

5 GATTGGCTGG ATGCCATCAA GATGGGGCGG TACAAGGAGA GCTTCGTACG TGGGGGTTT 2880  
 GCATCTTTTG ACCTGGTGGC CCAGATGACG GCAGAAGACC TGCTCCGTAT TGGGGTCAAC 2940  
 CTGGCCGGCC ACCAGAAGAA GATCCTGAGC AGTATCCAGG ACATGCGGCT GCAGATGAAC 3000  
 CAGACGCTGC CTGTGCAGGT CTGACACCGG CTCCACGGG GACCTGAGG ACCGTGCAGG 3060  
 GATGCCAAGC AGCGGGCTGG ACTTTGGGAC TCTTGGACTT TTGGATGCTT GGCCTTAGGC 3120  
 TGTGGCCCAAG AAGCTGGAAG TTTGGGAAAG GCCAAGCTG GGACTTCTCC AGGCCTGTGT 3180  
 TCCCTCCCCA GGAAGTGGCG CCCAAACCTC TTCAATTGA AGATGGATTA GGAGAGGGGG 3240  
 TGATGACCCC TCCCCAAGCC CCTCAGGGCC CAGACCTTCC TGCTCTCCAG CAGGGGATCC 3300  
 CCACAACCTC ACACCTGTCT GTTCTTCAGT GCTGGAGGTC CTGGCAGGGT CAGGCTGGGG 3360  
 10 TAAGCCGGGG TTCCACAGGG CCCAGCCCTG GCAGGGGTCT GGCCCCCCAG GTAGGCGGAG 3420  
 AGCAGTCCCT CCCTCAGGAA CTGAGGAGG GGACTCCAGG AATGGGAAA TGTGACACCA 3480  
 CCATCCTGAA GCCAGCTTGC ACCTCCAGTT TGCACAGGGA TTTGTCTGG GGGCTGAGGG 3540  
 CCCTGTCCCC ACCCCCGCCC TTGGTGTCTG CATAAAAGGG CAGGCGAGGG CAGGCTGAGG 3600  
 15 AGTTGOCCTT TGCCCCCAG AGACTGACTC TCAGAGCCAG AGATGGGATG TGTGAGTGTG 3660  
 TGTGTGTGTG TGTGGCGCG CGCGCGGTG TGTGTGTGCA CGCACTGGCC TGCACAGAGA 3720  
 GCATGGGTGA GCGTGTAAAA GCTTGGCCCT GTGCCCTACA ATGGGGCCAG CTGGGCGGAC 3780  
 AGCAGAATAA AGGCAATAAG ATGAA 3805

20 Seq ID NO: C21 DNA Sequence  
 Nucleic Acid Accession #: NM\_001804  
 Coding sequence: 82..879

25 1 11 21 31 41 51  
 AGGTGAGCGG TTGCTCGTGG TCGGGGCGGC CGGCAGCGGC GGCTCCAGGG CCCAGCATGC 60  
 CGGGGGGACC CGCGGGCCAC CATGTATGTG GGTATGTGTC TGGACAAGGA TTCCGCCGTG 120  
 TACCCCGGCC CAGCCAGGCC AGCCAGCCTC GGCTTGGGCC CGGCAAACTA CGGCCCCCGG 180  
 30 GCCCCGCCCC CGGCGCCCCC GCAGTACCCC GACTTCTCCA GCTACTCTCA CGTGGAGCCG 240  
 GCCCCGCGCG CCCCAGCGCG CTGGGGGGCG CCTTCCCTG CGCCCAAGGA CGACTGGGCC 300  
 GCGCGCTACG GCGCGGGCCC CGCGGCCCTT GCGCCAGGCC CAGCTTCGCT GGCATTGGGG 360  
 CCGCTCCAG ACTTTAGCCC GGTGCCGCGC CCGCTGGGC CGGCCCCGGG CCTCTGGGG 420  
 CAGCCCCCTG GGGGCCCGGG CACACCGTCC TCGCCCGGAG CGCAGAGGCC GACGCCCTAC 480  
 35 GAGTGGATGC GCGCGAGCGT GCGCGCGGGA GCGCGCGGTG GCAGCGGTAA GACTCGGACC 540  
 AAGGACAAGT ACOCGCTGGT CTACACCGAC CACCAACGCC TGGAGCTGGA GAAGGAGTTT 600  
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 40 ACCCCAGCCG GGCCTCCCTT GGGGGGCGCT TGTCCAGCA ACACCAAGCT CCGTGGCCAC 840  
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Seq ID NO: C22 DNA Sequence  
 Nucleic Acid Accession #: NM\_021978  
 Coding sequence: 36..2603

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 65 TGAATGGCTT GGAGGAAGGC GTGGAGTTCC TGCCAGTCAA CAACGTCAAG AAGGTGGAAA 180  
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Seq ID NO: C23 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2268

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Seq ID NO: C24 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2424

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	AGCGTCGGGA	AAGGGAGCTT	TGAAAGGTCC	AAGCACTTTG	CCATCACAGT	CTGTGACGGT	240
	CTGGACATCA	GCCCCGAGAG	GGTCAGAGTG	GGAGCATTCC	AGTTCACTTC	CACTCCTCAT	300
	CTGGAATTCC	CCTTGGATTG	ATTTTCAACC	CAACAGGAAG	TGAAGGCAAG	AATCAAGAGG	360
	ATGGTTTTC	AAGSAGGCG	CACGGAGAG	GAACCTGCTC	TGAAATACCT	TCTGCACAGA	420
	GGGTGCGCTG	GAGGCAGAAA	TGCTTCTGTG	CCCCAGATCC	TCATCATCTG	CACTGATGGG	480
	AAGTCCCAAG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
	TTTGCTGTGG	GGGTGAGGTT	TCCCAGGTGG	GAGGAGCTGC	ATGCACCTGG	CAGCGAGCCT	600
10	AGAGGGCAGC	ACGTGCTGTT	GGCTGAGCAG	GTGGAGGATG	CCACCAACGG	CCTCTTCAGC	660
	ACCTCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
	CCCTGTGAGC	ACAGGACGCT	GGAGATGGTC	CGGAGGTTGG	CTGGCAATGC	CCCATGCTGG	780
	AGAGGATCGC	GCGGACCCCT	TGCGGTGCTG	GCTGCACACT	GTCCCTTCTA	CAGCTGGAAG	840
	AGAGTGTTC	TAACCCACCC	TGCCACCTGC	TACAGGACCA	CCTGCCCAGG	CCCCTGTGAC	900
15	TGCGAGCCCT	GCCAGAATGG	AGGCACATGT	GTTCAGAAAG	GACTGGACGG	CTACCACTGC	960
	CTCTGCCCG	TGGCCTTTGG	AGGGGAGGCT	AACCTGTGCC	TGAAGCTGAG	CCTGGAATGC	1020
	AGGGTCGACC	TCTCTTCTCT	GCTGGACAGC	TCTGCGGGCA	CCACTCTGGA	CGGCTTCTGT	1080
	CGGGCCAAAG	TCTTGTGAA	GCGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
	CGAGTGGGTG	TGGCCACATA	CAGCAGGGAG	CTGCTGTGTG	CGGTGCTCTG	GGGGGAGTAC	1200
20	CAGGATGTGC	CTGACCTGGT	CTGGAGCCTC	GATGGCATTG	CCTTCCGTGG	TGGCCCCACC	1260
	CTGACCGGCA	TGGCCTTGGG	GCAGGCGGCA	GAGCGTGGCT	TGGGAGCGCG	CACCAAGACA	1320
	GGCCAGGACC	GGCCACGTAG	AGTGGTGGTT	TTGCTCACTG	AGTCACACTC	CGAGGATGAG	1380
	GTGCGGGCGC	CAGCGCGTCA	CGCAAGGGCG	CGAGAGCTGC	TCCTGCTGGG	TGTAGGCAGT	1440
	GAGGCGGTGC	GGGCAGAGCT	GGAGGAGATC	ACAGGCAGCC	CAAAGCATGT	GATGGTCTAC	1500
25	TGCGATCCTC	AGGATCTGTT	CAACCAATAT	CCTGAGCTGC	AGGGGAAGCT	GTGCAGCGCG	1560
	CAGCGGCGAG	GGTGCCTGGC	ACAAGCCCTG	GACCTGCTCT	TCATGTTGGA	CACCTCTGCC	1620
	TCAGTAGGGC	CGAGAAATTT	TGCTCAGATG	CAGAGCTTTG	TGAGAAGCTG	TGCCCTCCAG	1680
	TTTAGGTTGA	ACCCTGAGCT	GACACAGGTC	GGCCTGGTGG	TGTATGGCAG	CCAGGTGCAG	1740
	ACTGCTCTCG	GGCTGGACAC	CAAAACCCAC	CGGGCTGCGA	TGCTGCGGGC	CATTAGCCAG	1800
30	GGCCCTTACC	TAGGTGGGGT	GGGCTCAGCC	GGCACCGCCC	TGCTGCACAT	CTATGACAAA	1860
	GTGATGACCG	TCCAGAGGGG	TGCCCGGCTT	GGTGTCCCCA	AAGCTGTGGT	GGTGTCTACA	1920
	GGCGGGAGAG	GGCAGAGGGA	TGCAGCGGTT	CCTGCCCAGA	AGCTGAGGAA	CAATGGCATC	1980
	TCGTCTCTGG	TGCTGGGCGT	GGGGCCTGTC	CTAAGTGAGG	GTCTGCGGAG	GCTTGCAGGT	2040
	CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGACGTG	2100
35	CTCATTTAGT	GGCTGTGTGG	AGAAGCCAAG	CAGCCAGCTA	ACCTCTGCAA	ACCCAGCCCG	2160
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	GGCTGGGAGG	GCCCCACATG	CGAGAACCGT	GAGTGGAGCT	CTTGCTCTGT	ATGTGTGAGC	2280
	CAGGGATGGA	TTCTTGAGAC	GCCCCGTAGG	CACATGGCTC	CGGTGCAGGA	GGGCGAGCAG	2340
	CGTACCCCTC	CCAGCAACTA	CAGAGAAGGC	CTGGGCACTG	AAATGGTGCC	TACCTTCTGG	2400
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Seq ID NO: C25 DNA Sequence  
Nucleic Acid Accession #: XM\_097386.3  
Coding sequence: 142..795

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	CTACCTCAGG	TCTGACTTTT	GATGCCAAAA	TCTGAGCCCC	TGGGGTGCCT	CTCCCCCGCC	180
50	TCCCGTGCAC	CAGGGTCTGC	AGCAGCCACT	GGGGCCTGGC	TGCCGTCTGC	ATCTGGCGGC	240
	CCTGGACCCC	TGGGGCCCCC	GTGCACCTGC	CCACCTCGGA	GCCTGGGGAG	GGGCGGTGCA	300
	GGGTGAGGGG	CTGGGTCTGC	TCCCTCGGGC	TGCGTGTGTG	TGTGCGGAAT	CCTGCGTGTG	360
	GTGTCTGTGG	GCGATCGGGC	CTCCCGGCGG	TGGGTGGACC	TGGATTCTAA	CTCAGAGGAC	420
55	TTGAGCCTGC	TGTTAACTCC	GATGATTGTA	GGGACAGGCG	GGGTGGGTGG	GGGTGGGGCG	480
	CGAGGCTGGG	TCCCGGCCCA	GGAGAAGGAA	GTGCTGAAG	GCAGTGCCCA	TGCTGGCGGT	540
	GGAAATGGGA	GGGGGTGCA	GAGGGTCTAT	GGGGCCCGGT	CCTGGTACT	CGGCGAGGAG	600
	CGGTGTCTGC	AGAGGCTCCT	CCCTGCCTCA	GGTGGCCCCG	TTCAACCCCA	CGCGTGCCCA	660
	TCCTCTGTGA	CGGCTGTGCG	GTGGGGGTTT	AAATTGCGTG	TGGCTTTCTG	GGGTGCAGCT	720
60	CAGCACCCCC	CCTTATGCAG	ACTGGGAGGG	GGTGGGCGAG	TCCCTCAGC	CACGAGGACC	780
	CTGATGGGTT	TCTAGTTTAC	TTGGGACCGT	GGGGCCTGGC	TGCGTACTGA	GTGGGTGCCC	840
	CACAGTCAAG	AGCAACGGGG	GCTCCCCCTG	CTCTGAGATG	TTGGGAGAAA	GGCGGCTTCT	900
	GGAACTTCCC	GTGGGACCGG	TAAGTGGCTG	TCCAGAAAGG	CGGGAGGGTG	GGCAGGGGGC	960
	ACGGGGGGCA	GCTGGGTTGG	TTGTTAAGGG	TCAAGCATCT	GTACAGTTGA	ATTTCTTTTC	1020
65	TCTTATCATG	TTTTACCCAC	CTTGTCCCTT	TTTTCCCCAA	TGTGCTTTT	GCATTTTTTT	1080
	CCTTGGCAAA	TGTAACCTCA	GCCTTTCATT	CATGAAGTGT	GAAATTTTCA	TTTCTCTGGA	1140
	GTTTGTGAGA	CGGCGTGGGA	ACCACGCGTG	AAACTCAGGT	AATAGGAGGA	AAAAAAAAAA	1200
	AACTTAAAAA	AATTTTAAAA	AAACATAAAA	CTACTCTCTA	CCTCTGGCTG	GGCCCAAGCT	1260
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70	GTATTAAAAA	AAAAAA					1337

Seq ID NO: C26 DNA Sequence  
Nucleic Acid Accession #: Bos sequence  
Coding sequence: 95..2128

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	TGCTTCTCGG	GAGCTTGTGG	TCCGCGTTGA	CCATCCCAAT	GAAGAGCAGC	AGAAAGACGT	180
80	CACACTGAGA	GTATCTGGAG	ACCTTTCATG	TGGAGGAGTG	ATGCTCAAGT	TAGTAGAACA	240
	GATCAATATA	TCCCAAGACT	GSTCAGACTT	TGCTTTTGG	TGGGAACAGA	AGCATTGCTG	300
	GCTTCTGAAA	ACCCACTGGA	CCCTGGACAA	ATATGGGGTC	CAGGCAGATG	CAAAGCTTCT	360
	CTTACCCCTT	CAGCATAAAA	TGCTGGCGCT	TGCTCTGCGG	AATTTGAAGA	TGTTGAGGTT	420
	GCGAGTCAGC	TTCTCAGCTG	TGGTTTTTAA	AGCTGTCAAT	GATATCTGCA	AAATGCTGAA	480

5	TATTAGAAGA	TCAGAAGAGC	TTTCCCTTGT	AAAGCCGCTCT	GGTGACTATT	TTAAGAAGAA	540
	GAAGAAAAAA	GACAAAAATA	ATAAGGAACC	CATAATTGAA	GATATTCTAA	ACCTGGAGAG	600
	TTCTCCAACA	GCTTCAGGTT	CATCAGTAAG	TCCTGGTTTA	TACAGTAAAA	CCATGACCCC	660
	TATATATGAC	CCCATCAATG	GAACACCAGC	ATCATCCACC	ATGACTTGGT	TCAGTGACAG	720
	CCCTTTGACG	GAACAAAAC	SCAGCATCCT	CGCATTACAG	CAACCCCCC	AGTCCCCAGA	780
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	CTTAGCATTT	AAATATTATT	CTTTCTTCGA	CTTGAATCCT	AAATATGATG	CTGTCCGAAT	960
10	AAACCAACTC	TATGAGCAAG	CCAGGTGGGC	CAITCTCTTA	GAAGAAATTG	ATTGCACAGA	1020
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	TGAAACACAG	GATTTTGAG	GCGAGTCCGA	GGTTGATGAA	ATAGAAGCGG	CGCTTTCTAA	1140
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	CCCTAAACTT	GCAGATAATC	TCAAAATTAT	TAGGCCCAAG	AAGTTACTAC	CAAAAGCTTT	1260
15	CAAAACATAT	TGGTTTATCT	TTAAAGACAC	ATCCATAGCA	TACTTTAAAA	ATAAGGAACT	1320
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	AAATGTAGCA	GGAAAGAAAT	TTGGAATCAA	GTTACTAAATC	CCTGTTGCCG	ATGGTATGAA	1440
	TGAAATGTAT	TTGAGATGTG	ACCATGAGAA	TCAATACGCC	CAATGGATGG	CTGCGTCGAT	1500
	GTGGCATCG	AAGGGCAAAA	CCATGGCAGA	CAGCTCCTAC	CAGCCAGAGG	TCCTCAACAT	1560
20	CCTTTCATTT	CTGAGGATGA	AAAACAGGAA	CTCTGCATCT	CAGGTGGCTT	CCAGTCTCGA	1620
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	CTTTACTGCT	TTCACTGCC	TGAGTGCAGA	TTGCAAGATT	GTGCAAGAGT	ACATTGGCGG	2040
	CTACATTTTC	TTGTCCACCC	GCTCCAAGGA	CCAGAATGAA	ACACTCGATG	AGGACTTGTT	2100
	CCACAAATGG	ACCGGCGGTC	AGGATTGAAA	CAAGCACGGG	TGCTCGGCTC	ACACCAACAA	2160
30	GGCAAGCCAA	AGGCGCCCTC	CCCCAGAGGG	ATCCCTAACG	TGCCCGCAT	GTAGATTCTG	2220
	GACTAACAGA	CAACATACAT	TCACCGCTGG	TCACCCAGAT	CCTCATTCAA	ACCCACTGCT	2280
	GGCAGATCCC	TTTCTTACT	TTGCCCTGTG	CTACCAGCCA	CGGAAGGAGC	CTCTCTTGTT	2340
	TTTTCTATAA	AATGGGTAGG	CAGGAGAAAA	GCAGGTGCC	TAAGATTGCT	CTAAGGCCCA	2400
	GCATGTGGTT	ACAGTTCTCT	GACTTGCAGA	ACCTGCCAGG	TGTATGGCTA	CAAGTTATCC	2460
35	TGCTGCTGAT	CTGTCTCATT	ACTAAGTCAA	TGGAGAAGAC	AGAAAGGTAA	AAATCAGCTG	2520
	TAGCAAGTAA	AATCTTATTT	TCACAACTC	AGGTATGAAA	CGAAACGCTT	GTCTCTCATG	2580
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	TTCAACATGC	TTCTTAGCT	TTTCATAGTT	GTCTGACATT	TCCATGAAAA	CAAGGGAACC	4140
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65	AATGCTACTG	TTCCAAAGAG	CAACTTGATG	GTTTTTTTTA	ATACTGAGTG	CAAAAGGTCA	4320
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	TATCTACAGT	TGATTTCAGAA	ATCTGCATTT	TTTATTCTTT	TATATGACTT	TTAAGTAAAA	4440
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Seq ID NO: C27 Protein Sequence  
Protein Accession #: NP\_005161.1

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	RPQAVRPSAP	RGPPGTTTVA	ASPSRASSSP	GRGGSSEPGS	PRSAVSDDDS	CEGEGALSPAE	180
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Seq ID NO: C28 DNA Sequence  
Nucleic Acid Accession #: NM\_017763  
Coding sequence: 169..2520

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5	CACCAGCTGC	AGCTGGCTGC	CCTCTGGCCC	TGGCTGCTGA	TGGCTACCC	GCAGGCAGGC	240	
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	AAAGCTGTTA	TCAGAGTGAT	CCCCTTGAAA	ATGGACCCCA	CAGGAAAACT	GAATCTCACT	360	
	TTGGAAGGTG	TGTTTGTCTGG	TGTTGCTGAA	ATAACTCCAG	CAGAAGGAAA	ATTATGCGAG	420	
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	AGCTGCAGCT	CAGCCCTGT	GTGTGCCATC	TGTCTGGAGG	AGTTCTCTGA	GGGGCAGGAG	1020	
	CTACGGGTCA	TTTCTTGCCT	CCATGAGTTC	CATCGTAACT	GTGTGGACCC	CTGGTTACAT	1080	
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	GGCCCTTCGG	GGCGGCTCTC	TAAACCCAG	TGCCCCAGGG	CCCTCCCTGA	GCCAGCCCCC	2040	
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	ACCCCACTTG	TGGCATATCC	TTGGTCCCCA	GAGGCACACC	CCTTGATCTG	TGGACCTCCA	2280	
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Seq ID NO: C29 Protein Sequence  
Protein Accession #: NP\_004280.2

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	PDSDSLGLSD	SSHNNTSVIK	SNSSHSVDE	GAIGYCTDHE	SSSHDLEGA	VGGYYPEPSK	180
75	LCHLDQSDSD	PHGDLTFQHV	FHMHTYHLQP	TAPESTSEPF	PWPGKSQKIR	SRYLEDTDRN	240
	LSRDEQRARA	LHIPPVSDEI	VGMPVDSFNS	MLSRYLLTDL	QVSLIRDIRR	RGNKRVAAQN	300
	CRKKLDIIL	MLEDDVCNLQ	AKKETLKREQ	AQCNKAINIM	KQKLHDLYHD	IFSRLEDDQG	360
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80 Seq ID NO: C30 DNA Sequence  
Nucleic Acid Accession #: NM\_004442  
Coding sequence: 19..2982

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1216

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Seq ID NO: C31 DNA Sequence  
 Nucleic Acid Accession #: NM\_031942.1  
 Coding sequence: 145..1260

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Seq ID NO: C32 DNA Sequence  
 Nucleic Acid Accession #: NM\_012445.1  
 Coding sequence: 276..1271

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Seq ID NO: C33 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1314

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GGCTCAGACA AACTGGGCGC CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCCCTCA TGAAGCTGCA GTTCCCACT 900
ACTTCTCAG GCACAGTCA GGCATCTGT CTGCCCTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGATCAT TGGATGGGG TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GCGTACCAAG GGAAGTGCAC CGAAGAATG ATGTGTGCG GCATCCCGGA AGGGGGTGTG 1140
GACACCTGCG AGGGTATGAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAT AATGTCTGGA AGGCTGAGCT GTAA 1314

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Seq ID NO: C34 DNA Sequence

Nucleic Acid Accession #: NM\_003045.1

Coding sequence: 148..2037

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60  
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70  
75  
80

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1 11 21 31 41 51
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CGTCAATATC CAGCTCTGAA CAGCAACATG GGTGCAAGG TCCTGCTCAA CATTTGGCAG 180
CAGATGCTGC GCGGGAAGGT GGTGACTGT AGCGGGAGG AGACGCGGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCTCGGG GTGGGACGCA CACTGGGTGC TGGTGTCTAC 300
TCTCTGGCTG GAGCTGTGGC CGTGAGAAAT GCAGGCCCTG CCATTGTCTAT CTCTTCTCTG 360
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CCCAAGACGG GCTCAGCTTA CCTCTACAG TATGTACCG TTGAGAGCT CTGGGCCCTC 480
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ATGCCCTACT TCTGCTGGA CAATAACAGC CCGCTGCCCG AGCCTTTAA GCAGCTGGG 1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC CGCCAGTCTT 1200
CTAGGTTCCA TGTTTCCCAT GCCTGGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260
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TCGGGTGCGG TTGCTGCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380
ATGTCCATGT GCACTCTCTT GGCCTTACTG TTGGTGGCTG CTTGTGTGTT GGTCTTACGG 1440
TACCAGCCAG AGCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
CCAGCAGACC AAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACAGAG 1560
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5 TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC 1680  
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 TTCTGTAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCOG GTTGTCTGTG 1920  
 TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG 1980  
 TCCCTGGATG CGGACCAAGC AAGGACTCCT GACGGCAACT TGGACCACTG CAAGTGACGC 2040  
 ACAGCCCGC CCCCAGGAG TGGCAGCAGC CCGAGGGAC GCCCCAGAG GACCGGAGG 2100  
 10 CACCCACCC TOCCACCAG TGCAACAGAA ACCACCTGGG TCCACACCT CACTGCA 2157

Seq ID NO: C35 DNA Sequence  
 Nucleic Acid Accession #: NM\_002776.1  
 Coding sequence: 82..912

15 1 11 21 31 41 51  
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 GGCGACTCCC AGATCCTGGC CATGAGAGCT CCGCACTCC ACCTCTCCGC CGCCTCTGGC 120  
 20 GCGCGGGCTC TGGCGAAGCT GCTGCCGCTG CTGATGGCGC AACTCTGGGC CGCAGAGGCG 180  
 GCGCTGCTCC CCGAAAACGA CACGCGCTTG GACCCGAAAG CCTATGGCGC CCGGTGCGCG 240  
 CGCGCTCGC AGCCCTGGCA GGTCTGCTC TTCAACGGCC TCTGTTCCA CTGCGCGGGT 300  
 GTCCCTGGTG ACCAGAGTTG GGTGCTGACG GCGCGCACT GCGGAACAA GCCACTGTGG 360  
 GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAGGGCG AGCAGCTCG CGGACGACT 420  
 25 CGCTCTGTG TCCATCCCAA GTACCAACAG GGTCTAGGCC CCATCTCGCC AAGCGAAAG 480  
 GATGAGCAG ATCTCATGTT GCTAAAGCTG GCCAGGCCG TAGTCCGGG GCCCGCGTC 540  
 CGGGCCCTGC AGCTTCCCTA CCGCTGTGCT CAGCCGGAG ACCAGTGCCA GGTGTCTGGC 600  
 TGGGCGACCA CGGCGCCCG GAGAGTGAAG TACAACAAG GCCTGACCTG CTCACGATC 660  
 ACTATCCTGA GCCCTAAGA GTGTGAGGTC TTCTACCTG CGGTGGTTC CAACAACATG 720  
 30 ATATGTGCTG GACTGGACCG GGGCCAGGAC CCTTGCCAGA GTGACTCTGG AGGCCCCCTG 780  
 GTCTGTGACG AGACCTCCA AGGCATCCTC TCGTGGGTG TTTACCCCTG TGGCTCTGCC 840  
 CAGCATCCAG CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA 900  
 CGCTCCAACT GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT CCTGTGATC 960  
 CAGATGCCCA GAGGCTCCAT CGTCCATCCT CTCTCCCTCC AGTCCGCTGA ACTCTCCCT 1020  
 35 TGTCTGCACT GTTCAAACT CTGCGCCCT CCACACTCT AAACATCTCC CCTCTACCT 1080  
 CATTCCCCCA CTTATCCCCA TTCTCTGCT GTACTGAAG TGAATGCAG GAAGTGGTG 1140  
 CAAAGGTTTA TTCCAGAGAA GCCAGGAAG CGGTCTACAC CCAGCCCTCT AGAGCAGTTA 1200  
 CTGGGGTCTC CCAACTGAC TTCTCTGCC ACTCCCGCT GTGTGACTTT GGGCAAGCCA 1260  
 AGTGCCCTCT GTGAACCTCA GTTCTCTCAT CTGCAAAATG GGAACAATGA CGTGCCCTACC 1320  
 40 TCTTAGACAT GTGTGAGGA GACTATGATA TAACATGTGT ATGTAAATCT TCATGTGATT 1380  
 GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTCTGACT AAAGGTACC TGTGTGCTG 1440  
 AAAAAAAAAA AAAA 1454

Seq ID NO: C36 DNA Sequence  
 Nucleic Acid Accession #: XM\_095088  
 Coding sequence: 1..4074

45 1 11 21 31 41 51  
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 50 ACGCGGGGCC TGCGCGGCGC CTTCCTGCAG AGCCTGCGCA CCCTGTAGGA CATCTGGAC 120  
 GACTGCGCAG CGCGCTGCGT GCACCTGCGA GAGATCCAGT CCCTCTGGGT CGAAGCGCGG 180  
 GAGCTGCCAA GCGGGTGTCT GGAGGGCCTG AGCCAGCGGC GCGGGCCGCA GCGCGAGCA 240  
 GCTGTACGCT CCGCGCGAGG CGGCGCAGTG CCGCGCGGG CCGAGCGGT TCCAGAGCGC 300  
 55 TGCGCTGGA CCGAGACCGG GCGCGACGC AGGTGCGCG GCCTGCGCG CCTTGGAGGC 360  
 GGATTCAAGG GATGCCCGGC GGAACCTGT GCGCGAGGG AACACCGGAG GCACACCATC 420  
 ACCAGCGCG TGAGCTGCGG CCTGCTGAAG CAGATGAAG AGCTGGAGCA GGAGAGGAG 480  
 GTGCTGTAC AGGTTTGA GATGATGGCG CAGGGCCGCG ATTGTACCA GCAGCAGCTG 540  
 CAAACAAGT AGAGCGCCA GTGCGCCTG GGCAGAGCA GAGCCAGCG CCACTTGGG 600  
 60 GCGTGGGGA GCCCTGCGC ACTGGGACG CTACTGCCCA AGGTACAGGA GGTGGCCCG 660  
 TGGCTGGGG AGCTGTGCG TGAGGCTGT GCGCGTGGG CCCTGCCAC ATCTCTCTCC 720  
 GGGCCCCCTT GCTCTGCCCT GAOGTCCACC TCGTCCCGG GCTGGCAGCA GCAGATCATC 780  
 CTCATGCTGA AGGAGCAGAA CCGACTCTC ACCCAGGAG TGACCGAGAA GAGTGAGCGC 840  
 ATCAOGCAGC TGGAGCAGAA GTGCGCGCTC ATTAAGCAGC TATTGAGGC CCGCGCCCTG 900  
 65 AGCCAGCAG ATGGGGGCT GTCCCGGCT GCGCCCACTA TTGAGCCCTT GACTCGGTTT 960  
 CGGCTTCGCG TGCTGACATG GGTGGGGCT CTCTTGAGTC CGCATAGTCC GCAGCTACTA 1020  
 CTGCGCTGT CAGCGACAG TGGGGGACCC CTCACGAGT TACCAGATAC CTGTTTCCA 1080  
 GCGGTGCTGC TTTGGGTCCC ATCTCCAGGG AAAAGAACTG CTCAGCCAG GCTGCACCTC 1140  
 70 CACCAAGGC CAGCAGAGGG CGCGTGCGAG CTGGATGCG GCGCTGAGGC TGGCGCCGAG 1200  
 ACCTGCGGGA CGCTGCCCA CTTTGAGTCC CACAAAACAA CCTGTGAGCC TGACTCCCTC 1260  
 GGAGGGCCCT GTCCCCAGGA GGGGATCGC AGCTGGAGCC ACCTGGGCGC AGCGTTTGTAT 1320  
 GTGGCACTG CAGTGCCCAA AGTGACACC AACCGTGAG AGCTGCGAG GAGTGGCAC 1380  
 GGAGACATCT GTCCCTCTG TCCCAAGGGA CTGTTGACAT TCAGAGACAT AGCTATAGAA 1440  
 75 TTCTCTCTGG CGAGTGGA ATGCTGGAT CATGCTCAGC AGAATTTATA TAGAGATGTG 1500  
 ATGTTAGAGA ACTACAGAA CCTGTTCTCC CTGGGTATGA CTGCTCTAA GCCAGACTTG 1560  
 ATCGCTGTG TGGAGCAAAA TAAAGAGCCC CAGAATATA AGAGAAATGA GATGGCAGCC 1620  
 AAAACCCAG TTACATGTT TCAITTTCAAC CAAGACCTTC AGCCAGAGCA GAGCATAAAA 1680  
 GATTCACTCC AAAAAGTAAT ACCAAGACA TATGGAATA GTGGACATGA GAATTTACAA 1740  
 TTAATAAAT GTTGTAAAG AGTAGATGAG TGTGAGGTGC ACAAGGAGG TTAATATGAC 1800  
 80 CTTAAACAT GTTGTCAAA TACCCAAAAC AAAATATTTC AGACTATAA ATGTGTCAAA 1860  
 GTCTTCAGTA AATTTTCAAA TTCCAATAGA CAAATGCAA GATATACTGG AAAGAAACAT 1920  
 TTGAATGTA AAAAATATGG CAAATCATTT TGCAATGTTT CACACCTAAA TCAACATCAG 1980  
 ATAAATCAT TAAAGAGAA GTCTACAAA TGTGAAGAA GTGGCAATC CTTAAACAC 2040  
 TCCTCAAGCG GTACTACAA TAAAGAAAT CTTACTGGAG AGAAACCTCA CAGATGTGAG 2100  
 GAATGTGCA AAGCCTTAG GTGGCCCTCA AACCTTACTA GACATAAGAG AATTCACT 2160

5	GGAGAGAAAC	CCTACGCACTG	TGAAGAATGT	GGCCAAGCCT	TTAGGCGCTC	CTCAACACTT	2220
	ACTAACCACA	AGAGAATTCA	TACTGGAGAG	AGACCTTACA	AATGTGAAGA	ATGTGGCAAA	2280
	GCCTTTAGCG	TATCCTCAGC	CCTCATTTAC	CACAAGAGAA	TTCACTCTGG	AGAGAAACCC	2340
	TACACATGTG	AAGAATGTGG	CAAAGCCTTT	AACGTCTCCT	CGACTCTTAA	GACACATAAG	2400
	ATAATTCATA	CTGGAGAGAA	ACCCTACACA	TGTGAAGAAT	GTGSCAGAAC	CTTTAACTGC	2460
	TCCTCAACTG	TAAAGGCACA	TAAGAGAATT	CATACTGSAG	AGAAACCATA	CAAAATGTGA	2520
	GAATGTGACA	AAGCTTTTAA	GTGGCATTCA	AGTCTTGCTA	AACATAAGAT	AATTCACACT	2580
	GGAGAGAAAC	CCTACAAATG	CAGTGACAGC	AAAGCCTTAG	CCAAATCATC	AGAAATGCAA	2640
10	AAGGTCTACT	CTGGAGATGG	GGAAAATGGA	ATCCGTGTAC	ATAAGAAAAA	GGAGACACAG	2700
	GGCTGGCTTG	TGAGAAACAA	GAACGAAAAT	AGAACAGGGC	TGTTCCAGAT	CCGGCTGCGC	2760
	GTGAGACCTA	ACAGGACCCC	TTCAATGGGA	CAGCAAGAAG	GTTCACAGAC	TGACCCCAAT	2820
	CAGAGGAAGG	AGGAACCTGA	CCTTCAAAAT	CACATGAGCC	ATCAGAATGC	CTTAGAAGAT	2880
	CAAGAAATA	CTGGAGTGGG	TGGACTGTGT	ACATTGAGAG	ATGTAGTCAT	AGAATTCCTC	2940
15	CTGGAGGAGT	GGCAATGCCT	GGATCACGCT	CAGCAGAAIT	TATATAGAGA	TGTGATGTTA	3000
	GAGAACTACA	GAAACCTGGT	CTCCTGGGT	ATTGCTGTCT	CTAAGCCAGA	CTTGATCACC	3060
	TGTCTGGAGC	AAAAATAAGA	GCCTTGAAT	ATAAGAGAG	ATGAGATGGT	AACCAACAC	3120
	CCAGACCTTC	CGCCAGAGCT	AGGCATAAAA	GATTCACTCC	AAAAAGTAAT	ACCAAGAGA	3180
	TATGGAAAAA	GTGGACATGA	CAATTTACAA	GTAAGAACAT	GTAAGAACAT	GGGTGAGTGT	3240
20	GAGGTGCAAA	AAGGAGGTGT	TAATGAAGTT	AACCAATGTT	TGTCAACTAC	CCAAAAACAA	3300
	ATATTTTACA	CTCATAAATG	TGTCAAAGTC	TTGGGCAAT	TTTCAAAATC	CAATAGACAT	3360
	AAGACNAGAC	ATACTGGAAA	GAAACATTTT	AAATGTAAAA	AATATGGCAA	ATCATTTTGC	3420
	ATGGTTTCAC	AACATACATCA	ACATCAGATA	ATTCACTACT	GGGAGAATTC	CTACCAATGT	3480
	GAAGAATGCG	GCAAAACCTT	CAACTGCTCT	TCAACCCCTT	CTAAACATAA	AAGAATTCAT	3540
25	ACTGGAGAGA	AACCCATACAG	ATGTGAGGAA	TGTGGCAAGG	CTTTTACCTG	GTCTTCAACC	3600
	CTTACTAAAC	ATAGGAGAAT	TCATACTGGA	GAAAAACCTT	ACACATGTGA	AGAATGTGGC	3660
	CAAGCCCTTA	GCCGCTCTCT	AACACTTGCT	AACCACAAGA	GAATTCATAC	TGAGAGAGAA	3720
	CCATACACAT	GTGAAGAATG	TGGCAAGGCC	TTTAGCTTAT	CCTCATCCCT	CACCTACACC	3780
	AAGAGAATTC	ATACTGGAGA	GAAACCTTAC	ACATGTGAAG	AATGTGGCAA	AGCCTTTAAC	3840
30	TGCTCTCTCA	CCCTTAAGAA	ACATAAGATA	ATTCTACTGT	GAGAGAAACC	CTACAAATGT	3900
	AAAGAATGTG	GGAAAGCCTT	TGCCCTTCCC	TCAACTCTTA	ATACTCATAA	GAGGATTCAT	3960
	ACTGGAGAGG	AACCCATCAA	ATGTGAAGAA	TGTGACAAAG	CTTTTAAGTG	GTCTTCAAGT	4020
	CTTGTCTAAT	ATAAGAGTAT	GCATACTGGA	GAGAAACCTT	ACAAATGTGA	ATAA	4074

Seq ID NO: C37 DNA Sequence  
Nucleic Acid Accession #: NM\_032044  
Coding sequence: 182..658

40	1	11	21	31	41	51	
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	GCCCTTAGAG	TCTTGGTTGC	CAAAAGAGAT	TGCAGATCAA	GGAGAACCCA	GGAGTTTCAA	120
	AGAAGCGCTA	GTAAGGTTCT	TGAGATCCTT	GCACTAGCTA	CATCCTCAGG	GTAGGAGGAA	180
	GATGGCTTCC	AGAAGCATGC	GGCTGCTCCT	ATTGCTGAGC	TGCTTGGCCA	AAACAGGAGT	240
45	CCTGGGTGAT	ATCATCATGA	GACCCAGCTG	TGCTCCTGGA	TGGTTTACC	ACAAGTCCAA	300
	TTGCTATGGT	TACTTCAAGG	AGCTGAGGAA	CTGGTCTGAT	GCGAGCTCG	AGTGTCACTC	360
	TTACGGAAAC	GGAGCCCAAC	TGGCATCTAT	CCTGAGTTTA	AAGGAAGCCA	GCACCATAGC	420
	AGAGTACATA	AGTGGCTATC	AGAGAAGCCA	GCCGATATGG	ATTGGCTGCG	ACGACCCACA	480
	GAAGAGGCAG	CAGTGGCAGT	GGATTGATGG	GGCCATGTAT	CTGTACAGAT	CCTGGTCTGG	540
50	CAAGTCCATG	GGTGGGAACA	AGCACTGTGC	TGAGATGAGC	TCCAATAACA	ACTTTTAAAC	600
	TTGGAGGAGC	AACGAATGCA	ACAAGCGCCA	ACACTTCTCG	TGCAAGTACC	GAACCATAGG	660
	CAAGAATCAA	GATTCTGCTA	ACTCTGCAC	AGCCCGCTCC	TCTTCTTTTC	TGCTAGCCTG	720
	GCTAAATCTG	CTCATTTATT	CAGAGGGGAA	ACCTAGCAAA	CTAAGAGTGA	TAAGGGCCCT	780
	ACTACACTGG	CTTTTATTAG	CTTAGAGACA	GAAACTTTAG	CATTGGCCCA	GTATGGCTTT	840
55	CTAGCTCTAA	ATGTTTGGCC	CGCCATCCCT	TTCCACAGTA	TCTTCTTCCC	CTCCTCCCTC	900
	GTCTCTGGCT	GTCTCGAGCA	GTCTAGAAGA	GTGCTCTCC	AGCCTATGAA	ACAGCTGGGT	960
	CTTTGGCCAT	AAGAAGTAAA	GATTGAAGA	CAGAAGGAAG	AAACTCAGGA	GTAAGCTTCT	1020
	AGACCCCTTC	AGCTTCTACA	CCCTTCTGCC	CTCTCTCCAT	TGCTTGCACC	CCACCCACGC	1080
	CACCTCAACT	CTGCTTGTGT	TTCTTTGGC	CATAGGAAGG	TTTACAGTA	GAATCCTTGC	1140
60	TAGGTTGATG	TGGGCCATAC	ATTCTCTTAA	TAAACCATG	TGTACATAAG	AAAAAAAAAA	1200

Seq ID NO: C38 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 52..3042

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	GCTCACCAG	GAAAAATATG	CAATCGTCCC	ATTGATATAC	AGGCCACTAC	AATGGATGGA	60
	GTTAACTCTA	GCACCGAGGT	TGTCTACAAA	AAAGGCCAGG	ATTATAGGTT	TGCTTGCTAC	120
70	GACCGGGGCA	GAGCCTGCGG	GAGCTACCGT	GTAAGGTTCC	TCTGTGGGAA	GCCTGTGAGG	180
	CCCAAACTCA	CAGTCACCAT	TGACACCAAT	GTGAACAGCA	CCATTCTGAA	CTTGGAGGAT	240
	AATGTACAGT	CATGGAAACC	TGGAGATACC	CTGGTCATTG	CCAGTACTGA	TTACTCCATG	300
	TACCAGGAG	AAGAGTTCCA	GGTGCTTCCC	TGCAGATCCT	GCGCCCCCAA	CCAGGTCAAA	360
	GTGGCAGGGA	AACCAATGTA	CCTGCACATC	GGGAGGGAGA	TAGAGGGGCT	GGACATGGGG	420
75	GCGGAGGTG	GGCTTCTGAG	COGGAACATC	ATAGTGATGG	GGGAGATGGA	GGACAAATGC	480
	TACCCCTACA	GAAACCATAT	CTGCAATTTT	TTTGACTTCG	ATACCTTTGG	GGGCCACATC	540
	AAGTTTGCTC	TGGGATTATA	GGCAGCACAC	TTGGAGGGCA	CGGAGCTGAA	GCATATGGGA	600
	CAGCAGCTGG	TGGGTCAAGT	COCGATTAC	TTCCACCTGG	COGCTGATGT	AGACGAAAGG	660
	GGAGGTTATG	ACCCACCCAC	ATACATCAGG	GACCTCTCCA	TCCATCATAC	ATTCTCTGCG	720
80	TGCGTCACAG	TCCATGGCTC	CAATGGCTTG	TTGATCAAGG	ACGTTGTGGG	CTATAACTCT	780
	TTGGGCCACT	GCTTCTTCC	GGAAGATGGG	COGAGGGAAC	GCAACACTTT	TGACCACTGT	840
	CTTGGCCCTC	TTGTCAAGTC	TGGAACCCCTC	CTCCCTCTGG	ACCGTGACAG	CAAGATGTGC	900
	AAGATGATCA	CAGGAGACTC	CTACCCAGGG	TACATCCCCA	AGCCAGGSCA	AGACTGCAAT	960
	CGCTGTGTC	CCTTCTGGAT	GGCCAAATCC	AACAACAACC	TCATCAACTG	TGCGCTGCA	1020
	GGATCTGAGG	AAACTGGAAT	TTGCTTTATT	TTTACCAAGG	TACCAACGGG	CCCCCTCCTG	1080

Seq ID NO: C39 DNA Sequence  
Nucleic Acid Accession #: NM\_014373  
Coding sequence: 322.1338

1 11 21 31 41 51  
| | | | |  
5 GTGGCCCTCGA GGTGGTGGCA GGGCGGCCCC CTGCAGTCCG GAGACGAAAC CACGGACCGG 60  
GCTCCGGAG GCAGGTTCGG CTGGAAGGAA CCGCTCTCGC TTCGTCTTAC ACTTGCGCAA 120  
ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180  
AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240  
GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATT T CAGCAGGTCT 300  
TCTTGAATTT TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAAGTCTCT TTTTCAGTAC 360  
CAGTTACGTC AAACAAACCA GCCCCTAGAC GTTAACATATC TGCTATTCTT GATCATACTT 420  
GGGAAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAAT 480  
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TCCATTATAT TGTATTTCAG GGATTTTGTA CTTTAAAGCA TTAGGTTTAC TAAATACCAC 600  
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CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCTAAAA CAACCAAGCT TTCATTAAAG 720  
TGTCAAAAAT TATTTTATTT CTTTACAGTA ATTTTAAATTT GGATTTTCACT CCTTGCTTAT 780  
GTTTGGGAG ACCCAGCCAT CTACCAAGC CTGAAGGCA AGAATGCTTA TTCTCGTCAC 840  
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TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960  
ACTTCTCTATA TGAATGAAGC TATCTTATAT TTCTCTTTTT CATCCCACTC CAGTTATACT 1020  
GTGAGATCTA AAAAATATTT CTTATCCAAG CTCATTGTCT GTTTCTCAG TACCTGGTAT 1080  
CCATTGTGAC TACTTCAGGT AATCATTGTT TTACTTAAAG TTCAGATTCC AGCATATATT 1140  
GAGATGAATA TTCCTGGTT ATACTTTGTC AATAGTTTTC TCATTGCTAC AGTGTATTGG 1200  
TTTAAATGTC ACAAGCTTAA TTTAAAAGAC ATTGGATTAC CTTTGGATCC ATTTGTCAAC 1260  
TGGAAGTGCT GCTTCATTCC ACTTACAATT CCTAATCTTG AGCAAAATGA AAAGCCTATA 1320  
TCAATAATGA TTTGTTAATA TTATTAATTA AAAGTTACAG CTGTATAAG ATCATAATTT 1380  
TATGAACAGA AAGAACTCAG GACATATTAA AAAATAAACT GAACATAAAC AACTTTTGCC 1440  
CCCTGACTAG TAGCATTTC AATGTGTCT TTTGAAGGCG TATACCAGTT ATTAATATAGT 1500  
GTTTATTTT AAAACAAAAA TAATTCCAAG AAGTTTATAT AGTTATTACG GGACACTATA 1560  
TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACATT TGGCTATACT 1620  
GATGTTGTG TGTCTCAAAA AAACCTACTG ATGCAAACTG TTATGTAAAT CTGAGATTTC 1680  
ACTGACAAC TTAAGATATC AACCTAAACA TTTTATTTAA ATGTTCAAAT GTAAGCAAGA 1740  
AAAAAAA 1749

35 Seq ID NO: C40 DNA Sequence  
Nucleic Acid Accession #: BC012089  
Coding sequence: 1..2571

1 11 21 31 41 51  
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TATGAGACCC AAGACTCCCA TAAAGCTGGA CCCATTGGCA TTCTCTTTGA ACTAGTGCA 180  
ATCTTCTCT ATGTGGTACA GCGCGTGAT TTCCAGAAAG ATACTTTGAG AAAATTCITA 240  
CAGAAGGCAT ATGAATCCAA AATTGATTAT GACAAGATTG TCTACTATGA AGCAGGGATT 300  
45 ATTCTATGCT GTGCTCTGGG GCTGCTGTTT ATTATTTGTA TGCTCTGTT GGGGTATTTC 360  
TTTTGTATGT GTCGTTGCTG TAACAAATGT GGTGGAGAAA TGCAACAGCG ACAGAAAGGA 420  
AATGGGCCCT TCCTGAGGAA ATGCTTTGCA ATCTCCCTGT TGGTATTGG TATAATAATA 480  
AGCATTGGCA TCTTCTATGG TTTTGTGGCA AATCACCAGG TAAGAACCOC GATCAAAAGG 540  
AGTCGAAAC TGCCAGATAG CAATTTCAAG GACTTGCGAA CTCTCTTGAA TGAACCTCCA 600  
50 GAGCAATATCA AATATATATT GGCCTAGTAC AACACTACCA AGGACAAGGC GTTCACAGAT 660  
CTGAACAGTA TCAATTCAAT GCTAGGAGGC GGAATTTCTG ACCGACTGAG ACCCAACATC 720  
ATCCCTGTCT TTGATGAGAT TAAGTCCATG GCAACAGCGA TCAAGGAGAC CAAGAGGCG 780  
TTGGAGAAC TGAACAGCAC CTTGAAGAGC TTGCACCAAC AAAGTACACA GCTTAGCAGC 840  
55 AGTCTGACCA GCGTGAAGAC TAGCCTGCGG TCATCTCTCA ATGACCCTCT GTGCTTGGTG 900  
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Seq ID NO: C41 DNA Sequence



Seq ID NO: C42 DNA Sequence  
Nucleic Acid Accession #: NM\_001432.1  
Coding sequence: 167..676

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65	GAGGATGGAG	ATGCTCTGTG	CGCGCAGGGT	CACTCGGCTG	CTGCTCTGCC	TGGGTTTCCA	240
	TCCTTCTACG	CGAGTCTCTA	GTCACACTGT	GATTCCATCA	TGTATCCGAC	GAGAGTCCAG	300
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	TATATGAGGG	GCAGTGGACA	TTTCCCTATG	CCAACTCACG	ACTCTCAGAG	GTAAGTGTCA	1380



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	AAAGATTTC	TCTGCACTCT	GAGCCCATAG	GTCTCAGAGA	GTTAATAGGA	GTATTTTGG	2040
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35	AAAAACAAGT	CATTTTGTGA	TTTTTCTATC	TTAAGAAATG	TTAAAAAAGC	TAATCCCTAA	3420
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	TTTGAAGAGC	CATTTTGTGA	AACGGTTTTT	ATTAAGATG	CTATGGAAAC	TAAAGTTGTA	4440
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55	AAATAGATAA	TTTACAGAT	ATTATTAAAT	TTTATTATT	TTTCTTGGGA	ATTGAAAAAA	4620
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Seq ID NO: C43 DNA Sequence  
Nucleic Acid Accession #: AF011468.1  
Coding sequence: 257..1468

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 Coding sequence: 63..617

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Seq ID NO: C45 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 200..2932

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Seq ID NO: C46 DNA Sequence  
Nucleic Acid Accession #: NM\_000584.1  
Coding sequence: 75..374

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Seq ID NO: C47 DNA Sequence  
 Nucleic Acid Accession #: NM\_005603.1  
 Coding sequence: 1..3756

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Seq ID NO: C48 DNA Sequence  
Nucleic Acid Accession #: XM\_044533  
Coding sequence: 238..2751

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Nucleic Acid Accession #: NM\_007019.1  
Coding sequence: 41..580

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Seq ID NO: C50 DNA Sequence  
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ACAGCGATTG GATGGAATTT TGACTGAAGG AGAAGGTCCA AGAAGGCTTA AGAATCTGTA 1140
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GGAAATACTT CATGAATCA AGTCATTTC TTTGCATTTT GATGAGAATT CATTTTTTGC 1320
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TTCAAGAAAT ATGATTTGTG TTGGTTGTTT TAAATGTGCT CTGTGGGGAA AGCTTCAGAC 1440
TCAGGGTTTG GCTCAGCTC TGAAGATCTT ATTTTCTGAG AAATGATAG CAAATATGCC 1500
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CGCATTTGGA AGAATTTCTA CAAGTGTGAA AGAATTAGAA AACTTCAGGA ACTTGTATCA 1620
GAATATTCAT TAAAGAAAAA AAGCTGATAT GTGCTGTITT CTGGACAATG GAGGCGAAG 1680
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TTGCCAGTT AGATTGGAAT TTCAGATAAA CAATTAGTTT TTTAATATT TACATGGAAT 2160
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TATTGCTATT TTGATTGGGT TGTTTTGTG TGTAGAAAAG TACAATAACA ACTCAAAGGC 2340
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GGGCTGAAGT GATCTTCCCA CCTCAGCCTC CCAAGTAGCT GGGAAACAG GTGCTGCGCA 2940
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AAAACTGTGC CCTCTTTACA TATGCTTAT CAGGTATAAC ATGTTGAAAT GTCACATTAG 3180
TAGTAAAGTG GGGTTTATTT ATATAGTGTG TAAGAAATGT CAGTTTACAC TGCTGTATAC 3240
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Seq ID NO: C51 DNA Sequence  
 Nucleic Acid Accession #: NM\_002888.1  
 Coding sequence: 37..723

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CTGTTGCTCG CCCCGGTGGC GGGGCCCGCG GGGTCCGGGG GCCCGGACGA CCTCGGGCAG 180
CCTCAGGATG CTGGGGTCCC GCGCAGGCTC CTGCAGCAGA AGCGCGCGGC GGCGCTTCA 240
TTCTTCAACT TCGGTCGCGG CTGCGCCAGC GCGCTGCGAG TGCTGGCCGA GGTGCAGGAG 300
GGCGCGCGGT GGATTAATCC AAAAGAGGGA TGTAAAGTTC ACGTGGTCTT CAGCACAGAG 360
CGCTACAACC CAGAGTCTTT ACTTCAGGAA GGTGAGGGAC GTTTGGGGAA ATGTTCTGCT 420
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CAGTGTGCAC ACTACTACTT GGCACAGCTC ACTAGTGTGA GGCAGTGGGT AAGAAAAACC 720
TGAAAAATTA CTGTGCCAC AAGAGTTACA ATCAAAGTGG TCTCCTTAGA CTGAATTCT 780
GTGAACCTCT AATTTCATAT CAAGAGTTGT AATCACTTT ATTTCAATAA ATATGTGAGT 840
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Seq ID NO: C52 DNA Sequence  
Nucleic Acid Accession #: NM\_005409.3  
Coding sequence: 94..378

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TGTCTTTGCA TAGGCCCTGG GGTAAAAACA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAAT 300
AAAGGACAAC GATGCCATAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGT 360
GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAAGG GCATCTGAAA 420
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GCATTTCTAG GCTAGAGAAC CTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
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Seq ID NO: C53 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..609

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CACAGCCGCG CCAAGATCGA GCGCAGCCTG GCCAGCAGCC TTTTCCCTT GGACCAAGTCC 240
AAAAGCCAGC TCTATTGGGA CTACACACC CCGGGGAGGT ATGGCAGGCT GATCCTCCTC 300
TCCCCAACCG GGGACAATAT TTTGCTCCAG GCTGAGGGGA TCTTCGAGAC CCACCGAGCC 360
GTGCTGGAAA TGAAGGTGAA CCACAAGGCG TATAATTATA CTTTTTCCCA TCTGTGTGTG 420
TTGAGAAATC AGGATAAGAA ATGOGTGCTG GATGATATTA TTTCACTGCT AGAGGATCTC 480
AGGCAGGCTG CCGTCTCCAA TAAGACAACA GCCAGGGTGC AAGTGAGGTA TCCCAACACT 540
AAATTAAAGG TATGCTCCTT CTGCATGCTT CTGCCAATTA AAGAGGCAGC ACTTCATTTT 600
TTGCCCTAA 609

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Seq ID NO: C54 DNA Sequence  
Nucleic Acid Accession #: NM\_002438.1  
Coding sequence: 104..4474

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GCCCTCTCTG CCATCAGGAG AAGGAAAGGA TAAACCTCG GCCATGAGGC TACCCCTGCT 120
CCTGTGTTTT GCCTCTGTCA TTCCGGGTGC TGTTCCTCTA CTGACACCA GGCAATTTTT 180
AATCTATAAT GAAGATACAA AGCGCTGCGT GGATGCAAGT AGTCCCAAGT CCGTCCAAAC 240
CGCAGCTTGC AACCGGATG CCGAATCACA GAAATTCGA TGGGTGTCCG AATCTCAGAT 300
TATGAGTGTG GCATTTAAAT TATGCTCGG AGTGCCATCA AAAACAGACT GGGTTGCTAT 360
CACTCTCTAT GCCTGTGACT CAAAAAGTGA ATTTAGAAA TGGGAGTGCA AAAATGACAC 420
ACTTTTGGGG ATCAAGGAG AAGATTATTT TTTTAACCTAC GGCAACAGAC AAGAAAAGAA 480
TATTATGCTC TACAAGGGAT CGGTTTATG GAGCAGGTGG AAGATCTATG GAACCAAGA 540
CAATCTGTGC TCAGAGGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGAGC 600
AACCTGTGCA TTCCCGTTCA AGTTTGAAAA CAAGTGGTAC GCAGATTGCA CGAGTGTG 660
GCGGTGCGAT GGTGGCTCT GGTGCGGAAC CACTACTGAC TATGACACAG ACAAGCTATT 720

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5	TGGATATGT	CCATTGAAAT	TTGAGGGCAG	TGAAAGCTTA	TGGAATAAAG	ACCCGCTGAC	780
	CAGCGTTTCC	TACCAGATAA	ACTCCAAATC	CGCTTTAAGC	TGGCACCAG	CGAGGAAAAG	840
	CTGCCAACAA	CAGAACGCTG	AGCTCTCTGAG	CATCACAGAG	ATACATGAGC	AAACATACCT	900
	GACAGGATTA	ACCCAGTTCT	TGACCTCAGG	ACTCTGGATT	GGACTTAACA	GTCTGAGCTT	960
	CAACAGCGGT	TGGCAGTGG	GTGACCGCAG	TCCTTTCCGA	TATTTGAACT	GGTTACCAGG	1020
	AAGTCCATCA	SGTGAACCTG	GAAAAGCTG	TGTGTCACTA	AATCCTGGAA	AAAAATGCTAA	1080
	ATGGGAAAAT	CTGGAATGTG	TTCAGAAACT	GGGCTATATT	TGCAAAAAGG	GCAACACCAC	1140
	TTTAAATCT	TTTGTATTTC	CCTCAGAAAG	TGATGTGCCT	ACTCAGTCTC	CTAGTCAGTG	1200
10	GTGGCCGTAT	GCCGCTCACT	GTTACAAGAT	TCACAGAGAT	GAGAAAAAAA	TCCAGAGGGA	1260
	TGCTCTGACC	ACCTGCAGGA	AGGAAGGCGG	TGACCTCACA	AGTATCCACA	CCATCGAGGA	1320
	ATTGGACTTT	ATTATCTCCC	AGCTAGGATA	TGAGCCAAAT	GACGAATTGT	GGATCGGCTT	1380
	AAATGACATT	AAGATTCAAA	TGTACTTTGA	GTGGAGTGAT	GGGACCCCTG	TAAAGTTTAC	1440
	CAAAATGGCTT	CGTGAGAAAC	CAAGCCATGA	AAACAACAGA	CAGGAGGATT	GTGTGGTGAT	1500
15	GAAAGGCAAG	GATGGTACT	GGGCAGATCG	GGGCTGTGAG	TGGCCTCTTG	GCTACATCTG	1560
	CAAGATGAAA	TCACGAAGCC	AAGGTCCAGA	AATAGTGGAA	GTGCAAAAAG	GCTGCAGGAA	1620
	AGGCTGGAAA	AAACATCACT	TTTACTGCTA	TATGATTGGA	CATACGCTTT	CAACATTGTC	1680
	AGAAGCAAAC	CAAGCTCTGA	ATAATGAGAA	TGCTTATTTA	ACAACTATTG	AAGACAGATA	1740
	TGAACAGACC	TTCTGAGCTA	GTTTCGTGG	CTTAAGGCCCT	GAAAAATATT	TCTGGACAGG	1800
20	ACTTTCAGAT	ATACAAACCA	AAGGGACTTT	TCAGTGGACC	ATCGAGGAAG	AGGTTTCGGTT	1860
	CACCCACTGG	AATTGAGATA	TGCCAGGGCG	AAAGCCAGGG	TGTGTTGCCA	TGAGAACCGG	1920
	GATTGCAAGG	GGCTTATGGG	ATGTTTTGAA	ATGTGATGAA	AAGGCAAAAT	TTGTGTGCAA	1980
	GCATGTGGCA	GAAGGAGTAA	CCCAACCCAC	GAAGCCACAG	ACGACTCCCG	AACCCAAATG	2040
	TCGGGAGGAT	TGGGGCGCCA	GCAGTAGAAC	AAGCTTGTGT	TTCAAGCTGT	ATGCAAAAAG	2100
25	AAAACATGAG	AAGAAAAGT	GGTTTGAATC	TCGAGATTTT	TGTCGAGCTC	TGGGTGGAGA	2160
	CTTAGCTAGC	ATCAATAACA	AAGAGGAACA	GCAAAACAATA	TGGCGATTAA	TAAACAGTAG	2220
	TGGAAGCTAC	CACAAACTGT	TTTGGTTGGG	ATTGACATAT	GGAAAGCCCTT	CAGAAGGTTT	2280
	TACTTGGATT	GATGGTTCTC	CTGTTTCATA	TGAAAACCTG	GCTTATGGAG	AACCTAATAA	2340
	TTATCAAAAT	GTGTAATACT	GTGGTGAAGT	GAAAGGTGAC	CCTACTATGT	CTTGGAAATGA	2400
30	TATTAATTTG	GAACACCTTA	ACAACTGGAT	TTGCCAGATA	CAAAAAGGAC	AAACACCAAA	2460
	ACCTGAGTGA	ACACAGCTCT	CTCAAGACAA	TCCACCAAGT	ACTGAAGATG	GGTGGGTTAT	2520
	TTACAAAGAC	TACCAATATT	ATTTCAGCAA	AGAGAAGGAA	ACCAATGGACA	ATGCGGAGAC	2580
	GTTTTCGAAG	AGGAATTTTG	GTGATCTTGT	TTCTATTCAA	AGTGAAGTGA	AAAAGAAAGT	2640
	TCTATGGAAA	TATGTAAACA	GAAATGATGC	ACAGTCTGCA	TATTTTATTG	GTTTATTGAT	2700
35	CAGCTTGGAT	AAAAAGTTTG	CTTGGATGGA	TGGAAGCAAA	GTGGATTACG	TGCTCTGGGC	2760
	CACAGGATGA	CCCAAGTTTG	CAAAATGAAGA	TGAAAACCTG	GTGACCATGT	ATTCAAAATC	2820
	AGGGTTTGGG	AATGACATTA	ACTGTGGCTA	TCCAAACGCC	TTCAATTGGC	AGCGACATAA	2880
	CAGTAGTATC	AATGCTACCA	CAGTTATGCC	TACCATGCCC	TCGGTCCCAT	CAGGGTGCAA	2940
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	CATACAAAGT	GAAACAGAGC	AAGCAATTCT	TACCTATCAC	ATGAAGGACT	CCACTTTCAG	3120
	TGCTGGACT	GGGCTGAATG	ATGTCAATTG	AGAACACACG	TTCTTTTGGG	CGGATGGAGC	3180
	AGGAGTCCAT	TACACAAACT	GGGGGAAAGG	TTACCTTGGT	GGGAAGAGAA	GCAGTCTTTC	3240
	TTATGAAGAT	GCTGACTGTG	TTGTTATTAT	TGGAGGTGCA	TCAAAATGAAG	CAGGAAAATG	3300
45	GATGTGATGAT	ACCTCGGACA	GTAACAGGAG	CTACATATGC	CAGACACGAT	CCGACCCCTC	3360
	CTTGACTAAT	CCTTCAGCAA	CGATTCAAAC	AGATGGCTTT	GTTAAATATG	GCAAAAGCAG	3420
	CTATTCACTC	ATGAGACAAA	AATTTCAATG	GCATGAAGCG	GAGACATACT	GCAAGCTTCA	3480
	CAATTTCCCTT	ATAGCCAGCA	TTCTGGATCC	CTACAGTAAT	GCATTGTGGT	GGCTGCAGAT	3540
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50	CACCTGGACT	GATAAGTGGG	GGGTGAGGTA	CACCTAAGTG	GCTGCTGATG	AGCCCAAATT	3660
	GAAATCAGCA	TGTGTTTATC	TGGATCTTGA	TGGCTACTGG	AAGACAGCAC	ATTGCAATGA	3720
	AAGTTTITAC	TTTCTCTGTA	AAAGATCAGA	TGAAATCCCT	GCTACTGAAC	CCCCACAATC	3780
	GCCTGGCAGA	TGCCCGGAGT	CAGATCACAC	AGCATGGATT	CCTTTCCATG	GTCACTGTTA	3840
	CTATATTAG	TCTCATATA	CAAGAAACTG	GGGCCAAGCT	TCTCTGGAAT	GTCTTCGAAT	3900
55	GGGTTCCTCT	CTGGTTTCCA	TTGAAAGTGC	TGCAGAAATC	AGTTTCTCTG	CATATCGGGT	3960
	TGAGCCACTT	AAAAGTAAAA	CCAATTTTGT	GATAGGATTG	TTCAAGAAATG	TTGAAGGGAC	4020
	GTGGCTGTGG	ATAAATAACA	GTCCGGTCTC	CTTTGTCAAC	TGGAACACAG	GAGATCCCTC	4080
	TGGTGAACGG	AATGATTGTG	TAGCTTTACA	TGCGTCTTCT	GGGTTTGGGA	GTAATATTCA	4140
	CTGTCTTCTC	TACAAAGGAT	ATATTGTGAA	AAGACCAAAA	ATTATTGATG	CTAAACCTAC	4200
60	TCATGAATTA	CTTACACAAA	AAGCTGACAC	AAGGAAGATG	GACCCCTCTA	AACCGTCTTC	4260
	CAACGTGGCC	GGAGTAGTCA	TCATTGTGAT	CCTCCTGATT	TTAAGCGGTG	CTGGCCTTGC	4320
	CGCCTATTTC	TTTTATAAGA	AAAGACGTGT	GCACCTACCT	CAAGAGGGGG	CCTTTGAAAA	4380
	CACCTCTGAT	TTTAACAGTC	AGTCAAGCCC	AGGAACATAGT	GATATGAAAG	ATCTCGTGGG	4440
	CAATATTGAA	CAGAATGAAC	ACTCGGTCAAT	CTAGTACCTC	AATGCGATTG	TGAGATATTT	4500
65	GAATTTTATA	AAATTGTAAAC	TGAAATTTAA	AATTTTATGT	TCAATGTGAT	TGTTTTCTTT	4560
	AAATGAGTA	CTGAATTGTA	CTGGTCTGTC	CTTTTCTCTT	TTGCCTAATT	GAAGAAATAA	4620
	TTGCTTGTTT	TCTAGCTTGG	CAAGATATTT	TCATAAAAAG	GGGATAACAA	TGCTGATTAC	4680
	TACCTTTTAA	AATATTTTAG	ATRAATGCAC	AGCACCACAG	CACCACATCT	AAGCATTAGT	4740
	GATGGGTAGC	TGATGTCAGC	TTCAATGTGA	TTTAAAGCAC	TCTAGAAAAC	ATGAAGCTTC	4800
70	TTGSCATATT	TTAAGGAGCT	CCCAAAATGT	GTTACCTATT	AAATTGTAAC	TCAGCAAGTA	4860
	GAAGACCAAT	TGAAAAGTCA	GGTACAAAAT	TCCTCAAGTG	GCATAAAAAT	GTAGTCAGTT	4920
	TTCTCTTTTC	CCAGTTTFTA	TTTCCACTCC	AATTATTTAG	AACCTTATTT	GTACATGTGC	4980
	AGAAGAATAA	GGCAGCTGAG	AATCTGTGTT	CCCCCAAGAG	AGTTTTCAG	GCTGAGTGTT	5040
	GCAAAATGTT	TCITTTGCTT	GTTATATGTA	TATCAGGAAT	ACAAGGATGT	GAATAAATAC	5100
75	TGTAATTTTG	CATAACTGGA	TGTACTTAGA	TAATGTGAAA	TAAACATTTA	AGACAAAGTC	5160
	TATTTTAAAT	AAAAAAAATA	AAAAA				5185

Seq ID NO: C55 DNA Sequence  
Nucleic Acid Accession #: NM\_024574.2  
Coding sequence: 424..2130

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5	CGCTGCCCGG	GGATTCCCA	GCCCCGCGG	GCTCCCTACT	CCACTTGGCA	GCAACTTGGG	180
	CGACCGCGCG	CGCCCCGCCC	TGCCCCGCGT	TTGAAGTTTG	CTGTGCGGAC	CGCAAAGTTG	240
	GGACACTTCA	GGGATTGAA	TTTTTCTCTT	TTATCTGCGT	CGTCCCCGCG	CCTCCAGGCT	300
	TCTCGTTTCT	GGATTATTGGT	GCTTAGCATC	TTGGCAGGGT	CGGGGAAGT	GGACTATTTC	360
	GCACACCACA	CCACGGGGAG	GGATTTTTTT	CTATTTTCCC	TACGAAAAAC	AGATCTTTTT	420
	AAGGATGGTG	CTGCTCCACT	GGTGCTGCT	GTGGCTCCTG	TTTCCACTCA	GCTCAAGGAC	480
	CCAGAAGTTA	CCCAACCGGG	ATGAGGAAC	TTTTCAGATG	CAGATCOGGG	ACAAGGCATT	540
	TTTTCATGAT	TGGTCAGTAA	TTCCAGATGG	AGCTGAAATT	AGCAGTTATC	TCTTTAGAGA	600
10	TACACCTAAA	AGGTATTCTT	TTGTGGTTGA	AGAAGACAAT	ACTCCATTAT	CAGTCACAGT	660
	GACGCGCTGT	GATGCGCCTT	TGGAGTGGAA	GCTGAGCCTC	CAGGAGCTGC	CAGAGGCAGC	720
	GAGCGGGGAA	GGCTCAGGTG	ATCTGGAACC	TCTTGAGCAG	CAGAAGCAGC	AGATCATTAA	780
	TGAGGAAGGC	ACTGAGTTAT	TCTCCTACAA	AGGCAATGAT	GTTGAGTATT	TTATATOGTC	840
	TAGTTCCCCA	TCCGGTTTAT	ATCAGTTGGA	TCTTCTTTCA	ACAGAGAAGG	ACACACATTT	900
15	CAAAGTATAT	GCCACCAAA	CTCCAGAAATC	TGATCAGCCA	TACCTGAGT	TACCTTATGA	960
	CCCAAGAGTA	GATGTGACCT	CACTGGGGCG	CACCACGGTC	ACTTTGGCCT	GGAAACCAAG	1020
	CCCCACTGCC	TCTTTGCTGA	AACAACCCAT	TCAGTACTGT	GTGGTCATCA	ACAAAGAGCA	1080
	CAATTTCAAA	AGTCTCTGTG	CAGTGGAAAG	AAAACTGAGT	GCAGATGATG	CTTTTATGAT	1140
	GGCACCGAAA	CCTGGTCTGG	ACTTCAGCCC	CTTTGACTTT	GCCACTTTTG	GAITTCCTTC	1200
20	TGATAATTCA	GGTAAGAAC	GCAGTTTCCA	GGCAAGCCT	TCTCCAAAC	TGGGGCGTCA	1260
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30	CGTACCTGT	TCCTCGGCCA	CGTGGCTTGG	GCTAGGCAC	CAGGAAAGGA	ACAAGTTTGG	1860
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	CCAATGTCTA	GGACACAGTA	TAAGGAAGAA	GTGAGAAAG	GTCTCTGTA	AATATTTCAC	1980
	CAGTCAAAAC	CTGCAGAAAG	CAGTGACCAC	AGAAACAATT	AAAGTCTTTC	AGCTGGCCAA	2040
	ATCTTACCTG	CTGGATGTTT	ATGTCATAGG	ACATGGGGGG	CACCTCTGTA	AGTATCAGAG	2100
35	TAAGGTGTGT	AAAACAGAAA	AGTTCTGTGA	GTTACCTTCT	TATAGAGATA	TATTATGTAG	2160
	AACTCCAGGA	GGGACATTAA	ATCACTTTAA	GTATAAATCT	ACTACTCCCA	CAGTTGAGAG	2220
	AAGTTGTGAC	CTGTACTTGT	ACTATGGAAG	GAAGGATATC	AACGTGTGTA	TATTGATGTT	2280
	TATATAAGTA	ACTCTTGAAG	GAGACTTGT	CTAGCGTGCC	CCATGGTACC	TAGTGTGTGT	2340
	CTGATGCCGG	TTGGTGTCAA	AGATAGAGGG	CTTCTTGAGG	GAACCTGGCA	TTCTTGCTT	2400
40	TGACCACCTG	ATGAACCTGT	TCTAAATTAT	TTTATTACCT	AAAAATTAA	AATATGCCAT	2460
	TCATTGCACA	CACCCACAAA	TGCAAAATCAT	TCCTCTCTAT	AGATGCTAGG	ATATATATAA	2520
	ATTATTTTAT	AAATCTCTGT	TTTAAATGTC	AGTGTCTCTA	TGATTGTAAA	CTATTAAATT	2580
	CTTTTCTTAT	TAAAGTACAG	ATCTAATCTA	AGTATTATTA	AGTTGATAGC	CCTCTAGTCA	2640
	GTTATATTGC	TATGTGAAAT	TCTTGTTTGT	TGAGTAAAT	GTTTAAATAC	TATATGTATC	2700
45	TCATGTACAA	AGTTGACATA	CATTATATTC	ATGTACATAA	AATTAAAGAG	ATTAGATTAT	2760
	ATACTGTATA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		2808

Seq ID NO: C56 DNA Sequence  
Nucleic Acid Accession #: BC034229.1  
Coding sequence: 373..1422

50	1	11	21	31	41	51	
	ATCCGGCGGT	GGTGACGCGA	GAGGCTGGGG	TCTCCAGGAC	CAACTCCTCT	TCATCTTCGT	60
55	CTTCTCAGC	CTGCTCAATG	TGAAGCCCTT	GATCATGATT	CACCTCCACT	TAATAAATAA	120
	AGTGTTTACA	AATCAGAATA	ACTTTTAGAC	AATATTAAGG	TGGTAATCAT	GAACAGAAAA	180
	GATTTGTAGT	TTCTTCCATG	GGGAAACCTT	GGAAATCTGT	TAAAGCTAAA	ATATAGCAAT	240
	GTAATAATTA	AAACAAAAGT	CTAAGATTGG	AAGAGATAAT	TTGCTTCAGG	ATTTTGTATG	300
60	AAGGCAATG	CTAACTTTAA	AAACCAGATT	TCCGAGAAAT	ACAAAAGAAA	TAGAAATGCT	360
	CAAGAACTGC	GAATGGAGAA	AGTACAGTTA	GAGTTTGAGA	ACCAAGAGAT	GGAGAAGAAA	420
	CTGCAAGAA	TCCGATCCAC	AAGAAACRAA	GAAAAGGAAG	ATAGAGAGTC	AAGCGAGTAT	480
	TACTGGAAAT	CTGGAAGAGT	GGGCAAAATG	GTCAATCAAT	CATATATGAT	GTCACAAAAT	540
	AAAGGAAATG	TTGTTAAGTT	TTCTGCTGGA	AAAGTGAAAT	TAAAATTGCT	GAAGGAACAG	600
65	ATTCAAGAGC	CAGTGAAACC	AACAGTTAAT	TATAAAATGG	CAAATTCCTC	AGAAATGTGA	660
	AAACCCAAGA	TAAATGGGAA	AGTTTGTGGA	CAGTGTGAGA	ACAAAGCTGC	TCTACTGGTA	720
	TGCTTGAAT	GTGGAGAAGA	TTATTGTGTA	GGATGCTTTG	CTAATGTGTA	CCAGAAAGGG	780
	GCACTAAAGC	TCCACAGAAC	AACTCTTTTG	CAGGCAAGAT	CTCAAAATAT	ATTCAATGTA	840
	TTGGATGTTG	CCCATCAGTT	TATAAAGGAT	GTTAATCCAG	ATGAACCCAA	AGAGGAGAA	900
70	AATTCTACAA	AGGAAACCCG	TAAAATTCAA	CATAAACCCA	AATCTGTACT	TCTCCAGAGG	960
	AGCAGCTCTG	AGGTAGAAAT	TACAACGATG	AAAAGAGCAC	AACGTACAAA	ACCAAGAAAG	1020
	AGTCTGTTGT	GTGAAGGGTC	ATTGATGATA	GAAAGCTTCT	CACAGTCTCT	TCAGGAAGTG	1080
	TTAAGTCAAT	GGAGAACCGG	AAATCATGAT	GACAAACAAG	AACAGAAATT	ACATGCAGCA	1140
	GTAAAAGACT	CATTGGGAAG	ATGCGAAGTA	CAGACTAATC	TGAAAATTGG	GAGAGAACCA	1200
75	CTTAATATTG	AACTTAAAGA	AGACATTCTA	TCCTATATGG	AAAAATTATG	GCTTAAAAAA	1260
	CACAGGAGAA	CTCCACAAGA	GCAACTTTTT	AAATGCTACC	AGATACGTTT	CCACATCCAC	1320
	ATGAAACCA	TGGTGAATCA	CAGTGTCTCT	AAATGAAAAA	CGATGAAGAT	AGTGATGGTG	1380
	AGGAGACCAA	AGTACAAAC	ACAGCTCTTT	TATTGCCAGT	AGAAACATTA	AACATAGAGA	1440
	GACCTGAACC	ATCTCTGAAG	ATAGTGAAC	TGGATGATAC	TTATGAAGAG	GAATTTGAAG	1500
80	AAGCAGAAAA	TATTTGTGCT	TACAAAGTTA	AATTAGCTGA	TGCAGACAGT	CAAGAAAGTT	1560
	GTGCTTTTCA	TGATTGTGAG	AAGAATAGCT	TTCCATATGA	AAATGGCATC	CATCAACATC	1620
	ATGTTTTTGA	TAAAGGAAAG	AGAGACTTCT	TAAATCTTTG	TCTGAGAAAC	AGCTCTACTT	1680
	ATTATAAAGA	TAATTCAAAA	GGAGAAACTT	CAAAACAGAA	TTTTGACAAC	ATCGTGGATC	1740
	CTGATGTGTA	TTCTTCTGAC	ATTGAAAAAA	TTGAGGAAAG	CACCTCCTTT	GAAGAAATTT	1800
	TAAAGGAGAA	AAATATAGST	TTAGAAAGTA	ATCAAAAGTC	TGATGATTCC	TGTGTATCAC	1860

5 TTGAAAGCAA GGACACTTTG CTAGGTAGAG ATTTAGAAAA AGCTCCCAT T GAGGAGAAAT 1920  
 TATCTCAAGA CATCAAGAGAA TCCTTGGAAT TGAGCAATCT GTATAAGAGG CCAAGCTTTG 1980  
 AAGAATCAAA AACTACAAAG TCATCACTGT TGTACAAGA AATAGCCTGC AGAAGTAAGC 2040  
 CTATAACAAA ACAATATCAA GGACITGAGA GATTCTTTAT TTTTGATACA AATGAAAGAC 2100  
 TCAACTTACT TCCTTCTCAT CGTTTAGAAT GCAACAATTC CAGTACTAGG ATTACACTTG 2160  
 CAGGTCAGAA ATCAGAGAGA CCTTCAACAG CAAATTTTCC ACTTTCCAC TCTGTTAAAG 2220  
 AAAGCTCCAG TTGCCTTTCA TCCTCTCATC CTGATCAAG AAGTGCAGCT GCTCAATCAT 2280  
 CATCTAGAGC TGCTTCTGAA ATTTAGAAA TTGAATATAT TGATATTACT GACCAGAATG 2340  
 10 AGCTTTCTCT AGATGACACT ACTGATCAAC ATACTTTAGA CAATTTGGAA AAAGAATTAC 2400  
 AAGTGCTGAG ATCTCTTGCA GATACTTCAG AAAAGCTTTA CAGCTTAACC TCAGAAGAGT 2460  
 TCCAGATTTT CAGCAGCCAA TCACTGAATA TAAGTCAGAT TTCCACAGAT TTCCTTAAGA 2520  
 CCTCACATGT GAGGGGTCCC TGTGGAGTTG AGGAATTGAG CTGTTCTGGA AGAGATACCA 2580  
 AAATTTCAGT TTTGCTGTCA CTTTCTGAGA GCAGTACAGA TGAGGAGGAG GAAGATTTTC 2640  
 TCAACAAGCA ACATGTCATC ACACCTACCGT GGTCAAAGAG TACTTAAAGA TTATTTGTTT 2700  
 15 ATTACTGTTT CCATTTTGTA CCCAGAGTAA AGCAAAACAC TGAGAAAAGT AACCAAGTGA 2760  
 TTACCTATCC AAGTGCTGGA GATTTTGATT ACTAATGTCT TTGATGTTTC AAGGCTACAA 2820  
 ACTAATAAAA GTAAAATTAT AAGTTCAAAA AAATTTTATA AAAAAAAAT AAAAAA 2876

20 Seq ID NO: C57 DNA Sequence  
 Nucleic Acid Accession #: NM\_024687.1  
 Coding sequence: 138..1706

25 1 11 21 31 41 51  
 AAAAAACATGA TGACAACAAG AAACAGAAAT TACATGCAGC AGTAAAAGAC TCATTGGAAG 60  
 AATGCGAAGT ACAGACTAAT CTGAAAAATTT GGAGAGAACC ACTTAATATT GAACCTTAAAG 120  
 AAGACATTTT ATCCTATATG GAAAAAATTTT GGCTTAAAAA ACACAGGAGA ACTCCACAAG 180  
 30 AGCAACTTTT TAAATATGCTA TCAGATACGT TCCACATCC ACATGAAACC ACTGGTGATG 240  
 CACAGTGTTC TCAAAATGAA AACGATGAAG ATAGTGATGG TGAGGAGACC AAAGTACAAC 300  
 ACACAGCTCT TTTATTGCCA GTAGAAACAT TAAACATAGA GAGAGCTGAA CCATCTCTGA 360  
 AGATAGTCGA ACTGGATGAT ACTTATGAAG AGGAATTTGA AGAAGCAGAA AATATTGTGC 420  
 CTTACAAAGT TAAATTAGCT GATGCAGACA GTCAACGAAG TTGTGCTTTT CATGATTGTC 480  
 AGAAGATAG CTTTCCATAT GAAAAATGGCA TCCATCAACA TCATGTTTTC GATAAGGGAA 540  
 35 AGAGAGACTT CTTAAATCTT TGTCTGAGAA ACAGCTCTAC TTATTATAAA GATAATTCAA 600  
 AAGGAGAAAC TTCAACACA GATTTTGACA ACATCGTGGA TCCTGATGTG TATTCTCTG 660  
 ACATTGAAAA AATTGAGGAA AGCACCTCCT TTGAAAGAAA TTTAAAGGAG AAAAAATAG 720  
 GTTTAGAAAG TAATCAAAAG TCTGATGATT CCTGTGTATC ACTTGAAAGC AAGGACACTT 780  
 40 TGCTAGGTAG AGATTTAGAA AAAGCTCCCA TTGAGGAGAA ATTATCTCAA GACATCAAAG 840  
 AATCCTTGGA ATTGAGCAAT CTGTATAAGA GGCCAAGCTT TGAAGAATCA AAAACTACAA 900  
 AGTCATCATC GTTGTACAA GAAATAGCCT GCAGAAGTAA GCCTATAACA AAACAATATC 960  
 AAGGACTTGA GAGATTCTTT ATTTTGATA CAAATGAAAG ACTCAACTTA CTTCCTCTC 1020  
 ATCGTTTGA ATGCAACAAT TCCAGTACTA GGATTACACT TGCAGAGAC AGAGAATGGA 1080  
 45 TTCCAGACCA TAGCTTAAGT GAATATGCTG ATAATGCAAT TGTCTTGGGT GTTCTGCAGG 1140  
 GTGCTCAGAG TCCATCATCA AGTAGAAAAC AGCAAAAGAT GGGTCAGAAA TCACAGAGAC 1200  
 CTTCAACAGC AAATTTTCCA CTTTCCAAC TGTGTAAGA AAGCTCCAGT TGCCCTTCAT 1260  
 CCTCTCATCC TCGATCAAGA AGTGCAGCTG CTCATCATC ATCTAGAGCT GCTTCTGAAA 1320  
 TTTCAAGAA TGAATATATT GATATTACTG ACCAGAATGA GCTTTCCTTA GATGACACTA 1380  
 50 CTGATCAACA TACTTTAGAC AATTTGGAAG AAGAATTACA AGTGCTGAGA TCTCTTGAG 1440  
 ATACTTCAGA AAAGCTTTAC AGCTTAACCT CAGAAGAGTT CCCGATTTC AGCAGCCAA 1500  
 CACTGAATAT AAGTCAGATT TCCACAGATT TCCTTAAGAC CTCACATGTG AGGGGTCCCT 1560  
 GTGGAGTTGA GGAATTGAGC TGTCTGGAAG GAGATACCAA AATTCAGTCT TTGCTGTCTC 1620  
 TTTCTGAGAG CAGTACAGAT GAGGAGGAGG AAGATTTTCT CAACAAGCAA CATGTCATCA 1680  
 55 CACTACGCTG GTCAAAGAGT ACTTAAAGAT TATTTGTGTA TTACTGTTTC CATTTTGATC 1740  
 CCAGAGTAAA GCAACAACCT GAGAAAAGTA ACCAAGTGAT TACCTATCCA AGTGCTGGAG 1800  
 ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAATAAAG TAAATTATA 1860  
 AGTTCAAAAA AAAAAA AAAA 1884

60 Seq ID NO: C58 DNA Sequence  
 Nucleic Acid Accession #: NM\_005408.1  
 Coding sequence: 76..372

65 1 11 21 31 41 51  
 AAAAGGCCGG CGGAACAGCC AGAGGAGCAG AGAGGCCAAG AAACATGTGT AAATCTCCAA 60  
 CTCTTAACCT TCAACATGAA AGTCTCTGCA GTGCTTCTGT GCCTGCTGCT CATGACAGCA 120  
 GCTTTCAACC CCCAGGGACT TGCTCAGCCA GATGCACTCA ACGTCCCATC TACTTGCTGC 180  
 70 TTCACTTTA GCAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACCACC 240  
 AGCAGGTGTC CCCAGAAGGC TGTCTCTTC AGAACCAAC TGGGCAAGGA GATCTGTGCT 300  
 GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCGGAAA AGCTCACACC 360  
 CTGAAGACTT GAACCTCTGT ACCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT 420  
 TCCATTCTCC TCTGGCCTCC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT 480  
 AGGATGCATT CGGTTTGTG ATTCAAAATG TACTATGTGT TAAGTAATAT TGGCTATTAT 540  
 75 TTGACTTGTT GCTGGTTTGG AGTTTATTTG AGTATTGCTG ATCTTTTCTA AAGCAAGGCC 600  
 TTGAGCAAGT AGGTGTCTGT CTCTAAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT 660  
 GGGTTTGAT TGGTTTCCCA GGGGTTGAGA GCATGCCTGT GGGAGTCATG GACATGAAGG 720  
 GATGCTGCAA TGTAGGAAGG AGAGCTCTTT GTGAATGTGA GGTGTTGCTA AATATGTTAT 780  
 80 TGTGGAAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATTT 840  
 AAAATCTCCA AAAAAA AAAA 860

Seq ID NO: C59 DNA Sequence  
 Nucleic Acid Accession #: AK097746.1  
 Coding sequence: 185..2224

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1      11      21      31      41      51
5      CTTTCATGAC AGTAACAAAT CCAAGATTTT GGAAAAGGCG CTACGATATT TAAATGACCA 60
      CTTTCATATAC AACTTATATT GTAATATATG CCGATCAGTA TTTGAGAAGG ACAAGCTGTT 120
      ATTTTCCTTT TTATTATGTG CCAATCTTCT TCTGGCAAGG AAAGAGATTG AATACCAGGA 180
      ACTGATGTTT CTTTAACTG GAGGAGTAAG TCTTAAAGT GCTGAGAAAA ATCCTGATCC 240
      AACTTGGCTA CAGGACAAAA GCTGGGAGGA AATCTGTGCG GCAAGTGAAT TTCCTGCCTT 300
      CAGAGGACTC AGGCAACATT TTTGTGAACA TATATATGAA TGGCGAGAAA TCTATGACAG 360
10     TAAAGAGCCA CATAATGCTA AATTTCCAGC ACCAATGGAT AAGAACCTAA ATGAATACA 420
      GAAAATAATA ATTCCTGGGT GTTTAAGACC TGATAAGATA ACCCCAGCTA TAACAAACTA 480
      TGTAACTGAC AAAC TAGGGA AAAAGTTTGT AGAGCCTCCA CCATTGATT TGACAAAGAG 540
      TTACTTGGAT TCAAATGGCA CCATTCCCTT AATTTTGTGTT CTATCTCCAG GAGCAGATCC 600
      TATGGCCAGC CTGCTGAAAT TTGCAATGA TAAATCTATG TCTGGAAATA AGTTTCAAGC 660
15     TATTTCACTG GGACAGGGAC AAGGACCGAT TGCAGCAAAA ATGATTAAAG CAGCAATTGA 720
      AGAAGGAACCT TGGGTGTGCC TACAGAATTG CCATCTTGCA GTGTCTCGGA TGCCCATGTT 780
      GGAAAAAATA TTGAAGATT TTACCTCTGA AACCTGTAAC TCATCCTTTA GGCTTTGGCT 840
      GACAAGCTAT CCATCTTCAA AATTCOCAGT AACAACTCTA CAGAATGGAG TAAAAATGAC 900
      TAATGAACCT CCCACGGGTC TTCGGCTGAA TCTCCTTCAA TCATATCTCA CTGATCCAGT 960
20     TTCTGATCCT GAGTTTTCAT AGGGATGCGG TGGAAAGGAA CTGTTATTTA TCAATGAATA 1020
      TGATACAAAT CCATTGGAAG CTATATCTTA CCTGACTGGG GAGTGTAAAT ATGGAGGAAG 1080
      AGTGACAGAC GATTGGGACA GACGTCTTCT ATTAACCATG CTGGCTGACT TTTATAATCT 1140
      GTACATAGTT GAAAACCCCTC ATTATAAGTT TTCTCCCACT GGAACCTATT TTGCACTCC 1200
25     TAAAGGCAC TATGAGGACT ACATTGAATT CATTAAAGAA CTTCCTTTA CTCAACACCC 1260
      TGAGATATTT GGATTACATG AAAACGTTGA CATCTCCAAG GATCTTCAAC AAACAAAAAC 1320
      CCTCTTTGAG TCCTTGTCTC TCACCCAGGG AGGCTCCAAA CAGACAGGAG CCTCAGGAAG 1380
      TACTGATCAG ATTCTGTTAG AAATTACCAA AGATATCCTC AACACGCTCC CTAGTGATT 1440
      CGACATTGAA ATGGCACTAC GGAAGTATCC TGTGAGATAT GAAGAAAGCA TGAATACTGT 1500
      GTTAGTACAA GAAATGGAAA GATTTAACAA TTTAATTATA ACTATACGTA AACTCTACG 1560
      GGACCTTGAA AAGGTTATTA AGGGTGTGGT TGTGATGGAT TCTGCATTGG AGGCATCTCT 1620
      CAGTAGCTTA CTGTGTGGA AGGTTCAGGA AATATGGGCC AAACGTTTAT ACCCAAGCCT 1680
      TAAGCCCTCG GGAAGTTACA TCACAGATT TCTAGCCCGG TTGAACCTTT TACAGCACTG 1740
      GTATAATTCA GAAAAACCTT GTGTGTTTTG GCTGTCAAGT TTCTTTTTC CACAGGCCTT 1800
      TTTAACTGGA GCTATGCAGA ATTATGCCAG AAAATATACC ACCCCTATTG ATTTGCTAGG 1860
35     ATATGAATTT ATAAAGTATC CATCTGATAC ATCTGACACA TCACCAGAA ATGGTGTTTA 1920
      TATCCACGGA CTGTATCTCG ATGGCGCAGC CTGGACCGGA GAAAGTGGAT TGCTTGTCTGA 1980
      ACAATATCCC AAATCTCTGT TTGACCTGAT GCCCATCATA TGGATAAAAC CAACTCAAAA 2040
      ATCTCGGATT ATGAGTTCGG ATGCCCTATG CTGTCCCTTC TACAAGACAA GTGAACGTAA 2100
      AGGAACCTCT TCCACTACGG GACATCTAC TAACTTTGTC ATTGCAATGT TGTTAAAAAC 2160
40     AGACCAACCT ACTCGGCACT GGATCAAGCG CGGGGTGCT TTGCTTTGTC AGTTGGATGA 2220
      CTAAATTTGA CAAATTTATA AAACATCCAA AAGTTT 2256

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Seq ID NO: C60 DNA Sequence  
Nucleic Acid Accession #: J02761.1  
Coding sequence: 14..1159

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1      11      21      31      41      51
50     GAATTCGGGT GGCATGGCTG AGTCACACCT GCTGCAGTGG CTGCTGCTGC TGCTGCCAC 60
      GCTCTGTGGC CCAGGCACTG CTGCCCTGGAC CACCTCATCC TTGGCCTGTG CCCAGGGGCC 120
      TGAGTTCCTG TGCCAAAGCC TGGAGCAAGC ATTGCAGTGC AGAGCCCTAG GGCATTGCC 180
      ACAGGAAGCT TGGGACATCG TGGGAGCCGA TGACCTATGC CAAGAGTGTG AGGCATGCT 240
      CCACATCCTT AACAAAGATG CCAAGGAGGC CATTTTCCAG GACACGATGA GGAAGTTCT 300
      GGAGCAGGAG TGCAAGCTCC TCCCTTGAA GCTGCTCATG CCCAGTGA ACCAAGTGCT 360
55     TGACGACTAC TTCCCTCTGG TCATCGACTA CTTCAGAAC CAGACTGACT CAAACGGCAT 420
      CTGTATGCAC TGGGCGCTGT GCAAAATCCG GCAGCCAGAG CCAGAGCAGG AGCCAGGGAT 480
      GTCAGACCCC CTGCCAAAC CTCTGCGGGA CCCTCTGCCA GACCTCTGCT TGGCAAGCT 540
      CGTCTCCTCT GTGCTGCGCG GGGCCCTCCA GGGGAGGCTT GGGCTCACA CACAGGATCT 600
      CTCGAGCAG CAATTCCCCA TTCTCTGCC CTATTGCTGG CTCTGACGG CTCTGATCAA 660
60     GCGGATCCAA GCCATGATTC CCAAGGGTGC GCTAGCTGTG GCAGTGGCCC AGGTGTGCG 720
      CGTGGTACCT CTGGTGCGCG GCGGCATCTG CCAGTGCTCG GCTGAGGCTT ACTCCGTCAT 780
      CCTGCTCGAC AGCTGCTGCG GCGGCATGCT GCCCAGCTG GTCTGCGGCC TCGTCTCTCG 840
      GTGCTCCATG GATGACAGCG CTGGCCCAAG GTGCGGACA GGAAGATGGC TGCCGCGAGA 900
      CTCTGAGTGC CACCTCTGCA TGTCCGTGAC CACCCAGGCC GGAACAGCA GCGAGCAGGC 960
65     CATACCACAG GCAATGCTCC AGGCCTGTGT TGGCTCTGCG CTGACAGGG AAAAGTGCAA 1020
      GCAATTTGTG CAGCAGCACA GCCTCCAGCT GCTGACCTCG GTGCCAGGG GCTGGGATGC 1080
      CCACACACCT TGCCAGGCC TCGGGGTGTG TGGGAACATG TCCAGCCCTC TCCAGTGTAT 1140
      CCACAGCCCC GACCTTTGAT GAGAACTCAG CTGTCCAGCT GCAAGAGAAA AGCCAAGTGA 1200
      GAOGGCTCTT GGGACCATGG TGACCAAGCT CTTCCTCTGC TCCCTGGCCC TCGCCAGCTG 1260
70     CCAGGCTGAA AAGAAGCCTC AGCTCCACCA CCGCCCTCCT CACCTCCCTT CCTCGGCAGT 1320
      CACTTCCACT GGTGGAGCCG GGGCCCCCAG CCCTGTGTG GCTTGTGCTG TCTCAGCTCA 1380
      ACCACAGTCT GACACAGAG CCCACTTCCA TCCTCTCTGG TGTGAGGCAC AGCGAGGGCA 1440
      GCATCTGGAG GAGCTCTGCA GCCTCCACAC CTACCAAGAC CTCCAGGGC TGGGCTCAGG 1500
      AAAAAACGAC CACTGCTTTA CAGGACAGGG GGTGAAGCT GAGCCCGGCC TCACACCCAC 1560
      CCCCATGAC TCAAGATTG GATTTTACAG CTACTTGCAA TTCAAAATTC AGAAGATAA 1620
75     AAAAAAGGAA CATACAGAAC TCTAAAGAT AGACATCAGA AATTGTTAAG TTAAGCTTTT 1680
      TCAAAAAATC AGCAATTCOC CAGGTAGTC AAGGTGAGC ACTGCAGCT CTGGCATGAT 1740
      GGGATGGCGA CCGGGCAAGC TTTCTTCTC GAGATGCTCT GCTGCTTGAG AGCTATTGCT 1800
      TTGTTAAGAT ATAAAAAGG GTTTCTTTT GTCTTTCTGT AAGGTGGACT TCCAGATTTT 1860
      GATTGAAAGT CCTAGGGTGA TTCTATTTCT GCTGTGATTT ATCTGCTGAA AGCTCAGCTG 1920
80     GGGTGTGCA AGCTAGGGAC CCATTCTGT GTAATACAAT GTCTGCACCA ATGCTAATAA 1980
      AGTCTTATTC TCTTTTAAAA AAAAAAAGG AAAAAAACG GAATTC 2026

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Seq ID NO: C61 DNA Sequence

Nucleic Acid Accession #: NM\_139172.1  
Coding sequence: 19..552

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5      1      11      21      31      41      51
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      GGGGTCCTGGG GAGGTGACAT GTTGGGCTGT GGGATCCCAG CGCTGGGCTT GCTCCTGCTG 60
      CTGCAGGGCT CGGCAGACGG AAATGGAATC CAGGGATTCT TCTACCCATG GAGCTGTGAG 120
      GGTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC 180
      TGCTGCGTC TCGGTGCTG CTACCGCAAT GGGGTCTGCT ACCACCAGCG TCCAGACGAA 240
10     AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGGAAGT GCAGGGGCTT CCTCTCTCTG 300
      AGCTGCAGCA TCTGCTTGTT CTGGTGGGCC AAGCGCCGGG AGCTGCTGCA TATGCCCGGT 360
      TTCTTGGCGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCAA GCACCGAGGG 420
      ACCAAGAAGA CGCCGTCCAC GGGCAGCGTG CCAGTCCGCC TGTCCAAGA GTCCAGGGAT 480
      GTGGAGGAG GCACCGAGGG GGAAGGGACG GAGGAGGGTG AGGAGACAGA GGGCGAGGAA 540
15     GAGGAGGATT AGGGGAGTCC CCGGGGAGCT GCTCAATACA GATACGGTGG ACG 593

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Seq ID NO: C62 DNA Sequence  
Nucleic Acid Accession #: NM\_054023.2  
Coding sequence: 98..379

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20     1      11      21      31      41      51
      |      |      |      |      |      |
      GGGGACACTT TGTATGGCAA GTGGAACCCAC TGGCTTGGTG GATTTTGCTA GATTTTCTG 60
      ATTTTAAAC TCCTGAAAAA TATCCAGAT AACTGTCTAT AAGCTGGTAA CTATCTTCTT 120
      GCTGGTGACC ATCAGCCTTT GTAGTTACTC TGCTACTGCC TTCCTCATCA ACAAAGTGCC 180
      CCTTCTCTGT GACAAGTTGG CACCTTTACC TCTGGACAAC ATCTCTCCCT TTATGGATCC 240
      ATTAAGCTT CTCTGAAAAA CTCTGGGCAT TTCTGTGAG CACCTTGTGG AGGGGCTAAG 300
      GAAGTGTGTA AATGAGCTGG GACCAGAGGC TTCTGAAGCT GTGAAGAAAC TGCTGGAGGC 360
      GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGAAGATGA 420
      TGCTCCTATC TCCTCTGCCT GAAACCTGTT CTACCAATTA TAGATCAAAAT GCCCTAAAAA 480
      GTAGTGACCC GTGAAAAGGA CAAATAAAGC AATGAATACT AAAAAAAAAA AAAAAAAAAA 540
      AAAAAAAAAA

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35 Seq ID NO: C63 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2874

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40     1      11      21      31      41      51
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      ATGCCCTCTG CTATGCTCTA TAAAAACGCT GAGACCTAG CAGGCAGACA CACAAGCAGC 60
      TGGATGTCGA GAGGAGCATA TCAGCGGAGG AACACACGGG CAGCTGGAGC TCCAGAGGAA 120
      TGCACTGACA GAAACTGGCA TGCTGGCAGA ACACGTGGAA TTTGGCTGGG GCAGTTGGAG 180
      GAGAGATGTT CAGATGTGTT CGGAGTTTCT TTCTTCTGTT GGGTTCTGGT TCTCGCTGGC 240
      TCAGGAGCGA AGCTCGAGAC CTTCAGCCCA GCCCAGGAAG GGGCTCCCACT AGTGCAAGCG 300
      CAGGCTGAAG CGCTCTGAA GTGCCGCCAG AGTGGGCGTC CAGGCAGAGG AGGCGCCGAG 360
      AGCGAGCGAG CGAGGGATGC CAGCATGCTG TCACCTCTCA GTGCTGCCAT GCGAAACTAC 420
      CCAAGCTCCT CTACCATCCC TCCAAGAAGA TCCTACTCTC CAACGAAAT TGCTCACAAG 480
      AGTTACTCCT GCAGCCTTCC AGACATGAAA ATCTCCATGG CAGAATCTGG CCCCTCCTTG 540
      GATAGCCTTG ACATTCTGGA GGATGGCGAG TCTGGGTAC CATTCTTGT GACTCATTTG 600
      TACTTTCTGG GGGTTGTGAC CACTGGGATG GAACAACTAG ATTTGAAAC AGGACCAAAC 660
      ATATTTGATT TGCAGATTTA TGTGAAGGAT GAGGTGGTG TCACAGACCT GCAAGTCCTG 720
      ACTGTCCAGG TAACAGATGT GAACGAGCCA CCTCAGTTTC AAGGCAACTT GGCAGAAGAT 780
      CATCTCCGTT CAGACCCAGC ACATTTCAAT GCTCATAGTC ACACGTACGT GAGGGTAGTG 840
      GCTACTGCTAT TGGCCAGGCA CAGGCTTAGA TCTAGCAATT GTTCCCTCTT CCTGGGCACC 900
      TTCTGTGTTG TGGTGGGCAT GCAGTATTTC CTGATTTCTC CCCCAAGAG CTTCAGAATG 960
      TCTGCTAATG GCACCTCTT CTCCACAACA GAATTGGACT TTGAAGCAGG ACACAGAAGT 1020
      TTCCATCTCA TCGTGGAGGT GAGGGACAGT GGAGGCCCTA AAGCCTCCAC AGAGCTCCAG 1080
      GTGAACATCG TGAACCTCAA CGACGAAATC CCGCTCTTTC CCAGCCGAC ACAGGTGTAC 1140
      ACAGTCTCGG AGGAACTGAG TCCAGGAACC ATCGTGGCCA ATATCACAGC GGAGGATCCT 1200
      GATGATGAAG GTTTTCCAG CCACCTCCTC TACAGCATTA CCACTGTTAG CAAATATTTC 1260
      ATGATAAATC AGTTGACTGG TACAATCCAA GTGGCCCAA GGATAGACCG AGATGCAGGT 1320
      GAATTGAGAC AAAATCCAC CATTTCCCTG GAAGTCTAG TGAAGGACAG ACCATATGGG 1380
      GGTCCAGGAG ATCGCATCCA GATAACCTTC ATTGTGGAAG ACGTCAACGA CAATCCTGCC 1440
      ACATGCCAAA AGTTACCTT CAGATCCAGT CTCACCCCTG CTCTGTGCTC CAAGAAGCTG 1500
      ACCTGGATGG ATACCGTATT AGACTGTTT CATGCTGCTG ATAAAGATAT ACCTGTGACT 1560
      GGGCGATTTA CAAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAAGC 1620
      CTCACAATCA TGGCAGAAGG CAAGGAGGAG CAAGTACAT CTTACATGGA TGGCAGCAGG 1680
      CAAAGAGATA GAGCTTGTGT AGGGAAACTC CTCCTTATAA AGCCATCAGA TCTCATGAGA 1740
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      AATTTCAAGC TGACATGTAC CGAOCCTGAT TCCAGCCCA GATCTTTCCG TTATTCCATT 2040
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      CGCTGCTGCG TTACATCTCG CTTTGACTAT GCTGGTGGGT TTGATAAGAT CTGGGACTAC 2160
      AAGCTACTTC TCTACGTAA TCATGACAAC TGATGTCTG ACAGGAAGAA AGCGGAGGCT 2220
      CTTGTTGAGA CAGGAACAGT GACACTGAGT ATTAAGATCA TTCCCAACCC AACCACTATC 2280
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      CTGCTGATCC TGGTGTCTCT ATTGGCCAAA GCCATCCACA GACACTGCCC CTGCAAGACT 2460
      GGGAGAGACA AGGAACCTCT GACAAAGAAA GGAGAAACGA AGACTGCAGA GAGAGACGTC 2520
      GTGGTGGAAA CTATCCAGAT GAACACTATC TTTGATGGAG AAGCCATAGA TCCAGAGCCT 2580
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GCTGAACGGT GCATTGGATT GGTCTCTAGT CTGAAAAAGT ACAGTTCTGA TTAA 2874

5

Seq ID NO: C64 DNA Sequence  
Nucleic Acid Accession #: XM\_168571.1  
Coding sequence: 155..988

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20 GCCGCAATA AATATACGGT GATAATCCAG GTGCAGGATG TGGCCCCCCC TTACTATAAA 600  
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45 ACTACAGAAAT GTGCTGATG GCTCATGCCT GTAATGCCAG CACTTTGCCA AGGTGGGCAG 2100  
ATCACCTAAG GTGAGGAGTT CAAGATCAGC CTGGCTTAGA TGGCAAAACC CTGTCTCTAC 2160  
TAAAAAATAC AAAAATTAGC TTGGTGTGGT GGTGGGCACA TGTAATCCCA GCTACTTGGG 2220  
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Seq ID NO: C65 DNA Sequence  
Nucleic Acid Accession #: NM\_005266.3  
Coding sequence: 122..1198

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1 11 21 31 41 51  
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60 GATGGGCGAT TGGAGCTTCC TGGGAAATTT CCTGGAGGAA GTACACAAGC ACTCGACCGT 180  
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TGCTGAGTCT TCCTGGGGGG ATGAGCAGGC TGATTTCCGG TGTGATACGA TTCAGCCTGG 300  
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65 GCAGATCATC TTGCTCTCCA CGCCCTCTCT GGTGTACATG GGCCAAGCCA TGCACACTGT 420  
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70 CACCCTGCAT GTCTGCGCGA GGAGTCCCTG TCCCACCCCG GTCAACTGTT ACGTATCCCG 720  
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5 AAAGTTCOCA GCCAATAGAC AGCATGAATC AAGGAACTTG CATTATATGT GCTCTTGAAT 1680  
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 10 GCTGTTGTCC TCTCTCGAAC CCGTACCAGA TCATCAGCA CTGAGGCCAG TGAATTTTCC 2160  
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Seq ID NO: C66 DNA Sequence  
 Nucleic Acid Accession #: NM\_014459.2  
 Coding sequence: 738..3407

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 TTTTCATCAG GGAGGCGAGC AGCAAGTAAG AATTTCACTT TCGGATCTGC CTAGAGACAC 240  
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5 TCCGATCAG ATGGCAAGGG TCTTTGCAGA TGTGCATTCC AGAGCCAGCC GGGATTCCAG 4080  
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 15 ATAAACACAA GGAACATTCC ATATCATTAG TCGAAAACAA AAACAAAAAA AAAACCTTTG 4860  
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Seq ID NO: C67 DNA Sequence

Nucleic Acid Accession #: NM\_005601.2

Coding sequence: 101..598

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Seq ID NO: C68 DNA Sequence

Nucleic Acid Accession #: NM\_006433.2

Coding sequence: 129..566

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 50 GTCTGCTCTT CTCTGCTCTG AGCCCTGAGT ACTACGACCT GGCAGAGCC CACTGCGTGT 240  
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 AGATGTTGGA TAAGCCCAAC CAGAGAAGTG TTTCCAATGC TGCGACCCCG GTGTGTAGGA 420  
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 CTCCTGTCTT CAGATCCCGG GAACCTCAGC AACCTCTGCC GGCTCTCGC TTCTCTGATC 660  
 CAGAAATCCAC TCTCCAGTCT CCTCCCTCTG ACTCCCTCTG CTGTCTCTCC CTCTCACGAG 720  
 AATAAAGTGT CAAGCAAG 738

Seq ID NO: C69 DNA Sequence

Nucleic Acid Accession #: NM\_002985.2

Coding sequence: 69..344

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 65 1 | 11 | 21 | 31 | 41 | 51  
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 70 GCGCTCCTGC ATCTGCTCTC CCATATTCTT CGGACACCAC ACCCTGCTGC TTTGCCTACA 180  
 TTGCCCGCCC ACTGCCCGGT GCCCACATCA AGGAGTATTT CTACACCACT GGCAAGTGCT 240  
 CCAACCCAGC AGTCGTCTTT GTCAACCGAA AGAACCGCCA AGTGTGTGCC AACCCAGAGA 300  
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 GAGGCCAAGG TGGGTGGATC ACTTGAGGTC AGGAGTTGGA GACCAGCCTG GCCAACATGA 600  
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TGTGACCAGG AAGGAAGTCA GCATGCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACCTC 1140  
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 TACCATTAAA GTTCTCAATG CAACCATAAA AAAAAA 1237

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Seq ID NO: C70 DNA Sequence  
 Nucleic Acid Accession #: NM\_022154.2  
 Coding sequence: 1381..1722

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CATATGTACG	CAAACTCTGG	GGCGTTTGCA	AACCCGGATC	CGGGGCGTCT	GGCCCCATGC	120
CCGGCCGGGC	TTTGTAGGGC	TACTGCCACG	CAGCGTTTCT	GGAGCCTGCC	GGCTGGTGCC	180
CTGGTGGCCT	TATCTCTGTG	CCCCCTTTGT	CCTCTTTATC	TCAGGCTCTC	CAGGAGGCGG	240
GGGGGCCAC	TCCGCTATC	GCTCCCTCG	GCTACGCTGC	CACTCCAATG	CCCGGAGGCT	300
GGGAGCTCG	TGTTCTTTGG	AAGGCGCCGG	AGAACCCAGG	GGGTCCCGCG	CCACCTCTGA	360
CTCGAGCAG	CGCCGAGCAC	TGACGCTCCC	GGCCTTGGGC	AAGGACGCCA	GTGGGCCCGC	420
CGCGCTCCCT	CTGGCGGGCA	GGCCGTGCGC	GGCCCTCAAG	GGGAAGCCCA	GGCCAGGATG	480
GCCCGGGTTC	GCGCGGTGGC	CGGGCTCCTG	TTGCTGGCGG	CGCCCGGCTC	CGGAGGAGTG	540
GCGGAGGGGC	CAGGGCTAGC	CTTCAGCGAG	GATGTGCTGA	GGGTGTTCCG	CGCGAATCTG	600
AGCCTGTCCG	GCGCGCAGCT	CCAGCACTTG	CTGGAGCAGA	TGGGAGCCGC	CTCCCGCGTG	660
GGCGTCCCGG	AGCCTGGCCA	GCTGCACCTC	AACCACTGTT	TAACTGCTGA	AGAGATCTTT	720
TCCCTTCATG	GCTTTTCAAA	TGCTACCCAA	ATAACCAAGT	CCAAATTCCT	TGTCATCTGT	780
CCAGCAGTCT	TACAGCAATT	GAACCTTCAC	CCATGTGAGG	ATCGGCCCAA	GCACAAAAAC	840
AGACCAAGTC	ATTGAGAGT	TTGGGGATAT	GGATTCTCTG	CAGTGACCAT	TATTAACTCTG	900
GCATCTCTCC	TGGGATTGAT	TTTGAATCCA	CTGATAAAGA	AATCTTATTT	CCCAAGAGTT	960
TTGACCTTTT	TTGTGGGGCT	GGCTATTGGG	ACTCTTTTTT	CAATGCAAT	TTTCCAACTT	1020
ATTCCAGAGG	CAITTTGGATT	TGATCCCAAA	GTGACAGATT	ATGTTGAGAA	GGCAGTTGCT	1080
GTGTTTGGTG	GATTTTACCT	ACTTTTCTTT	TTTGAAGAGG	TGCTAAAGAT	GTTATTAAGA	1140
ACATATGGTC	AGAATGTGCA	TACCCACTTT	GGAAATGATA	ACTTTGGTCC	TCAAGAAAAA	1200
ACTCATCAAC	CTAAAGCATT	ACCTGCCATC	AATGGTGTGA	CATGCTATGC	AAATCCTGCT	1260
GTACAGAAAG	CTAATGGACA	TATCCATTTT	GATAATGTCA	GTGTGGTATC	TCTACAGGAT	1320
GGAAAAAAG	AGCCCAAGTTC	ATGTACCTGT	TTGAAGGGGC	CCAACTGTGC	AGAAATAGGG	1380
ACGATTTGCT	GGATGATAAC	GCTCTGCGAT	GGCCTCCACA	ATTTCATCGA	TGGCCTGGCG	1440
ATTGGGGCTT	CCTGCACCTT	GTCTCTCTCT	CAGGGACTCA	GTACTTCCAT	AGCAATCCTA	1500
TGTGAGGAGT	TTCCCCACGA	GTTAGGAGAC	TTTGTGATCC	TACTCAATGC	AGGGATGAGC	1560
ACTCGACAAG	CCTTGCTATT	CAACTTCCTT	TCTGCATGTT	CCTGCTATGT	TGGGCTAGCT	1620
TTTGGCAATT	TGGTGGGCAA	CAATTTGCTG	CCAAATATTA	TATTGCACT	TGCTGGAGGC	1680
ATGTTCTCTT	ATATTTCTCT	GGCAGATATG	TTTCCAGAGA	TGAATGATAT	GCTGAGAGAA	1740
AAGTAACTG	GAAGAAAAAC	CGATTTCACC	TTCTTCATGA	TTCAAGATGC	TGGAATGTTA	1800
ACTGGATTCA	CAGCCATTCT	ACTCATTACC	TTGTATGCAG	GAGAAATCGA	ATTGGAGTAA	1860
TAGAAATGAG	AAGATGGTGT	TGTTAATAAA	GGCATTTAAT	AGATAAAAAAC	ATCTCCAAAA	1920
AGGATTTTGA	AGCTGATCCT	ATTAGTTTAA	AAAGATAATT	TTGCTTTCAA	CTGTAGGTCC	1980
AGAAAACTAA	TATTGGCAT	CAGTCTGTGA	AATAGTCCAT	TATTTGTTGT	TAAAAATGCT	2040
TCAAAAGGTT	TTCAAGTGCA	GTCTGAGATG	CCTGGTATAT	AGGAGCCTTT	GGGAAATACT	2100
TATTTTTCAG	TATTCATGTC	ATATTAGATA	TCACCATGAA	GCAAGAGACA	TGCAATCTAT	2160
AATCATGTAG	CACACTCAGC	TCAGGGGAAA	ATACAAGTTA	TATCCTGAAA	GCCTTTAAAA	2220
CTCTATGGTA	GGATCAAGA	TTCAATGGT	TTCAAGAGG	TTTTATTCTA	ATTAATTTGT	2280
TCTAGTGCTT	TCAGAGGCAA	GTACATCAAA	ATGTAGAAGG	TAAAAATGAT	GCAACACTAA	2340
TATAAATTAT	TCCAAGTCTT	TAAGGAGCCA	AAGAAAAAAA	AGATTTCTCA	CAGCTTTTGT	2400
TTCTGTTTGT	TATTTCAATT	AGGAACCTGC	AGTATTATTT	TGAAAAACAT	TCTAAAAATA	2460
TAGGAGTTAG	AGAAATAAATA	AAGTTTGTCT	AGCCCTGCTA	AGTTCAAGCT	TAGAGGCTTA	2520
TCGCTAAGTN	TAACTCTCAC	CAGATTCCAC	GMAAGCTGG	ATAGCTTTTT	TTCTGACTTA	2580
TGTTGTGGTT	GCACCCCTCA	CAATGGCAG	AACAGTATGT	AAAGCTGGTA	ACACCTCGGT	2640
TTCACTGCAC	CATGTGTTTG	CTTTGTGAAG	GTGAAGAATA	TGTTGGTTTA	GAGAAAGAAA	2700
TTGGATGTAA	TTTTATGCAA	TTTACTTTTA	AAGACAAACA	TAACTATTTA	GCAGAGAATA	2760
TTTTATAAAA	TGCAAAACAA	CAGCTGGACT	GCTGTACATC	AAGGACAGAT	TAACTGGAAA	2820
ACATATGTTC	CTTATGTGTG	ATTGAGAGCC	ATTGAGAAAA	GACTTCCTTT	GTGTTCAAGC	2880
TATACTTTTC	CATATGGTAT	ACCTTGAAAA	AAATTAGCAC	ACCATGGTTA	TTTTTCTACC	2940
TTTTATAAAA	GACAGAGCCT	GTTTACTCAT	TTAGAAGATA	GAGAAAATTG	GTCTAAAAAT	3000
GAACATCCTA	GATTCACACT	CCCAAGTCAC	TTAAGGTGAT	TTGATGGTGA	GGAAATGAT	3060
TGACAAAGCC	CAACAATGAT	CTCAGGAATT	ACATTTTCCA	ACAGACCAAA	AAATGTTTTT	3120
ATGTAGCAGC	AATGCAAGAT	TGGTGAATAT	TTAATATATA	TTTTAGTATG	TATTTCACTT	3180
TATGACTGAC	AATTAAAAAA	TATTTGTTGG	CCAAATAGTA	AACACCTTTT	TGAAACCATG	3240
AAAAAA						3246

Seq ID NO: C71 DNA Sequence  
 Nucleic Acid Accession #: NM\_004184.2  
 Coding sequence: 188..1603

1	11	21	31	41	51	
CGAAAAAAGA	GGGGAAGAGT	ATTAAAGACC	ATTTCTGGCT	GGGCAGGGCA	CTCTCAGCAG	60
CTCAACTGCC	CAGCGTGACC	AGTGCCACCC	TCTGCACTGT	CTTCCACAA	CTGGTCTTGA	120
CTGCTCTGCT	GAACAAATCC	TCTGACCTCA	GGCCGGCTGT	GAACGTAGTT	CCTGAGAGAT	180
AGCAAAACATG	CCCAACAGTG	AGCCCGCATC	TCTGCTGGAG	CTGTTCAACA	GCATCGCCAC	240
ACAAGGGGAG	CTGTAAAGGT	CCCTCAAAGC	GGGAAATGCG	TCAAAAGGATG	AAATTGATTC	300
TGCAGTAAAG	ATGTTGGTGT	CATTAAAAAT	GAGCTACAAA	GCTGCCGCGG	GGGAGGATTA	360
CAAGGCTGAC	TGTCCTCCAG	GGAACCCAGC	ACCTACCACT	AATCATGGCC	CAGATGCCAC	420
AGAAGCTGAA	GAGGATTTTG	TGGACCCATG	GACAGTACAG	ACAAGCAGTG	CAAAAGGCAT	480
AGACTACGAT	AAGCTCATTG	TTCCGTTTGG	AAGTAGTAAA	ATTGACAAAG	AGCTAATAAA	540
CCGAATAGAG	AGAGCCACCG	GCCAAAGACC	ACACCACTTC	CTGGCGCAGG	GCATCTTCTT	600



5	CTCACACAGA	GATATGAATC	AGGTTCTTGA	TGCCTATGAA	AATAAGAAGC	CATTTTATCT	660
	GTACACGGGC	CGGGCCCCCT	CTTCTGAAGC	AATGCATGTA	GGTCACCTCA	TTCCATTAT	720
	TTTCACAAAG	TGGCTCCAGG	ATGTATTATA	CGTGCCCTTG	GTCACTCCAGA	TGACGGATGA	780
	CGAGAAGTAT	CTGTGGAAGG	ACCTGACCCCT	GGACCCAGGCC	TATGGCGATG	CTGTTGAGAA	840
	TGCCAAGGAC	ATCATCGCCT	GTGGCTTTGA	CATCAACAAG	ACTTTCATAT	TCTCTGACCT	900
	GGACTACATG	GGGATGAGCT	CAGGTTTCTA	CAAAAATGTG	GTGAAGATTG	AAAAGCATGT	960
	TACCTTCAAC	CAAGTGAAAG	GCATTTTTCG	CTTCACTGAC	AGCGACTGCA	TGCGGAAGAT	1020
	CAGTTTTCCT	GCCATCCAGG	CTGCTCCCTC	CTTCAGCAAC	TCATTCCAC	AGATCTTCCG	1080
10	AGACAGGACG	GATATCCAGT	GCCTTATCCC	ATGTGCCATT	GACCAGGATC	CTTACTTTAG	1140
	AATGACAAGG	GAGTTCGCC	CCAGGATCGG	CTATCCTAAA	CCAGCCCTGT	TGCACTCCAC	1200
	CTTCTTCCCA	CGCTTCGAGG	GCGCCAGAC	CAAAATGAGT	GCCAGCGACC	CAAACTCCTC	1260
	CATCTTCTTC	ACCGACACGG	CCAGCAGAT	CAAAACCAAG	GTCAATAAGC	ATGCGTTTTC	1320
	TGGAGGGAGA	GACACCATCG	AGGAGCACAG	GCAGTTTGGG	GGCAACTGTG	ATGTGGACGT	1380
15	GTCTTTCATG	TACCTGACCT	TCTTCTCGA	GGACGACGAC	AAGCTCGAGC	AGATCAGSAA	1440
	GGATTACACC	AGCGGAGCCA	TGCTCACCGG	TGAGCTCAAG	AAGGCACTCA	TAGAGGTTCT	1500
	CGAGCCCTTG	ATCGCAGAGC	ACCAGGCCCG	GCGCAAGGAG	GTCAAGGATG	AGATAGTGAA	1560
	AGAGTTCATG	ACTCCCCGGA	AGCTGTCTCT	CGACTTTCAG	TAGCACTCGT	TTTACATATG	1620
	CTTATAAAAG	AAGTGATGTA	TCAGTAATGT	ATCAATAATC	CCAGCCCACT	CAAGCAACCG	1680
20	CCACCTGTAG	GCTTCTGTCT	CATGTAAT	ACTGGGCTGT	GCTCTGTAA	GCTCTGTAT	1740
	GTTATCAATA	CTGTTTCTTC	CTGTGAGTTC	CATTATTCTT	ATCTCTTATG	GGCAAAAGCAT	1800
	TGTGGGTAAT	TGGTGTCTGG	TAACATTGCA	TGGTTCGGATA	GAGAAGTCCA	GCTGTGAGTC	1860
	TCTCCCAAAA	CGAGCCCCAC	AGTGGAGCCT	TCCGCTGGAA	GTCCATGGGC	CACCCGTGTC	1920
	TGTTCATGAG	AGGACTTCCG	AGGGTTCCAA	GTATACTCTT	AAGACCCACT	CTGTTTAAAA	1980
25	ATATATATTC	TATGATGCG	TATATGGAAT	TGAAATGTCA	TTATTGTAAC	CTAGAAAGTG	2040
	CTTTGAAAAA	TTGATGTGGG	GAGGTTTAT	GAGCACAGA	TGTATTTCAG	CCCATGCCCC	2100
	CTCCCAAAAA	GAAATGTGTA	AGTAAAAGCT	TCGTATATCA	TTTGAATAAG	AAATCACCCA	2160
	GCTTTAAAGC	TGCTTTTAA	AATGAAAGAT	GAAACAGATT	CAGCAATTTT	GATTAAATTA	2220
	AGACTTGGGG	GTGAAACTTT	CCAGTTTACT	GAACTCCAGA	CCATGCATGT	AGTCCACTCC	2280
30	AGAAATCATG	CTCGCTTCCC	TTGGCACACC	AGTGTCTTCC	TGCCAAATGA	CCCTAGACCC	2340
	TCTGTCTCTG	AGAGTCAAGG	TGGCTTTTCC	CCTGACTGTG	TCOGATGCCA	AGGAGTCTGT	2400
	GCCTCCGACG	AGCTTTCATT	TTGACCCCTG	GCTGCAGTGG	AAGTCAGCAC	AGAGCAGTGC	2460
	CCTGGCTGTG	TCCTGGACGG	GTGGACTTAG	CTAGGGAGAA	AGTCGAGGCA	CGAGCCCTCG	2520
	AGGCCCTCAC	AGATGCTCAG	GCAGGCCCTCA	TTTCATCACG	CAGCATGTGC	AGGCCCTGGAA	2580
35	GAGCAAAGCC	AAATCTCAGG	GAAGTCCCTG	GTTGATGTAT	CTGGGTCTCC	TCTGGAGCAC	2640
	TCTGCCCTCC	TCTCACCCAG	TAGAGTAAAT	AAACTTCTCT	GGCTCCTAAA	AAA	2693

Seq ID NO: C72 DNA Sequence

Nucleic Acid Accession #: NM\_004938.1

Coding sequence: 337..4632

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45	GCAACTCGCA	GCGGACGGGT	CTGGGGCCCG	CGCCTGGGAG	GGATCTGCGC	CCCCCACTCA	120
	CTCCCTAGCT	GTGTTCCCGC	CGCCGCCCCG	GCTAGTCTCC	GGCGCTGGCG	CCTATGGTCG	180
	GCCTCCGACA	GCGCTCCGGA	GGGACCGGGG	GAGCTCCACG	GCGCCCGGGA	CTGGAGACTG	240
	ATGCATGAGG	GGCCTACGGA	GCGCGAGGAG	CGGTGGTGAT	GGTCTGGGAA	GCGGAGCTGA	300
	AGTCCCTCGG	GCTTTGGTGA	GGCGTGACAG	TTTATCATGA	CGGTGTTTCA	CGAGGAAATC	360
50	GTGGATGATT	ACTACGACAC	CGGCGAGGAA	CTTGGCAGTG	GACAGTTTGC	GGTGTGTAAG	420
	AAATGCGCTG	AGAAAGATAC	CGGCCCTCCG	TATGCCGCCA	AATTCAATCA	GAAAGAGGAG	480
	ACTAAGTCCA	GCGCGCGGGG	TGTGAGCCGC	GAGGACATCG	AGCGGGAGGT	CAGCATCTCT	540
	AAGGAGATCC	AGCACCCCAA	TGTATATCAC	CTGCACGAGG	TCTATGAGAA	CAAGAAGGAC	600
	GTCATCTCTG	TCTTGGAACT	GTTTGCAGGT	GGCGAGCTGT	TTGACTTCTT	AGCTGAAATG	660
55	GAATCTTTAA	CTGAAGAGGA	AGCAACTGAA	TTTCTCAAA	AAATTTCTAA	TGGTGTTCAT	720
	TACCTGCACT	CCCTTCAAT	CGCCCACTTT	GATCTTAAGC	CTGAGAACAT	AATGCTTTTG	780
	GATAGAAATG	TCCCAAAACC	TGGATCAAG	ATCATTGACT	TTGGGTTGGC	CCATAAAATT	840
	GACTTTGGAA	ATGAATTTAA	AAACATATTT	GGGACTCCAG	AGTTTGTGCG	TCTGAGATA	900
	GTCAACTATG	AACCTCTTGG	TCTTGAGGCA	GATATGTGGA	GTATCGGGGT	AATAACCTAT	960
60	ATCCTCTCAA	GTGGGGCCTC	CCCATTTCTT	GGAGACACTA	AGCAAGAAAC	GTTAGCAAA	1020
	GTATCCGCTG	TCAACTACGA	ATTGAGGAT	GAATACITCA	GTAATACCA	TGCCCTAGCC	1080
	AAAGATTTC	TAAGAAGACT	TCTGGTCAAG	GATCCAAAGA	AGAGAATGAC	AATTCAAGAT	1140
	AGTTTGCAGC	ATCCCTGGAT	CAAGCCTAAA	GATACACAAC	AGGCACCTAG	TAGAAAAGCA	1200
	TCAGCAGTAA	ACATGGAGAA	ATTCAAGAA	TTTGACGCCC	GGAAAAAATG	GAAACAATCC	1260
65	GTTGCTTTGA	TATCACTGTG	CCAAAGATTA	TCCAGGTCAT	TCCGTCCAG	AAGTAACATG	1320
	AGTGTGCGCA	GAAGCGATGA	TACTCTGGAT	GAGGAAGACT	CCTTTGTGAT	GAAAGCCATC	1380
	ATCCATGCCA	TCAACGATGA	CAATGTCCCA	GGCCTGCAGC	ACCTTCTGGG	CTCATTATCC	1440
	AACTATGATG	TTAACCAACC	CAACAAGCAC	GGGACACCTC	CATTACTCAT	TGCTGCTGGC	1500
70	TGTGGGAATA	TTCAAATACT	ACAGTTGCTC	ATTAAAAAG	GCTCGAGAA	OGATGTCCAG	1560
	GATAAGGGGG	GGTCCAATGC	CGTCTACTGG	GCTGCTCGGC	ATGGCCACGT	CGATACCTTG	1620
	AAATTTCTCA	GTGAGAACAA	ATGCCCTTTG	GATGTGAAAG	ACAAGTCTGG	AGAGATGGCC	1680
	CTCCACGTGG	CAGCTCGCTA	TGGCCATGCT	GACGTGGCTC	AAGTTACTTG	TGCAGCTTGG	1740
	GCTCAAAATC	CAATATCCAG	GACAAAGGAA	GAAGAAACCC	CCCTGCACCTG	TGCTGCTTGG	1800
	CACGGCTATT	ACTCTGTGGC	CAAGGCCCTT	TGTGAAGCCG	GCTGTAAAGT	GAACATCAAG	1860
75	AACCGAGAAG	GAGAGACGCC	CCTCCTGACA	GCCTCTGCCA	GGGGCTACCA	CGACATCGTG	1920
	GAGTGTCTGG	CCGAACATGG	AGCCGACCTT	AATGCTTGGC	ACAAGGACGG	ACACATTGCC	1980
	CTTCATCTGG	GTGTAAGACG	GTGTGAGATG	GAGGTAATCA	AGACTCTCCT	CAGCCAAAGG	2040
	TGTTTCTGTG	ATTATCAAGA	CAGGCACGGC	AATACTCCCC	TCCATGTGGC	ATGTAAAGAT	2100
	GGCAACATGG	TATCTGTGGT	GGCCCTCTGT	GAGCAAACT	GCAATTTGGA	CATCTCCAA	2160
80	AAGTATGGGC	GAAAGCCTCT	GCACCTTGGC	GCCAAACAG	GAATCTTAGA	CGTGTGCTGG	2220
	TATCTCTGTC	TGATGGGAGC	CAGCGTTGAG	GCGCTGACCA	CGGACGAGAA	GAOGGAGAG	2280
	GATCTTGCTA	GATCGGAACA	GCACGAGCAC	GTAGCAGGTC	TCCTTGCAAG	ACTTCGAAAG	2340
	GATACGCAAC	GAGGACTCTT	CATCCAGCAG	CTCCGACCCA	CACAGAACTT	GCAGCCAAAG	2400
	ATTAAGCTCA	AGCTGTTTGG	CCACTCGGGA	TCCGGGAAAA	CCACCTTGTG	AGAACTCTCT	2460
	AAGTGTGGGC	TGCTGAGGAG	CTTTTTTCAG	AGGCGTGGCC	CCAGACTGTC	TTCCACCAAC	2520

5	TCCAGCAGGT	TCCCACCTTC	ACCCCTGGCT	TCTAAGCCCA	CAGTCTCAGT	GAGCATCAAC	2580
	AACCTGTACC	CAGGCTGCGA	GAACGTGAGT	GTGAGGAGCC	GCAGCATGAT	GTTGAGCCG	2640
	GGTCTTACCA	AAGGGATGCT	GGAGGTGTTT	GTGGCCCCGA	CCCACCAACC	GCATGCTCG	2700
	GCCGATGACC	AGTCCACCAA	GGCCATCGAC	ATCCAGAACG	CTTATTTGAA	TGGAGTTGGC	2760
	GATTTACAGC	TGTGGGAGTT	CTCTGGAAAT	CCTGTGTAAT	TCTGCTGTTA	TGACATATTT	2820
	GCTGCAATG	ATCCACGTC	AATCCATGTT	GTGTCTTTA	GTCTAGAAGA	GCCCTATGAG	2880
	ATCCAGCTGA	ACCCAGTGAT	TTTCTGGCTC	AGTTTCTGTA	AGTCCCTTGT	CCCAGTTGAA	2940
	GAACCCATAG	CCTTGGGTGG	CAAGCTGAAG	AACCCACTCC	AAGTTGTCTT	GGTGGCCACC	3000
10	CACGCTGACA	TCATGAATGT	TCCTGAGCCG	GCTGAGGCG	AGTTTGGATA	TGACAAAGAC	3060
	ACATGTTGTC	TGAAAGAGAT	TAGGAACAGG	TTTGGAAATG	ATCTTCACAT	TTCAAAATAG	3120
	CTGTTTGTTC	TGGATGCTGG	GGCTTCTGGG	TCAAAGGACA	TGAAGGTACT	TGAAATCAT	3180
	CTGCAAGAAA	TACGAAGCCA	GATTGTTTCG	GTCTGTCTTC	CCATGACTCA	CCTGTGTGAG	3240
	AAAAATCATCT	CCACGCTGCC	TTCTGTGAGG	AAGCTCAATG	GAOCCAAACA	GCTGATGTGG	3300
15	CTGCAGCAGT	TTGTGTACGA	CGTGACGAC	CAGCTGAACC	CCCTGGCCAG	CGAGGAGGAC	3360
	CTCAGGCGCA	TTGCTCAGCA	GCTCCACAGC	ACAGGCGAGA	TCAACATCAT	GCAAAGTGAA	3420
	ACAGTTTCAGG	ACGTGCTGCT	CCTGGACCCC	CGCTGGCTCT	GCACAAACGT	CCTGGGGAGG	3480
	TTGCTGTCCG	TGGAGACCCC	ACGGGCGCTG	CACCACTACC	GGGGCCGCTA	CACCGTGGAG	3540
	GACATCCAGC	GCCTGGTGCC	CGACAGCGAC	GTGGAGGAGC	TGCTGCAGAT	CCTCGATGCG	3600
20	ATGGACATCT	GGCCCGCGGA	CCTGAGCAGC	GGGACCATGG	TGGACGTCCC	AGCCCTGATC	3660
	AAGACAGACA	ACCTGCACCG	CTCCTGGGCT	GATGAGGAGG	ACGAGGTGAT	GGTGTATGGT	3720
	GGCGTGCGCA	TGTGTCCCGT	GGAACACCTC	ACCCCTTCC	CATGTGGCAT	CTTTCACAA	3780
	GTCCAGGTGA	ACCTGTGCCG	GTGGATCCAC	CAGCAAGACA	CAGAGGGCGA	CGCGGACATC	3840
	CGCTGTGGG	TGAATGGCTG	CAAGCTGGCC	AACCGTGGG	CCGAGCTGCT	GGTGTCTCTG	3900
25	GTCAACCAAG	GCCAGGSCAT	TGAGGTCCAG	GTCCGTGGCC	TGGAGACGGA	GAAGATCAAG	3960
	TGCTGCCTGC	TGCTGGACTC	GGTGTGCAGC	ACCATTGAGA	ACGTCAATGGC	CACCACTGCT	4020
	CCAGGGCTCC	TGACCGTGAA	GCATTACCTG	AGCCCCCAGC	AGCTGCGGGA	GCACCATGAG	4080
	CCCGTCATCA	CTTACACGCC	ACGGGACTTC	TTCCGGGCAC	AGACTCTGAA	GGAAACCTCA	4140
	CTGACCAACA	CCATGGGGGG	GTACAAGGAA	AGCTTCAGCA	GCATCATGTG	CTTGGGTGT	4200
30	CACGACGCT	ACTCACAGGC	CAGCCTCGGC	ATGGACATCC	ATGCATCAGA	CCTGAACCTC	4260
	CTCATCGGAA	GGAACTGAG	TGCGCTGCTG	GACCCGCCCG	ACCCCTTGGG	GAAGGACTGG	4320
	TGCGCTCTCG	CCATGAACCT	AGGCCTCCCT	GACCTCGTGG	CAAGTACAA	CACCAATAAC	4380
	GGGGCTCCCA	AGGATTTCTT	CCCCAGCCCC	CTCCAGCCCC	TGCTCGGGGA	ATGGACCAAC	4440
	TACCTCTAGA	GCACAGTGGG	CACCTCATG	TCCAAACTGA	GGGAGCTGGG	TGCGCGGGAT	4500
35	GCGCGAGACC	TTTTGCTGAA	GGCATCCTCT	GTGTTCAAAA	TCAACCTGGA	TGGCAATGGC	4560
	CAGGAGGGCT	ATGCCCTGAG	CTGCAACAGC	GGCACCTCTT	ACAATTCCAT	TAGCTCTGTT	4620
	GTATCCCGGT	GAGGGCAGCC	TCTGGCTTGG	ACAGGGTCTG	TTTGGACTGC	AGAACCAAGG	4680
	GGGTGATGTA	GCCCATCTCT	CCCTTTGGAG	ATGCTGAGGG	TGTTTCTTCC	TGCACCCACA	4740
	GCCAGGGGGA	TGCCACTCCT	CCCTCGGCT	TGACCTGTTT	CTCTGCGCT	ACCTCCCTCC	4800
40	CGCTCTCATT	CGGTGTCTG	TGGATGGTCA	TTGCAGTTTA	AGAGCAGAAC	AGATCTTTTA	4860
	CTTTGGCGCG	TGAAAAGCT	AGTGTACCTC	CTCTCAGTGT	TTTGGACTCC	ATCTCTCATC	4920
	CTCCAGTACC	TTGCTCTTTA	CTGATAATTT	TGCTGGAATT	CCTAACTTTT	CAATGACATT	4980
	TTTTTTAACT	ATCATATTGA	TTGTCTTTTA	AAAAAGAAAA	GTGCATATTT	ATCCAAAATG	5040
	TGTAATTTCT	ATACGCTTTT	CTGTGTTATA	CCATTTCTTC	AGCTTATCTC	TTTTATATTT	5100
45	GTAGAGGAAA	CTCCCATGTA	TGGAATCCCA	CTGTATGATT	TATAAACAGA	CAATATGTGA	5160
	GTGCGCTTTG	CAGAAGAGGG	TGTGTTTGAA	ATCATCGGAG	TCAGCCAGGA	GCTGTCAACA	5220
	AGGAAAGCCT	ACCTCTCTGT	CCCTTGCTGT	ATGCTGATCA	TCGCCAGAGG	TGCTTCACCC	5280
	TGAGTTTGTG	TTTGTATTGT	TTTCTGACAG	TTTTTCTGTT	TTGTTTGGCA	AGGAAAGGGG	5340
	AGAAAGGAAAT	CCTCCTCCAG	GGTGATTTTA	TGATCAGTGT	TGTTGCTCTA	GGAAGACATT	5400
50	TTTCGGTTTG	CTTTTGTTC	AATGTCAATG	TGAACGTCCA	CATGAAACCT	ACACACTGTC	5460
	ATGCTTTCAT	ATTCCCTCTC	ATCTCAGSTA	GAAGGTTGAC	ACAGTTGTAG	GOTTACAGAG	5520
	ACCTATGTAA	GAATTACGAA	GACCCCTGAC	TCATCATTTG	TGGCAGTCCC	TTATAATTGG	5580
	TGCATAGCAG	ATGGTTTCCA	CATTTAGATC	CTGGTTTCAT	AACTTCTCTG	ACTTGAAGTC	5640
	TAAAGCAGA	AAATAAAGGA	AGCAAGTTTT	CTTCCATGAT	TTTAAATGTT	GATCGAGTTT	5700
55	TAAATGTATA	GGAGGGAACA	TGTCTTAATT	CTTCTGTCTT	GAGAAGCATG	TAATGTTAAT	5760
	GTATATATAT	ATATATATAT	ATATATGCAC	TATGTATATA	CATATATATT	AATACTGGTA	5820
	TTTTTACTTA	ATCTATAAAA	TGCTGTTAAA	AAGTTGTTTG	TTTTTTTCTT	TTTTTATAAA	5880
	TAAACTGTGT	CTGTTAAAAA	AAAAAATAAA				5910

Seq ID NO: C73 DNA Sequence  
Nucleic Acid Accession #: NM\_002081.1  
Coding sequence: 222..1898

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	GGCTGCCCGA	GCGAGGCTTC	GGACCTGCGA	CCCCGCGGCG	CCCGCGCGCG	CGCGCGCGCG	60
	GGCTTTTGTG	GTCTCGGCTT	CCTCGGCGCG	CGCGGCTCT	GGACCGGAG	CGCGCGCGCG	120
	CGGACCTTGG	GCTCTGCCCT	TGCGGGGCGG	GAACCTGCGA	GGACCGGCGC	AGGATCCGAG	180
	AGAGGGGCGG	GCGGGTGGCC	GGGGGCGCGG	CGGGCGCGCG	CATGGAGCTC	CGGGCGCGAG	240
70	GCTGGTGGCT	GCTATGTGCG	GCCGACGCGC	TGGTCGCGTG	CGCGCGCGCG	GACCGCGCCA	300
	GCAAGAGCCG	GAGCTGCGGC	GAGGTGCGGC	AGATCTACGG	AGCCAAGGGC	TTGAGCTTGA	360
	GCGACGTGCC	CCAGGGGCGG	ATCTCGGGTG	AGCACCTGCG	GATCTGTCCC	CAGGGCTACA	420
	CCTGCTGAC	CAGCGAGATG	GAGGAGAAAC	TGGCCAAACG	CAGCCATGCC	GAGCTGGAGA	480
	CCGCGCTCCG	GCGACGACGC	CGGCTCTGCG	AGGCCATGCT	TGCCACCCAG	CTGCGCAGCT	540
75	TGATGACCA	CTTCCAGCAC	CTGCTGAACG	ACTCGGAGCG	GACGCTGCAG	GCCACCTTCC	600
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80	GAGAGCTGCG	CCTGCGGGCC	ACCGTGCCTT	TCGTGGCTGC	TGCTTCTTTT	GTGCAAGGCC	900
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	CGAGAGCTGT	CTGTAAGCTG	GTCTACTGTG	CTCACTGCTT	GGGAGTCCCC	GGGCGCAGGC	1020
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	ACGCGGAGTG	GAGGAACCTC	CTGGACTCCA	TGGTGCTCAT	CACCGACAAG	TTCTGGGGTA	1140
	CATCGGCTGT	GGAGAGTGTC	ATCGGCAGCG	TGCACAGTGT	GCTGGCGGAG	GCCATCAACG	1200

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45 Seq ID NO: C74 DNA Sequence  
Nucleic Acid Accession #: BC030205.1  
Coding sequence: 45..878

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80 Seq ID NO: C75 DNA Sequence  
Nucleic Acid Accession #: NM\_001982.1  
Coding sequence: 199..4227

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	AGCCTGGCCC	GGGGCTCCGA	GGTGGGCAAC	TCTCAGGCAG	TGTGCTCGTG	GACTCTGAAT	300
5	GGCCTGAGTG	TGACCGGCGA	TGCTGAGAAC	CAATACCGA	CAGTGTACAA	GCTCTACGAG	360
	AGGTGTGAGG	TGGTGATGGG	GAACTTGAG	ATTGTGCTCA	CGGACACAA	TGCCGACCTC	420
	TCCTTCCTGC	AGTGGATTCG	AGAAGTGACA	GGCTATGTCC	TCGTGGCCAT	GAATGAATTC	480
	TCTACTCTAC	CATTGCCCAA	CCTCCGCGTG	GTGCGAGGGA	CCGAGGTCTA	CGATGGGAAG	540
	TTTGCCATCT	TGCTCATGTT	GAACTATAAC	ACCAACTCCA	GCCACGCTCT	GCGCCAGCTC	600
10	CGCTTGACT	AGCTCACOGA	GATTCTGTCA	GGGGGTGTTT	ATATTGAGAA	GAACGATAAG	660
	CTTTGTGACA	TGGACACAAT	TGACTGGAGG	GACATCGTGA	GGGACCGAGA	TGCTGAGATA	720
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	GCAGAGGSCA	AGTGTGTGA	CCCACTGTGC	TCTCTGGGG	GATGCTGGGG	CCCAGGCCCT	1740
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	CAATGTGCCC	ATTTTCGAGA	TGGGCCCCAC	TGTGTGAGCA	GCTGCCCCCA	TGGAGTCCCTA	1980
	GGTGCCAAAG	CGCCATCTTA	CAAGTACCCA	GATGTTGAGA	ATGAATGTGC	CGCCTGCCAT	2040
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Nucleic Acid Accession #: NM\_001216.1  
Coding sequence: 43..1422

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10 AGTGAAGAGG ATTACCCAG AGAGGAGGAT CCACCCGAG AGGAGGATCT ACCTGGAGAG 300
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Seq ID NO: C77 DNA Sequence

Nucleic Acid Accession #: NM\_004207.1  
Coding sequence: 63..1460

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Seq ID NO: C78 DNA Sequence

Nucleic Acid Accession #: NM\_000358.1  
Coding sequence: 48..2099

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80      1      11      21      31      41      51
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GCTTGGCCGT CGGTGCTAG CTGCTGTGCT GCGGTGCTGC CGCTCCATG GCGCTCTTGG 60
TGGGCTGCTT GGTCTTGGCC CTGGCTCTGG CCTTGGGCCC GCGCGGAGC CTGGGGGGTC 120
CGCCCAAGCT GGTCTACGAG CTGGTGTGTC AGCAGAGCAG GCTCGCGGGC CGCCAGCAGC 180
GCCCCAAGCT GTTGTCTGTG CAGAAGGTTA TTGGCACTAA TAGGAAGTAC TTCAACCACT 240
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5	GCAAGCAGTG	GTACCAAAAGG	AAAATCTGTG	GCAAATCAAC	AGTCATCAGC	TACGAGTGCT	300
	GTCTTGGATA	TGAAAAGGTC	CCTGGGGAGA	AGGGCTGTCC	AGCAGCCCTA	CCACTCTCAA	360
	ACCTTTAGGA	GACCCCTGGGA	GTGTTGGAT	CCACCAACAC	TCAGCTGTAC	ACGGACCGCA	420
	CGGAGAACT	GAGGCCTGAG	ATGGAGGGGC	CCGGCAGCTT	CACCATCTTC	GCCCCTAGCA	480
	ACGAGGCCCTG	GGCCTCCTTG	CCAGCTGAAG	TGCTGGACTC	CCTGGTCAGC	AATGTCAACA	540
	TTGAGCTGCT	CAATGCCCTC	CGCTACCATA	TGGTGGGCAG	GCGAGTCTTG	ACTGATGAGC	600
	TGAAACAAGG	CATGACCTTC	ACCTCTATGT	ACCAGAATTC	CAACATCCAG	ATCCACCACT	660
	ATCCTAATGG	GATTGTAAC	GTGAATCTGT	CCCGGCTCCT	GAAAGCCGAC	CACCATGCAA	720
10	CCAAAGGGGT	GGTGCACCTC	ATCGATAAGG	TCATCTCCAC	CATCACCAAC	AACATCCAGC	780
	AGATCATTGA	GATCGAGGAC	ACCTTTGAGA	CCCTTCGGGC	TGCTGTGGCT	GCATCAGGGC	840
	TCAACACGAT	GCTTGAAGGT	AACGGCCAGT	ACAOGCTTTT	GGCCCCGACC	AATGAGGCCT	900
	TGAGAGAAGT	CCCTAGTGAG	ACTTTGAACC	GTATCCTGGG	CGACCCAGAA	GCCCTGAGAG	960
	ACCTGTGAA	CAACCACATC	TTGAAGTCAG	CTATGTGTGC	TGAAGCCATC	GTTCGGGGGC	1020
15	TGCTGTGAGA	GACCCCTGGAG	GGCACGACAC	TGGAGGTGGG	CTGCAGCGGG	GACATGCTCA	1080
	CTATCAACGG	GAAGGCGATC	ATCTCCAATA	AAGACATCCT	AGCCACCAAC	GGGGTGATCC	1140
	ACTACATTGA	TGAGCTACTC	ATCCAGACT	CAGCCAGAC	ACTATTGAA	TGGCTGCAG	1200
	AGTCTGATGT	GTCCACAGCC	ATTGACCTTT	TCAGACAAGC	CGGCCTCGGC	AATCATCTCT	1260
	CTGGAAGTGA	GCGGTGACC	CTCCTGGCTC	CCCTGAATTC	TGTATTCAA	GATGGAACCC	1320
20	CTCCAAATGA	TGCCCATACA	AGGAATTTGC	TTGGAACCA	CATAATTAA	GACCAAGCTGG	1380
	CCTCTAAGTA	TCTGTACCAT	GGACAGACC	TGGAACTCT	GGGCGGCAAA	AAACTGAGAG	1440
	TTTTTGTTTA	TGTAATAGC	CTCTGATTG	AGAACAGCTG	CATCGCGGCC	CACGACAAGA	1500
	GGGGGAGGTA	CGGGACCTTG	TTACGATGG	ACCGGGTGCT	GACCCCCCA	ATGGGGACTG	1560
	TCATGGATGT	CCTGAAGGGA	GACAATCGCT	TTAGCATGCT	GGTAGCTGCC	ATCCAGTCTG	1620
25	CAGGACTGAC	GAGAGCCCTC	AACCGGGAAG	GAGTCTACAC	AGTCTTTGCT	CCCAAAATG	1680
	AAGCCCTCCG	AGCCCTGCCA	CCAAGAGAAC	GGAGCAGACT	CTTGGGAGAT	GCCAAGGAAC	1740
	TTGCCAACAT	CCTGAAATAC	CACATTGGTG	ATGAAATCCT	GGTTAGCGGA	GGCATCGGGG	1800
	CCCTGGTGCG	GCTAAAGTCT	CTCCAAGGTG	ACAAGCTGGA	AGTCAGCTTG	AAAAACAATG	1860
	TGGTGAGTGT	CAACAAGGAG	CCTGTTGCCG	AGCCTGACAT	CATGGCCACA	AATGGCGTGG	1920
30	TCCATGTGAT	CACCAATGTT	CTGCAGCCTC	CAGCCACAG	ACCTCAGGAA	AGAGGGGATG	1980
	AACTTGCAAG	CTCTGCGCTT	GAGATCTTCA	AACAAGCATC	AGCGTTTTC	AGGGCTTCCC	2040
	AGAGGTCTGT	GCGACTAGCC	CCTGTCTATC	AAAAGTTATT	AGAGAGGATG	AAGCATTAGC	2100
	TTGAAGCACT	ACAGGAGGAA	TGCACCAACG	CAGCTCTCCG	CCAATTCTC	TCAGATTTC	2160
	ACAGAGACTG	TTTGAATGTT	TTCAAAACCA	AGTATCACAC	TTTAATGTAC	ATGGGCCGCA	2220
35	CCATAATGAT	ATGTGAGCCT	TGTGCATGTG	GGGGAGGAGG	GAGAGAGATG	TACTTTTAA	2280
	ATCATGTTC	CCCTAAACAT	GGCTGTTAAC	CCAATGCATG	CAGAACTTG	GATGTCACTG	2340
	CCTGACATTC	ACTTCCAGAG	AGGACCTATC	CCAAATGTGG	AATTGACTGC	CTATGCCAAG	2400
	TCCCTGGAAA	AGGAGCTTCA	GTATTGTGGG	GCTCATAAAA	CATGAATCAA	GCAATCCAGC	2460
	CTCATGGGAA	GTCTGGGCAC	AGTTTTTGTA	AAGCCCTTGC	ACAGCTGGAG	AAATGGCATC	2520
40	ATTATTAAGT	ATGAGTTGAA	ATGTTCTGTC	AAATGTGTCT	CACATCTACA	CGTGGCTTGG	2580
	AGGCTTTTAT	GGGGCCCTGT	CCAGGTAGAA	AAGAAATGGT	ATGTAGAGCT	TAGATTTCCT	2640
	TATTGTGACA	GAGCCATGGT	GTGTTGTGTA	TAATAAAACC	AAAGAAACAT	A	2691

Seq ID NO: C79 DNA Sequence  
Nucleic Acid Accession #: NM\_006536.2  
Coding sequence: 109..2940

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	AGCATTCGAG	GTCCCTATTG	CAACCTGAAG	TTTGTGACTC	TCTTGGTTGC	CTTAAGTTCA	180
	GAATCCCAT	TCTTGGGAGC	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
55	ATTGCAATTA	ATCCTCAGGT	ACCTGAGAAT	CAGAACCTCA	TCTCAACAT	TAAGGAAATG	300
	ATAACTGAAG	CTTCAATTTA	CCTATTTAAT	GCTACCAAGA	GAAGAGTATT	TTTCAGAAAT	360
	ATAAAGATTT	TAATACCTGC	CACATGGAAA	GCTAATAATA	ACAGCAAAAT	AAACAAAGAA	420
	TACATAGAAA	AGGCAAAATG	CATAGTGACT	GACTGGTATG	GGGCACATGG	AGATGATCCA	480
	TACACCTTAC	AATACAGAGG	GTGTGGAATA	GAGGGAATAAT	ACATTCATTT	CACACCTAAT	540
60	TTCTTACTGA	ATGATAACTT	AACAGCTGGC	TACGGATCAC	GAGGCGGAGT	GTTTGTCCAT	600
	GAATGGGCC	ACCTCCGTTG	GGGTGTGTTT	GATGAGTATA	ACAATGACAA	ACCTTTCTAC	660
	ATAAATGGGC	AAAATCAAAAT	TAAAGTGACA	AGGTGTTTAT	CTGACATCAC	AGGCATTTTT	720
	GTGTGTGAAA	AAGGTCCCTG	CCCCAAGAA	AATGTATTAT	TTAGTAAGCT	TTTTAAAGAA	780
	GGATGCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	GTTCATGCAA	840
65	AGTTTATCTT	CTGTGGTTGA	ATTTTGTAA	GCAAGTACCC	ACAAACCAAG	AGCACCAAAC	900
	CTACAGAAAC	AGATGTGCAG	CCTCAGAAAT	GCAATGGGATG	TAATCACAGA	CTCTGCTGAC	960
	TTTACACACA	GCTTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCAC	ATTCCTGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCCAGCAA	GATGGCAGAG	1080
	GCTGACAGAC	TCCTTCAACT	ACAAACAAGCC	GCAGAATTTT	ATTGTATGCA	GATTGTTGAA	1140
70	ATTCAATCTT	TGTTGGGCTC	TGCCAGTTTC	GACAGCAAGG	GAGAGATCAG	AGCCAGGCTA	1200
	CACCAAAATTA	ACAGCAATGA	TGATCGAAAG	TTGCTGGTTT	CATATCTGCC	CACCACTGTA	1260
	TCAGCTAAAA	CAGACATCAG	CATTGTGTTA	GGGCTTAAGA	AAGGATTGGA	GGTGGTTGAA	1320
	AAACTGAATG	GAAAAGCTTA	TGGCTCTGTG	ATGATATTAG	TGACCAGCGG	AGATGATAAG	1380
	CTTCTTGCGA	ATTGCTTACC	CATGTGCTC	AGCAGTGGTT	CAACAATTCA	CTCCATTGCC	1440
75	CTGGGTTTCT	CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
	TTCTTTGTTT	CAGATATATC	AAACTCCAAT	AGCATGATTG	ATGCTTTCAG	TAGAATTTCC	1560
	TCTGGAACCTG	GAGACATTTT	CCAGCAACAT	ATTGAGCTTG	AAAGTACAGG	TGAAAATGTC	1620
	AAACCTCAC	ATCAATTGAA	AAACACAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
	ATGTTTCTAG	TTACGTGGCA	GGCCAGTGGT	CCTCTGAGA	TTATATTATT	TGATCCTGAT	1740
80	GGACGAAAT	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTGGGAC	AGCTAGTCTT	1800
	TGGATTCCAG	GACAGCTAAA	GCTGGGCGAC	TGGACTTACA	CCCTGAACAA	TACCCATCAT	1860
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGCGCCT	CCAATCAGC	TGTGCCCCCA	1920
	GCCACTGTGG	AAGCCTTTGT	GGAAAGAGAG	AGCCTCCATT	TTCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAACACGGG	ATTTTATCCC	ATTCTTAATG	CCACTGTGAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGAGAC	AGGTGCTGAT	2100

GTTATAAAAA ATGATGGAAT TTACTOGAGG TATTTTTTCT CCTTTGCTGC AAATGGTAGA 2160  
 TATAGCTTTGA AAGTGCACTGT CAATCACTCT CCCAGCATAA GCACCCACGC CCACCTCTATT 2220  
 CCAGGGAGTTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280  
 GCTCCAGGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340  
 5 AGCTCAGSAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACCCG TGATGTGTTT 2400  
 CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT 2460  
 TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520  
 AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580  
 10 AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC 2640  
 AGGAATGGAG CTGAACATCA GCCAATGGA GAAACACATG AAAGCCACAG AATTATGTT 2700  
 GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCACGGCG 2760  
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820  
 GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTGTCC TTATTATAGT TGTGACACAT 2880  
 15 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940  
 ATAAATATCC AAAGTGTCTT CCTTCTAGA TATAAGACCC ATGCCCTCG ACTACAACAAA 3000  
 CATACTAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060  
 ATACAGATAA GATTTTTCAC TGGTAGATCA ACAATTCTTT TTGGGGTAG ATTAGAAAAC 3120  
 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATCTT TTAAGTAAT GTCTTTAAAG 3180  
 20 GCAAGGGGAA GGGTAAAGTC GGACCAAGT CAAGGAAAGT TTGTTTATT GAGGTGGAAG 3240  
 AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACGTCTG TGTGAAGCAA 3300  
 TCATTAGTT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGCACTAG AGGTTGCTTG 3360  
 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAG CTCTTTACCT 3420  
 CTTGCTATTT TGTATATAT ATTTGAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480  
 25 TTTCACTGTA ACAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540  
 TTTATGACAA AGGTCTATTG AATTATTTG TGTGTAAGTT TCTACTCCCA TCAAGCAGC 3600  
 TTTCTAAGTT TATTGCCTTG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660  
 TACCTAGGAA A 3671

Seq ID NO: C80 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1413

1 11 21 31 41 51  
 35 ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCGTAAC 60  
 AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTTGGTG AAAGATACTT AGAAAAATTT 120  
 TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAAAATGA AATATAGTGG AAACCTTAATG 180  
 AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240  
 40 ACATCTACCC TGGAGATGAT GCAAGCACCT CGATGTGGAG TCCCGATGT CCATCAITTC 300  
 AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360  
 TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCGGAAAGC TTTCCAAGTA 420  
 TGGAGTAGTG TTACCCCTT GAAATTACAG AAGATTAAAC CAGGCATGGC TGACATTTTG 480  
 GTGTTTITG CCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540  
 45 CTAGCCCATG CTTTGGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC 600  
 GAATTCCTGA CTACACATTC AGGAGGCACA AACTTGTTC TCACCTGCTG TCACGAGATT 660  
 GGCCATTCCT TAGGTCTTGG CCATCTTAGT GATCCAAAGG CCGTAATGTT CCCCACCTAC 720  
 AAATATGTTG ACATCAACAC ATTTGCTCTC TCTGCTGATG ACATACGTGG CATTCACTCC 780  
 CTGTATGGAG ACCCAAAGA GAACCAACGC TTGCCAAATC CTGACAATTC AGAACAGCT 840  
 50 CTCTGTGACC CCAATTTGAG TTTTGATGCT GTCACTACCG TGGGAAATAA GATCTTTTTT 900  
 TTCAAAGACA GGTCTCTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960  
 ATTTCTTCCT TATGGCCAAC CTGCTCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020  
 AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080  
 GAGCCAAATT ATCCCAAGAG CATACATCTT TTTGGTTTTC CTAACCTTGT GAAAAAATTT 1140  
 55 GATGCAGCTG TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAATAT 1200  
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCGTGTT ATCCCAAACT GATTACCAAG 1260  
 AACTTCCAAG GAAATCGGGC TAAATTTGAT GCAGTCTTCT ACTCTAAAAA CAAATACTAC 1320  
 TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAAAG TATCACCAAA 1380  
 60 ACACCTGAAA GCAATAGCTG GTTTGGTTGT TGA 1413

Seq ID NO: C81 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1413

1 11 21 31 41 51  
 65 ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCGTAAC 60  
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 TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAAAATGA AATATAGTGG AAACCTTAATG 180  
 70 AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240  
 ACATCTACCC TGGAGATGAT GCAAGCACCT CGATGTGGAG TCCCGATGT CCATCAITTC 300  
 AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360  
 TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCGGAAAGC TTTCCAAGTA 420  
 TGGAGTAATG TTACCCCTT GAAATTACAG AAGATTAAAC CAGGCATGGC TGACATTTTG 480  
 75 GTGTTTITG CCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540  
 CTAGCCCATG CTTTGGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC 600  
 GAATTCCTGA CTACACATTC AGGAGGCACA AACTTGTTC TCACCTGCTG TCACGCCATT 660  
 GGCCATTCCT TAGGTCTTGG CCATCTTAGT GATCCAAAGG CCGTAATGTT CCCCACCTAC 720  
 80 AAATATGTTG ACATCAACAC ATTTGCTCTC TCTGCTGATG ACATACGTGG CATTCACTCC 780  
 CTGTATGGAG ACCCAAAGA GAACCAACGC TTGCCAAATC CTGACAATTC AGAACAGCT 840  
 CTCTGTGACC CCAATTTGAG TTTTGATGCT GTCACTACCG TGGGAAATAA GATCTTTTTT 900  
 TTCAAAGACA GGTCTCTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960  
 ATTTCTTCCT TATGGCCAAC CTGCTCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020  
 AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080  
 GAGCCAAATT ATCCCAAGAG CATACATCTT TTTGGTTTTC CTAACCTTGT GAAAAAATTT 1140



5  
 10  
 15  
 20  
 25  
 30

GATGCAGCTG TTTTAAACCC ACGTTTTAT AGGACCTACT TCTTTGTAGA TAACCAAGTAT 1200  
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCGTGTT ATCCCAACT GATTACCAAG 1260  
 AACTTCCAAG GAATCGGGCC TAAAATTGAT GCAGTCTTCT ACTCTAAAAA CAAATACTAC 1320  
 TATTTCTTCC AAGGATCTAA CCAATTGAA TATGACTTCC TACTCCACG TATCACCATA 1380  
 AACTGAAAA GCAATAGCTG GTTTGGTTGT TGA 1413

Seq ID NO: C82 DNA Sequence  
 Nucleic Acid Accession #: NM\_006952.1  
 Coding sequence: 11..793

1 11 21 31 41 51  
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 TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTCAATC TGATGTTTAT 300  
 AGTATATGCC TTTGAAGTGG CATCTTGAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360  
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 TGATGACCAG TGGAAAAACA ATGGAGTCA CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480  
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 AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCC TGTGTTTATC ACAATCAGGG 660  
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGTTG CTGGTTTGG 720  
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 AATTGAATAT TAAGAA 796

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 Seq ID NO: C83 DNA Sequence  
 Nucleic Acid Accession #: NM\_001793.2  
 Coding sequence: 71..2560

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 CTGGCTCGAG TGCGCGGCT CCGAGCGGTG CCGGGCGGTC TTCCAGGGAG CTGAAGTGAC 180  
 CTGGAGGCG GAGGCGCGG AGCAGGAGCC CCGCCAGGCG CTGGGGAAG TATTCATGGG 240  
 CTGCGCTGG CAAGAGCCAG CTCTGTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300  
 TGGCGAGACA GTCCAGGAAA GAAGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360  
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCAA TATGCTTCCC 420  
 TGAAAAAGG AAGGTCCTCT TCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480  
 AGACACCGA ATTTTCTACA GCATCACGGG GCGGGGGCA GACAGCCCC CTGAGGGTGT 540  
 CTTGCTGTA GAGAAGGAGA CAGGCTGGT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600  
 GATTGCCAAG TATGAGCTCT TTGGCCAGCG TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660  
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 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCCCTACA GGTACTTCTG TGATGCAAGT 780  
 GACAGCCAG GATGAGGATG ATGCCATCTA CACCTACAT GGGTGGTTG CTTACTCCAT 840  
 CCATAGCCAA GAACCAAGG AOCACACGA CTTCTATGTC ACCATTCCAC GGAGCACAGG 900  
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 CAACTCACA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGAGC GGGACCATTT 1200  
 TACCATCACC ACCCACTCTG AGAGCAACCA GGGCATCCTG ACAACAGGA AGGGTTTGG 1260  
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 GCCTGTGTT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500  
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 ACTGATTGAT GTCAATGACC ATGGCCAGT CCTGAGCCC CGTCAGATCA CCATCTGCAA 1740  
 CCAAGGCCCT GTGCGCAGG TGCTGAACAT CACGACACAG GACCTGTCTC CCCACACCTC 1800  
 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860  
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGAOGT 1920  
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980  
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCTTGGACCC TGGAAAGGAG GTTTCTATCT 2040  
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 CGTCTTCTAC TATGGGGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCAACCA 2220  
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 CATCATCCCG ACACCATGAT ACCGTCTCTG CGCAGCCAC CCAGATGAAA TGGCAACTT 2340  
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 ACGTTAGAGT GGTGCTCTCC TTAGCCTTTC AGGATGAGG AATGTGGGCA GTTTGACTTC 2760  
 AGCACTGAAA ACCCTCTCCAC CTGGGCCAGG GTTGCTCTAG AGGCCAAGTT TCCAGAGCC 2820  
 TCTTACCTCG CGTAAATGAC TCAACCTGTG GTCCGTGGCC TGGGCTGCT GTGACTGACC 2880  
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940  
 TTTTTTTAA GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000  
 GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTCCAGAC CCCATGCTT CCCTTGGGA 3060



TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT 3120  
 GTTGGGTGTC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180  
 TAAAGAAACT TTCCACAGAA AAAAA 3205

5

Seq ID NO: C84 DNA Sequence  
 Nucleic Acid Accession #: NM\_005629.1  
 Coding sequence: 639..2546

10 1 11 21 31 41 51  
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 15 CCGATGTGCG CCGCGCGCGG TTAGGATGAG TCTCGGGTGC GCGGAGGAGC GCGCGCAGCC 300  
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 30 CCGTGGGCGC ATGTGGGCGC ACCTGGAACA CTCCGACTG GTGGAGATC TTCCGCGATG 1200  
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80

Seq ID NO: C85 DNA Sequence  
 Nucleic Acid Accession #: NM\_006516.1  
 Coding sequence: 180..1658

1 11 21 31 41 51  
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5 GTCAGAGTCG CAGTGGGAGT CCCCAGGACC GAGCAGAGC CTGAGCGGGA GAGCGCCGCT 120  
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 TCACCACGCT CTGGTCCCTC TCAGTGGCCA TCTTTTCTGT TGGGGGCATG ATTGGCTCCT 420  
 TCTCTGTGGG CCTTTTGGTT AACCGCTTGG GCGGGCGGAA TTCAATGCTG ATGATGAACC 480  
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 10 TGCTGATCCT GGGCCGCTTC ATCATCGGTG TGTACTGCGG CTGACCACA GGCTCGTGC 600  
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Seq ID NO: C86 DNA Sequence  
 Nucleic Acid Accession #: XM\_035292.2  
 Coding sequence: 53..1576

55 1 11 21 31 41 51  
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 CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGGTG GCCATCATCG TGGGGACCAT 240  
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 CTACGGCTCG CTGCCCGCTT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCOCGCCCTTC 480  
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 65 CTGCCCGGTG CCGGAGGAGG CAGCCAAGCT CGTGGCTGCT CTCTGCTGTC TGCTGCTCAC 600  
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 70 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCCTGCC 900  
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 75 CTCCATGATC CACCCACAGC TCCTCACCCC CGTCCGCTCC CTGCTGTTC CGTGTGTGAT 1200  
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 80 CATCATCTCT AGCGGCTGC CCGTCTACT CTTCGGGCTC TGGTGGAAAA ACAAGCCCAA 1500  
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Seq ID NO: C87 DNA Sequence  
 Nucleic Acid Accession #: NM\_005268.1

Coding sequence: 168..989

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   AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGGGTGG GTCCACCATG AACTGGAGTA 180
   TCTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
   TGTCTCTGGT CTTCATCTTC CGGTGCTGG TGTACCTGGT GACGGCGAG CGTGTGTGGA 300
10 GTGATGACCA CAAGGACTTC GACTGCAATA CTGCCAGCC CGGCTGCTCC AACGCTGTCT 360
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   CATGCCCTC ACTGTCTGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
   ACCGAGAAGC CCATGGGAGG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
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15 TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC 660
   AGCGAGATCC ATGTCCCAAT ATAGTGAGCT GTTCTATCTC CAAGCCCTCA GAGAAGAAC 720
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   TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
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20 CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCGCCCC 960
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   CTGAGGAGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
   CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
   TCAACTCCAG CCACCTGCCC CAGCTGACG GCACTGGGCC AGTTCCCTCT CTGCTCTGCA 1200
25 GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC 1243
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Seq ID NO: C88 DNA Sequence

Nucleic Acid Accession #: NM\_005130

Coding sequence: 98..802

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   GCTCTCCTTC CTCCTACTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAAGTGA 180
   GAATGGACTT CACAGCAAGG TGGTCTCAGA ACAAAGGAC ACTCTGGGCA ACACCCAGAT 240
   TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAGACC AAGCCAACTG 300
   CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT 360
   GGACCATGAA TTTTCTGTG TCTTTGCTGG CAATCCAAAC TCATGCTTAA AGCTCAAGGA 420
   TGAGAGATC TATTGGAACC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480
   ATATTCCAAG ACAGCTGTGA AAACCAAGAT GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540
   TAAGCTAGTC AGCTCCACTC TATTGGGAAA CAAAGAGCCC AGGAAGGAGA AAACAGAGAT 600
   GTCCCCCAGG GAGCAATCA GAGGCAAGGA GACCAACCCC TCTAGCTTAG CAGTGACCCA 660
   GACCATGGCC ACCAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720
   GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACTTCT TCCTCAGCAT 780
   AGTGCAGCAG ACCTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA 840
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   TGGAATTTGC CTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCTG CAGCATGTAT 1020
   TTCCATGGCC CACACAGCTA TGTGTTTGTG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
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Seq ID NO: C89 DNA Sequence

Nucleic Acid Accession #: BC022542

Coding sequence: 274..927

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   TGGCGGCTCG GTTGGCGGGG GTTGGGCGGG CCGCTCTGGT GCTCCTGGG GCGCGCACGG 180
   GGCTCACGCG CGGCGCCCGC ACGGCCTTCA CCGCGCGCGC CTCTGAAGCC GGCATAAGGG 240
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   ATTGTGCCAA GGAGTCTGAA GTTCTCATT ATGCCAGACG AGATTACAG TGCAATTGACT 540
   GTTTTCAAGC CTTTCTGCT GTGCACTGCC GCTATCATCG GCGCACAGT GAAGATGGAG 600
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   TTTTGAATG CTGGGCTCAC TCAGAAGTGG CAGCCCTCTG TGCTTTGGAT AATGAGGATA 720
   TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
   CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC 840
75 TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAAAATAGG CCATTTTTC CTATAAGTTT 900
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   TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAATG TAGTGTCTA TTGCATGGAT 1080
   CCTTGGTAAT CTTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATCTCG TAAATTAATG 1140
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5 GAGCCAAGAT CGCACCACCTG CACTACAGCC TGGGCGACAG AAGAGACCC TGTCTCCAAA 1560  
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 CTAAGAAATT AATATTAAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCCTTA 1740  
 ACGCACTCCA TTCTCCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800  
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10 Seq ID NO: C90 DNA Sequence  
 Nucleic Acid Accession #: NM\_004994  
 Coding sequence: 20..2143

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 CACTCGGGTG CGAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCTGCGC TGCTGCTTCT 240  
 CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300  
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 CAAGTGGCAC CACCAACAAC TCACCTATTG GATCCAAJAC TACTCGGAAG ACTTGGCCGG 420  
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 CATCTTCGAG GCGCTCTCTT ACTCTGCTTG CACCACGAC GGTGCTCCG ACGGCTTGCC 780  
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AGATCTGCTG  GGACCCCTGG  ATGCAACAC  CAGCCGAGGA  TGTACCCCT  CAACCCCTCC  1080
AAAGGAGGCC  CTGCCCCCTT  GGCTTGGTCC  TTGCTACCC  AAGCCTGGCC  TGGCTGGGCC  1140
TGGCCCCCAA  TGGTCAGAAG  AGCCATCCCA  TGGCCATGTC  ACAGGGATAG  ATGGACATTT  1200
GTTGACTTGG  TTTTACAGGT  CATTACCACT  CATTAAAGTC  CAGTATTACT  AAGGTAAGGG  1260
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CAAGGAGGCC  TTCTCCCGAG  AACCTGTGGT  CCCTGATTTT  GGAGGGGGAA  CTTCTTGCTT  1380
CTCATTTTGC  TATTTTGGTG  TATTTTGGTG  AAGTTGTTC  CATTTTGAGC  CCGGGGACTC  1440
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TCATATGCTT  TTACTTGGGC  AAGGGTGCTT  TCCTTCCAAT  ACCCCAGTAG  CTTTATTTT  1560
AGTAAAGGGA  CACTTTCCCC  TAGCCTAGGG  TCCCATATTG  GGTCAAGCTG  CTTACCTGCC  1620
TCAGCCGAGG  ATTTTATTAT  TTGGGGGAGG  TAAATGCCCT  TTGTACCCC  AAGGCTTCTT  1680
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CACCACCAGA  CAATAGGATG  GGATGGATGG  TTTTGTGGG  GATGGGCTAG  GGGAAATAAG  1860
GCTTGTCTGT  TGTTTTCTGT  GGGCGCTCCC  TCCAATTTG  CAGATTTTGT  CAACCTCTCT  1920
CTGAGCCGGG  ATTGTCGAAT  TACTAAATG  TAAATAATCA  CGTATTGTGG  GGAGGGGAGT  1980
TCCAAGTGTG  CCTCTCTTT  TTTCTCTGCC  TGGATTATT  AAAAAGCCAT  GTGTGGAAC  2040
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Seq ID NO: C95 DNA Sequence  
Nucleic Acid Accession #: NM\_002510.1  
Coding sequence: 92..1774

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TCTGCTCCTG  GCTGCAAGAT  TGCCACTTGA  TGCCGCCAAA  CGATTTCATG  ATGTGCTGGG  180
CAATGAAAGA  CCTTCTGCTT  ACATGAGGGA  GCACAATCAA  TTAATAGGCT  GGTCTTCTGA  240
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AAACTCCTGG  AAGGGAGGCC  GTGTGAGGCG  GGTCTGACCC  AGTGACTCAC  CAGCCCTGCT  360
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CAGACCTTCA  AAACCCACCC  CTCTTTAGG  ACCTGCTGGT  GACAAACCCC  TGGAGCTGAG  1140
TAGGATTCCT  GATGAAACT  GCCAGATTAA  CAGATATGGC  CACTTTCAG  CACCATCAC  1200
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5	GCCATGGCCT	GAAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCCAC	1320
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	CCCTGTGTGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCTT	1500
	GATTTCCTGT	CCTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAAAC	GTGCCCTGAT	1560
	CTCGTTTGGC	TGCTTGGCCA	TAITTTGTCAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAAACA	1620
	CAAGGAATAC	AACCCAATAG	AAAATAGTCC	TGGGAATGTG	GTGAGAACCA	AAGGCTGTAG	1680
	TGTCCTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCCAGAAA	AGGATCCGCT	1740
10	ACTCAAAAAC	CAAGAATTTA	AAGGAGTTTC	TTAAATTTCC	ACCTTGTTC	TGAAGCTCAC	1800
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	TTATTGTAA	ATAGATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGGT	TAAATGTCAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATCTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCATTATA	AAGTCTTAGG	2040
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	ATGCATAAAG	CCATGTAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
	TTCAATACAC	ACTCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
	GTGCACACTT	GCTAGACTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
20	TGACAACTCA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTTCCAT	2400
	GGACATTTAG	TTAGTGTCTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGTAT	2460
	ATTTCCAAAT	TTTTGTATAG	TCGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGTGC	CTGTGTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTCACC	TCTGTTTGTG	2580
25	ACTAAACCA	TCTACTATAT	GTTAGACATG	ACATTTCTTT	TCTCTCCTTC	CTGAAAAATA	2640
	AAGTGTGGGA	AGAGACAAAA	AAAAAAAAAA				2669

Seq ID NO: C96 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1\_4247

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35	ACAGGAGCAC	TGAATCAAAA	AAATTGGGGA	AAGAAATATC	CAACATGTAA	TAGCCCAAAA	180
	CAATCTCCTA	TTAATATTGA	TGAAGATCTT	ACACAAGTAA	ATGTGAATCT	TAAGAAACTT	240
	AAATTTTCAGG	GTGGGATAAA	AACATCATTG	GAAAAACAT	TCATTCTATA	CACTGGGAAA	300
	ACAGTGGAAA	TTAATCTCAC	TAATGACTAC	CGTGTGAGCG	GAGGAGTTTC	AGAAATGGTG	360
	TTTAAAGCAA	GCAAGATAAC	TTTTCACTGG	GGAAAATGCA	ATATGTCATC	TGATGGATCA	420
40	GAGCATAGTT	TAGAAGGACA	AAAATTCCA	CTTGAGATGC	AAATCTACTG	CTTTGATGCA	480
	GACCGATTTT	CAGTCTTTGA	GGAAGCAGTC	AAAGGAAAAG	GGAAGTTAAG	AGCTTTATCC	540
	ATTTTGTTTG	AGGTTGGGAC	AGAAGAAAAT	TTGATTTC	AAGCGATTAT	TGATGGAGTC	600
	GAAAGTGTTA	GTCGTTTTGG	GAAGCAGGCT	GCTTTAGATC	CATTCTACT	GTGAAACCTT	660
	CTGCCAAACT	ACTGACAAA	GTATTACATT	TACAATGGCT	CATTGACATC	TCCTCCCTGC	720
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	GCTGTTTTTT	GTGAAGTTCT	TACAATGCAA	CAATCTGGTT	ATGTCATGCT	GATGGACTAC	840
	TTACAAAACA	ATTTTGGAGA	GCAACAGTAC	AAGTTCTCTA	GACAGGTGTT	TTCTCTATAC	900
	ACTGGAAAGG	AAGAGATTCA	TGAAGCAGTT	TGTAGTTTCAG	AACCAGAAAA	TGTTTCCAGCT	960
	GACCCAGAGA	ATTATACCGA	CCTTCTTGT	ACATGGGAAA	GACCTCGAGT	CGTTTATGAT	1020
50	ACCATGATGG	AGAAGTTTGC	AGTTTGTGAC	CAGCAGTTGG	ATGGAGAGGA	CCAAACCAAG	1080
	CATGAATTTT	TGACATGAGG	CTATCAAGAC	TTGGGTGCTA	TTCTCAATAA	TTTGCTACCC	1140
	AATATGAGTT	ATGTTCTTCA	GATAGTAGCC	ATATGCACTA	ATGGCTTATA	TGAAAAATAC	1200
	AGCGACCAAC	TGATTGTGGA	CATGCCTACT	GATAATCCTG	AACTTGATCT	TTTCCCTGAA	1260
	TTAATTGGAA	CTGAAGAAAT	AATCAAGGAG	GAGGAAGAGG	GAAAAGACAT	TGAAGAAGGC	1320
55	GCTATTGTGA	ATCTCGTAG	AGACAGTGCT	ACAAACCAAA	TCAGGAAAAA	GGAACCCCAAG	1380
	ATTTCTACCA	CAACACACTA	CAATGSCATA	GGAACGAAAT	ACAAATGAAGC	CAAGACTAAC	1440
	CGATCCCCAA	CAAGAGGAAG	TGAATTCTCT	GGAAAGGGTG	ATGTTCCCAA	TACATCTTTA	1500
	AAATCCACTT	CCCAACCACT	CACTAAATTA	GCCACAGAAA	AAGATATTTC	CTTGACTTCT	1560
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60	GGCTCTAAAA	CTGTTCTTAG	ATCTCCACAT	ATGAACCTGT	CGGGGACTGC	AGAATCCTTA	1680
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	GAGAACATAT	CCCAAGGGTA	TATATTTTCC	TCCGAAAACC	CAGAGACAAT	AACATATGAT	1860
	GTCTCTATAC	CAGAACTCTG	TAGAAATGCT	TCCGAAAGATT	CAACTTCACT	AGGTTTCAGAA	1920
65	GAATCACTAA	AGGATCCTTC	TATGGAGGGA	AATGTGTGGT	TTCTAGCTC	TACAGACATA	1980
	ACAGCACAGC	CCGATGTTGG	ATCAGGCAGA	GAGAGCTTTC	TCCAGACTAA	TTCACTGAG	2040
	ATACGTTGTT	ATGAATCTGA	GAAAGCAACC	AAGTCTTTTT	CTGCAGGCCC	AGTGATGTCA	2100
	CAGGGTCCCT	CAGTTACAGA	TCTGGAAATG	CCACATTATT	CTACCTTTGC	CTACTTCCCA	2160
	ACTGAGGTAA	CACCTCATGC	TTTTACCCCA	TCCTCCAGAC	AACAGGATTT	GGTCTCCAG	2220
70	GTCAACGTGG	TATACTCGCA	GACAACCCAA	CCGATATACA	ATGAGGCCAG	TAATAGTAGC	2280
	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	2340
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	TACTGGAGGA	AATGCTTTCA	GACTGCACAC	TTTTACTTAG	AGGACAGTAC	ATCCCTTAGA	2460
	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	CCAATTTTCA	ATGATGTGCG	AGCAATTCCA	2520
75	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	2580
	TTTGAGGAAG	TGCAGAGCTG	TACTGTTGAC	TTAGGTATTA	CAGCAGACAG	CTCCAACCA	2640
	CCAGACAAACA	AGCAAGAGAA	TCGATACATA	AATATCGTTG	CCTATGATCA	TAGCAGGGTT	2700
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	GTTGATGGCT	ACAACAGACC	AAAAGCTTAT	ATTGCTGCC	AAGGCCCACT	GAAATCCACA	2820
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	AACCTCGTGG	AGAAAGGAAG	GAGAAAATGT	GATCAGTACT	GGCCTGCGGA	TGGGAGTGAG	2940
	GAGTACGGGA	ACTTCTGGT	CACCTCAGAA	AGTGTGCAAG	TGCTTGCTTA	TTATCTGTG	3000
	AGGAATTTTA	CTCTAAGAAA	CACAAAATA	AAAAAGGGCT	CCCAAGAAAG	AAGACCCAGT	3060
	GGACGTGTGG	TCACACAGTA	TCACATACAG	CAGTGGCCTG	ACATGGGAGT	ACCAGAGTAC	3120
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	ATCGTTTAC	AAAGAAATTA	TTTGGTACAA	ACTGAGGAGC	AAATGTCCTT	CATTTCATGAT	3360
	ACACTGTTTG	AGGCCATACT	TAGTAAAGAA	ACTGAGGTGC	TGGACAGTCA	TATTCATGCC	3420
	TATGTTAATG	CACCTCTCAT	TCTTGGACCA	GCAGGCAAAA	CAAAGCTAGA	GAAACAATTC	3480
	CAGCTCTGTA	GCCAGTCAAA	TATACAGCAG	AGTGACTATT	CTGCAGCCCT	AAAGCAATGC	3540
	AACAGGGAAA	AGAATCGAAC	TTCTTCTATC	ATCCCTGTGG	AAAGATCAAG	GGTTGGCATT	3600
	TCATCCCTGA	GTGGAGAAGG	CACAGACTAC	ATCAATGCCT	CCTATATCAT	GGGCTATTAC	3660
10	CAGAGCAATG	AATTCATCAT	TACCCAGCAC	CCTCTCCTTC	ATACCATCAA	GGATTTCTGG	3720
	AGGATGATAT	GGGACCATAA	TGCCCAACTG	GTGGTTATGA	TTCTGTATGG	CCAAAACATG	3780
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	AAGGTCACCT	TTATGGCTGA	AGAACACAAA	TGCTATCTTA	ATGAGGAAAA	ACTTATAATT	3900
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15	TGTCCTAAAT	GGCCAAATCC	AGATAGCCCC	ATTAGTAAAA	CTTTGAACT	TATAAGTGTT	4020
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	GTGACGGCAG	GAACCTTCTG	TGCTCTGACA	ACCCCTATGC	ACCAACTAGA	AAAAGAAAAA	4140
	TCCGTGGATG	TTTACCAGGT	AGCCAAGATG	ATCAATCTGA	TGAGGCCAGG	AGTCTTTGCT	4200
	GACATTGAGC	AGTATCAGTT	TCTCTACAAA	GTGATCCTCA	GCCTTGTGAG	CACAAGGCAG	4260
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Seq ID NO: C97 DNA Sequence  
Nucleic Acid Accession #: XM\_031379  
Coding sequence: 148..7095

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	CGCGAGGGGG	CGCGACACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGGAAG	AGATTGGCTG	GTCTTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
35	CAAGTAAATG	TGAATCTTAA	GAACCTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGGA	420
	AACACATTCG	TTCATTAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTACGCGGAG	GAGTTTCAGA	AAATGGTGT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCACATT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
40	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTTCAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	CGAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAACTCAA	CTGACAAGTA	TTACATTTC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCCTAC	AATGCAACAA	960
45	TCTGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACAG	1020
	TTCTCTAGAG	AGGTTTCTTC	TCATACACT	GGAAAGGAAG	AGATTTCATGA	AGCAATTTGT	1080
	AGTTTCAAGC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
50	GGTGCTATTG	TCATAAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
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	AATCTCTAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACAG	AAGAAATAT	CAAGGAGGAG	1440
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	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCACC	TCACACTGTG	1740
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60	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCCTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTATCAGG	TTTCAAGGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGTTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
65	AGCTTTCTCC	AGACTAAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
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	CATTATTCTA	CCTTTGCCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
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	GATAAGGTGC	CCTTGCAATG	TTCTCTGCCA	GTGGCTGGGG	GTGATTTGCT	ATTAGAGCCC	2760
75	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
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	GGGCTGCAG	CCCTTAAACAT	TTCTTCACTT	GTTCCTGTAG	CTGAATTATC	ATATACAACA	3240
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	TCTCAAGCAT CTGGTGACAC TTGCTTAAA CCTGTGCTTA GTGCAAACTC AGAGCCAGCA 3600
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Seq ID NO: C113 DNA Sequence  
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Nucleic Acid Accession #: NM\_006671.2  
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 Nucleic Acid Accession #: NM\_000676  
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	GCAGGCACTG	TCAGGCACT	GAGCTGATGG	ACCACTCGAG	GACCACCTTC	CAGCGGAGAA	1020
	TCCATGCAGC	CAAGTCACTG	GCCATGATTT	TGGGGATTTT	TGCCCTGTGC	TGGTTACCTG	1080
	TGCATGTCTG	TAACTGTGTC	ACTCTTTTCC	AGCCAGCTCA	GGGTAAAAAT	AAGCCCAAGT	1140
	GGGCAATGAA	TATGGCCATT	CTTCTGTAC	ATGCCAATTC	AGTTGTCAAT	CCCATTTGCT	1200
25	ATGCTTACGC	GAACCGAGAC	TTCCGCTACA	CTTTTCACAA	AATTATCTCC	AGGTATCTTC	1260
	TCTGCCAAGC	AGATGTCAAG	AGTGGGAATG	GTCAAGCTGG	GGTACAGCCT	GCTCTCGGTG	1320
	TGGGCTATG	ATCTAGGCTC	TGCGCTCTTC	CAGGAGAAGA	TACAATCCCA	CAAGAAACAA	1380
	AGAGGACACG	CGTGTGTTTC	ATTGTGAAG	ATAGCTACAC	CTCACAAGGA	AATGACTGCG	1440
	CTCTCTTGAG	CATTTCCCTG	GAGCTACACC	GTATCTAGCT	AATATGTATG	TGTCAGTAGT	1500
30	AGGCTCCAAG	ATGTGACAAA	TATATTTATG	ATCTATTACG	CTGCTTTTAC	TGTGTGGATT	1560
	ATGCCAACAG	CTTGAATGGA	TTCTAACAGA	CTCTTTTGTG	TTTAAAGTTC	TGCTTGTGTT	1620
	ATGGTGGAAA	ATTACTGAAA	CTATTTTACT	GTGAAACAGT	GTGAACATT	ATAATGCAAA	1680
	TACTTTTATA	CTTAGAGGCA	ATGGAATAAT	AAAAGTTGAC	TGTACTAAAA	ATG	1733

Seq ID NO: C120 DNA Sequence

Nucleic Acid Accession #: NM\_052932

Coding sequence: 217..786

	1	11	21	31	41	51	
40	CCCAGCCCCG	CCCCGCGGCC	CCGGCTGCGC	ACGCGAAGCC	CCCTCCAGGC	CCCGCTCCTG	60
	CGCCCTATTT	GGTCATTGCG	GGGGCAAGCG	CGGGGAGGGG	AAACGTGCGC	GGCCGAAGGG	120
	GAGGCGAGC	CGGCGCGGCG	TGCGCAGAGG	AGCCGCTCTC	GCGCGCGCCA	CCTCGCTGCG	180
	GAGCCACGA	GGCTGCCGCA	TCCTGCCCTC	GGAACAATGG	GACTCGGCGC	GCGAGGTGCT	240
45	TGGGCGCGCG	TGCTCCTGGG	GAGCTGCGAC	GTGCTAGCGC	TGCTGGGGGC	CGCCCATGAA	300
	AGCGCAGCCA	TGGCGGAGAC	TCTCCAACAT	GTGCTTCTG	ACCATACAAA	TGAAACTTCC	360
	AACAGTACTG	TGAAACCAAC	AACTTCAGTT	GCCTCAGACT	CCAGTAATAC	AACGGTCACC	420
	ACCATGAAC	CTCAGCGGCG	ATCTAATACA	ACAAACCCAG	GGATGGTCTC	AACAAATATG	480
	ACTTCTACCA	CCTTAAAGTC	TACACCCAAA	ACAAACAATG	TTTACAGAAA	CACATCTCAG	540
50	ATATCAACAT	CCACAATGAC	CGTAACCCAC	AATAGTTCAG	TGACATCTGC	TGCTTCTACA	600
	GTAAACATCA	CAACAACACT	GCATTCTGAA	GCAAGAAAG	GATCAAAAT	TGATAGTGGG	660
	AGCTTTGTTG	GTGGTATTGT	ATTAAACGCT	GGAGTTTAT	CTATTCTTTA	CATTGGATGC	720
	AAAAATGATT	ACTCAAGAAG	AGGCATTGCG	TATCGAACCA	TAGATGAACA	TGATGCCATC	780
	ATTTAAGGAA	ATCCATGGAC	CAAGGATGGA	ATACAGATTG	ATGCTGCCCT	ATCAATTAAAT	840
55	TTTGTTTAT	TAAATAGTTA	AAACAATATT	CTCTTTTGA	AAATAGTATA	AACAGGCCAT	900
	GCATATAAGT	TACAGTGAT	TACGTAAATA	TGTAAAGATT	CTTCAAGGTA	ACAAAGGGTT	960
	GGGTTTTGAA	ATAAACATCT	GGATCTTATA	GACCGTTCAT	ACAATGGTTT	TAGCAAGTTC	1020
	ATAGTAAGAC	AAACAAGTCC	TATCTTTTTC	TTTTTGGCTG	GGGTGGGGGC	ATTGGTCACA	1080
	TATGACCAGT	AATTGAAAGA	CGTCATCACT	GAAGACAGAA	ATGCCATCTG	GGCATAACAA	1140
60	TAAGAAATTT	GTACAGCAGC	TCAGGATTTT	GGGTATCTTT	TGTAGCTCAC	ATAAGAAACT	1200
	TCAGTGTCTT	TCAGAGCTGG	ATATATCTTA	ATTACTAATG	CCACACAGAA	ATTATACAAT	1260
	CAAACTAGAT	CTGAAGCATA	ATTTAAGAAA	AACATCAACA	TTTTTTGTGC	TTTAAACTGT	1320
	AGTAGTTGGT	CTAGAAACAA	AATACTCCAA	AAAAAAGAAA	ATTTTCAAAAT	AAAACCCAAA	1380
	ATAATAGCTT	TGCTTAGCCC	TGTTAGGGAT	CCATTGGAGC	ATTAAGGAGC	ACATATTTTT	1440
65	ATTAACCTCT	TTTGAGCTTT	CAATGTGTAT	GTAATTTTGT	TTCTCTGTGT	AATTTAGGTA	1500
	AACTGCAGTG	TTTAAACATA	TAATGTTTGA	AAGACTTAGT	TGTCAGTATT	AAATAATCCT	1560
	GGCATTATAG	GGAAAAAACC	TCCTAGAGAT	TAGATTATTT	GCTACTGTGA	GAATATTGTC	1620
	ACCACTGGAA	GTTACTTTAG	TTCAATTTAT	TTTAATTTTA	TATTTTGTGA	ATATTTTAAG	1680
	AACTGTAGAG	CTGCTTTCAA	TATCTAGAAA	TTTTTAATTG	AGTGTAAACA	CACCTAACTT	1740
70	TAAGAAAAAG	AACCGCTTGT	ATGATTTTCA	AAAGAACATT	TAGAATTTCT	TAGAGTCAAA	1800
	ACTATAGCGT	AATGCTGTGT	TTATTAAGCC	AGGATTTGTG	GGACTTCCCC	CAGGCAACTA	1860
	AACCTGCAGG	ATGAAAAATG	TATATTTTCT	TTCAATGCACT	GTCGATATTA	CTCAGATTTG	1920
	GGGAATGAC	ATTTTATATC	TAAACAAAC	ACCATAATAT	TTTAGAATAA	ATTTCTTAGAA	1980
	AGTTTGTAGA	GGAAATTTTGA	GAGAGGACAT	TTCTCTCTTC	CTGATTTTGA	TATTCCTTCA	2040
75	AATCCCTCCT	CTTACTCCAT	GCTGAAGGAG	AAGTACTCTC	AGATGCATTA	TGTTAATGGA	2100
	GAGAAAAAGC	ACAGATTATG	AGACACCA	ATATTAGCTA	ATGTATTTTG	GAGTGTTTTC	2160
	CATTTTACAG	TTTATATTCC	AGCACTCAAA	ACTCAGGCTC	AAGTTTAAAC	AAAAGAGGTA	2220
	TGTAGTCACA	GTAAATACTA	AGATGGCAAT	TCTATCTCAG	AGGGCCAAAG	TGAATCACAC	2280
	CAGTTTCTGA	AGGTCTCTAA	AATAGCTCAG	ATGTCTTAAT	GAACATGCAC	CTACATTTAA	2340
80	TAGGAGTACA	ATAAACTGT	TGTCAGCTTT	TGTTTACAG	AGAACGCTAG	ATATTAGAA	2400
	TTTTGAAATG	GATCATTTCT	ACTTGTCTGT	CAITTTAAAC	AATAATCTGA	TGAATATAGA	2460
	AAAAATGAT	CCAAATATG	GATATGATTG	GATGATGTGA	ACACATACAT	GGAGTATGGA	2520
	GGAAATTTTC	TGAAAAATAC	ATTTAGATTA	GTTTAGTTTG	AAGGAGAGGT	GGGCTGATGG	2580
	CTGAGTTTGA	TGTTACTAAC	TTGGCCCTGA	CTGGTTGTGC	AACCATTTGT	TCATTTCTTT	2640
	GCAAAAATGA	GTTAAGATAT	ACITTTATCT	AATGAAGGCC	TTTTAAATTT	GTCCACTGCA	2700

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TTCCTGGTAT TTCACTACT CAAGTCAGTC AGAACTTCGT AGACCGACCT GAAGTTTCTT 2760  
TTTGAATACT TGTTCCTTTA GCACCTTTGAA GATAGAAAAA CCACCTTTTAA AGTACTAAGT 2820  
CATCATTTCG CTGAAAGTTT TCCTCTGCAAT TGGGTTTGAA GTAGTTTAGT TATGCTCTTT 2880  
TCTCTGTATG TAAGTAGTAT AATTGTGTAC TTTCAAATAC CCGTACTTTG AATGTAGGTT 2940  
TTTTTGTGTG TGTATCTAT AAAAATTGAG GAAATGGTT ATGCAAAAAA ATATTTTGCT 3000  
TTGGACCAT TTTCTTAAGC ATAAAAAAT GCTCAGTTTT GCTTGCAATC CTTGAGAATG 3060  
TATTTATCTG AAGATCAAAA CAAACAATCC AGATGTATAA GTACTAGGCA GAAGCCAATT 3120  
TTAAATTTTC CTGAAATAAT CCATGAAAGG AATAATTCAA ATACAGATAA ACAGAGTTGG 3180  
CAGTATATTA TAGTGATAAT TTTGTATTTT CAAMAAAAAA AAAGTTAAAC TCTTCTTTTC 3240  
TTTTTATTAT AATGACCAGC TTTTGGTATT TCATTGTITAC CAAGTTCTAT TTTTAGATAA 3300  
AATTGTTCTC CTCTAAAAA AAAAAAATA AAAAAA 3338

Seq ID NO: C121 DNA Sequence

Nucleic Acid Accession #: NM\_004195

Coding sequence: 1..726

1 11 21 31 41 51  
| | | | |  
ATGGCAGCAGC ACGGGGCGAT GGGGCGGTTT CGGGCCCTGT GCGGCGCTGGC GCTGCTGTGC 60  
GCGCTCAGCC TGGGTTCAGC CCCACCGGG GGTCCCGGGT GCGGCGCTGG GCGCTCCTG 120  
CTTGGGACGG GAACGGACGC GCGCTGCTGC CGGTTCACA CGACGCGCTG CTGCGCGAT 180  
TACCGGGGCG AGGAGTGTCT TCCGAGTGG GACTGCATGT GTGTCCAGCC TGAATTCAC 240  
TGGGAGACCC CTGTGTCAC GACCTGCGCG CACCACCTT GTCCCGCAGG CCAGGGGGTA 300  
CAGTCCAGG GGAATTCAG TTTTGGCTTC CAGTGTATCG ACTGTGCTC GGGGACCTTC 360  
TCCGGGGGCC ACGAAGGCCA CTGCAAACTT TGGACAGACT GCACCCAGTT CGGGTTTCTC 420  
ACTGTGTTC CTGGGAACAA GACCCACAAC GCTGTGTGCG TCCAGGGTC CCGCGCGGCA 480  
GAGCGCTTG GGTGCTGAC CGTGTCTTC CTGGCGTGG CCGCTGCGT CCTCTCTG 540  
ACCTGCGGCC AGCTTGACT GCACATCTGG CAGCTGAGGA GTCACTGCAT GTGCCCCGA 600  
GAGACCCAGC TGCTGCTGGA GGTGCCGCCG TCGACCGAAG ACGCCAGAAG CTGCCAGTTC 660  
CCCGAGGAAG AGCGGGGCGA GCGATCGGCA GAGGAGAAGG GCGGCTGGG AGACCTGTG 720  
GTGTA 726

Seq ID NO: C122 DNA Sequence

Nucleic Acid Accession #: AK091896.1

Coding sequence: 28..1572

1 11 21 31 41 51  
| | | | |  
AGATCCGCGA GCCCGTCAGC CTGCGCCATG GGCTGCGACG GCGCGGTGTC GGGGCTGCTC 60  
CGCCCAACC TGCAGCCAC GCTCACCCTAC TGGAGCGTCT TCTTCAGCTT CGGCTGTGC 120  
ATCGCCTTCC TGGGGCCAC GCTGCTGGAC CTGCGCTGTC AGACGCACAG CTGCTGCC 180  
CAGATCTCT GGTCTTCTT CTGCGACAG CTCTGCTCC TGCTGGGACG CGCCCTCGGG 240  
GGCGTCTTCA AAAGGACCTT GGGCCAGTCA CTATGGGCC TGTTCACTCT CTCTCTGGCC 300  
ATCTCCCTGG TGTTTGGCGT CATCCCTTC TGGCGCGACG TGAAGGTGCT GGCCTCAGTC 360  
ATGGCGCTGG CGGGCTTGGC CATGGCTGCG ATCGACACCG TGGCCACAT GCAGCTGGTA 420  
AGGATGTACC AGAAGGACTC GGGCGTCTT CTCCAGGTGC TCCATTCTT CTGCGGCTTT 480  
GGTGTCTGCG TGAGCCCTCT TATGTCTGAC CCTTCTCTGT CTGAGGCCAA CTGCTTGCT 540  
GCCAATAGCA CGGCCAACAC CACCTCCGGA GGCACCTGT TCCATGTCTC CAGGGTCTG 600  
GGCCAGCACC ACGTAGATGC CAAGCCTTGG TCCAACCGA CGTTCCAGG GCTGACTCCA 660  
AAGGACGGGG CGGCGACCG AGTGTCTAT GCCTTCTGGA TCATGGCCCT CATGATCTT 720  
CCAGTGCCCA TGGCTGTGCT GATGCTGCTG TCCAAGGAGC GGCTGCTGAC CTGCTGTCCC 780  
CAGAGGAGGC CCTGCTTCT GTCTGCTGAT GAGCTTGCTT TGGAGACACA GCTCTGTGAG 840  
AAGGAAGATG CCTCTCACT GCGCCCAAG TTTCACTCAC ACCTAGGCGA TGAGGACCTG 900  
TTCACTGCTT GCCAAGGAA GAACCTCAGA GGAGCCCTT ATTCTTCTT TGCCATCCAC 960  
ATCAGCGGCG CCTGCTACT GTTCAATGAG GATGGGTGA GGGGTGCTTA TTCGCTTC 1020  
GTGTACAGCT ATGCTGTGGA GAAGCCCTG TCTGTGGAC ACAAGGTGGC TGGCTACCTC 1080  
CCCAGCTCT TCTGGGGCTT CATCACACT GCGCGGCTCC TCTCAATTCC CATATCTCTA 1140  
AGAATGAAGC CGGCCACCAT GGTTTTCATC AAGTGGTTG GCGTGGTGGT GACGTTCCCTG 1200  
GTGCTGCTTA TTTTCTCCTA CAACGTCGTC TTTCTGTTG TGGGACGGC AAGCTGGGC 1260  
CTGTTTCTCA GCAGCACCTT CCCCAGCATG CTGGCTTACA CGGAGGACT GCTGCACTAC 1320  
AAAGGCTGTG CAACCAAGT GCTGTGACA GGGGACAGAG TTGGCGAGAT GGTGCTGAC 1380  
ATGCTGGTTG GTTCGATATT CAGGCTCAG GGCAGCTATA GTTTCCTGGT CTGTGGCGTG 1440  
ATCTTGTGTT GTCTGGCTTT TAOCCTCTAT ATCTTGCTCC TGTTTTCCA CAGGATGCAC 1500  
CCTGAGTCCC CATCAGTCCC TAOCCTAGAC AGATCAATTG GAATGGAAAA CTCTGAGTGC 1560  
TACCAGAGGT AAACTGGGT GAAGAAGGCA AGAGAAGACT TTCAGCTCT TGATCACCAG 1620  
CAGACCATTA CTGTTTCAGA AAGCTGGGTG GTGGTGGAGG CGCTCTCTCA ATGGCTATTC 1680  
AAGTCTTCT CACTAAAAT TGGTTGGGTA GAGGAAATTA AATTGAGTCC TGGTACCTGG 1740  
TCAAATCAT TAGAAGTTTA CCTGGCTTCT CAAGTTATCT TCTTCCCTGG TTCAGACTGT 1800  
TGGTAAGAGC TGTCCAGATA CCCAGATGGG AAGGAAGGAG ACAGCGCGCG GCTTCACTCC 1860  
ATTTGTACC TCATGCTAG ACCATACTCT GGGTTGAGA TCATTCTTCA TTGAAGTTTG 1920  
TAAATATAGG TTGAATTTGT AAAGCTCCAT GATCACTGCT ATATGTAGAT ATATTCAAT 1980  
TTAAGCAAAA CAAGCTGCAA GTTATCCCT GGCATGCTCA AAGGATTTTC GTGCTTTTCA 2040  
CTTAATAGTC CAAAGTCTCT TAAATCCCT CTGCAGATAT CAATAGCTTA TCTATATTCT 2100  
CAACACCAA AAGGAAAGT TGAATCTTGC TCTCTTTGGT ATACTAATGT AGTGGTATGC 2160  
TAAGCTGGCT CATACCAACT TAGAAAAGCT GATTGTAAAA TTTTCATTTT GACAGCTGGT 2220  
TATTAATGTC AGGCATTATT AAAAATCAAA TCATACAAAC TTATAATTAA ATCAATTACA 2280  
TTTAAACAA AGGTAATAAA TATCAAAGC ATATCACTTC CT 2322

Seq ID NO: C123 DNA Sequence

Nucleic Acid Accession #: NM\_002203.2

Coding sequence: 43..3588

1 11 21 31 41 51  
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	CTGCAAAACC	AGOGCACTA	CGGTCCCCG	GTCAGACCA	GGATGGGGC	AGAAACGGA	60
	GGGGCCGGC	CGCTGCCGCT	GCTGCTGGT	TTAGCGCTCA	GTCAGGCAT	TTTAAATGT	120
	TGTTTGGCCT	ACAAATGTTG	TCTCCAGAA	GCAAAATAT	TTTCCGGTCC	TTCAAGTGAA	180
5	CAGTTTGGGT	ATGCAGTGCA	GCAGTTTATA	AATCCAAAG	GCAACTGGTT	ACTGGTTGGT	240
	TCACCCCTGGA	GTGGCTTTCC	TGAGAACOGA	ATGGGAGATG	TGTATAAATG	TCTGTTGAC	300
	CTATCCACTG	CCACATGTGA	AAAACATAAT	TTGCAAACTT	CAACAAGCAT	TCCAAATGTT	360
	ACTGAGATGA	AAACCAACAT	GAGCCTCGGC	TTGATCCTCA	CCAGGAACAT	GGGAACTGGA	420
	GGTTTTCTCA	CATGTGCTCC	TCTGTGGGCA	CAGCAATGTC	GGAAATCAGTA	TTACACAACG	480
10	GGTGTGTGTT	CTGACATCAG	TCCTGATTTT	CAGCTCTCAG	CCAGCTTCTC	ACCTGCAACT	540
	CAGCCCTGCC	CTTCCCTCAT	AGATGTTGTG	GTTGTGTGTG	ATGAATCAAA	TAGTATTAT	600
	CCTTGGGATG	CAGTAAAGAA	TTTTTTGGAA	AAATTTGTAC	AAGGCCTTGA	TATAGGCCCC	660
	ACAAAGACAC	AGGTGGGGTT	AATTCAGTAT	GCCAATAATC	CAAGAGTTGT	GTTAACTTGT	720
	AACACATATA	AAACCAAGA	AGAAATGATT	GTAGCAACAT	CCCAGACATC	CCAATATGGT	780
15	GGGACCTCA	CAAAACATT	CGGAGCAATT	CAATATGCAA	GAAATATGTC	CTATTCAGCA	840
	GCCTCTGGTG	GGCGACGAAG	TGCTACGAAA	GTAATGCTAG	TTGTAACATG	CGGTGAATCA	900
	CATGATGGTT	CAATGTTGAA	AGCTGTGATT	GATCAATGCA	ACCATGACAA	TATACGTAGG	960
	TTTGGCATAG	CAGTTCTTGG	GTACTTAAAC	AGAAACGCC	TTGATACTAA	AAATTTAATA	1020
	AAAGAAATAA	AAGCGATCGC	TAGTATTCCA	ACAGAAAGAT	ACTTTTTCAT	TGTTGCTGAT	1080
20	GAAGCAGCTC	TACTAGAAAA	GGCTGGGACA	TTAGGAGAAC	AAATTTTCAG	CATTGAAGGT	1140
	ACTGTTCAAG	GAGGAGACAA	CTTTCAGATG	GAAATGTCAC	AAGTGGGATT	CAGTGACGAT	1200
	TACTCTTCTC	AAAAATGATAT	TCTGATGCTG	GGTGCAGTGG	GAGCTTTTGG	CTGGAGTGGG	1260
	ACCATTGTCC	AGAAGACATC	TCATGGCCAT	TTGATCTTTC	CTAAACAAGC	CTTTGACCAA	1320
	ATTCTGCAAG	ACAGAAATCA	CAGTTTCATAT	TTAGGTTACT	CTGTGGCTGC	AATTTCTACT	1380
25	GGAGAAAGCA	CTCACTTTGT	TGCTGGTGT	CCTCGGGCAA	ATTATACCGG	CCAGATAGTG	1440
	CTATATAGTG	TGAATGAGAA	TGGCAATATC	ACGGTTATTC	AGGCTCACCG	AGGTGACCAG	1500
	ATTGGCTCCT	ATTTTGTGAT	TGTGCTGTGT	TCAGTTGATG	TGGATAAAGA	CACCATTTACA	1560
	GACGTGCTCT	TGGTAGGTGC	ACCAATGTAC	ATGAGTGACC	TAAAGAAAGA	GGAAGGAAGA	1620
	GTCTACCTGT	TACTATCAAA	AAAGGGCATT	TTGGGTGAGC	ACCAATTTCT	TGAAGGCCCC	1680
30	GAGGGCATTG	AAACACTGCG	ATTTGGTTCA	GCAATTCAG	CTCTTTCAGA	CATCAACATG	1740
	GATGGCTTTA	ATGATGTGAT	TGTTGGTTCA	CCACTAGAAA	ATCAGAAATC	TGGAGCTGTA	1800
	TACATTTTACA	ATGGTCATCA	GGGCACTATC	CGCACAAGT	ATTCCAGAA	AACTTTGGGA	1860
	TCCGATGGAG	CCTTTAGGAG	CCATCTCCAG	TACTTTGGGA	GGTCTTGGGA	TGGCTATGGA	1920
	GATTTAAATG	GGGATTCAT	CACCGATGTG	TCTATTGGTG	CCTTTGGACA	AGTGGTTCAA	1980
35	CTCTGGTCAC	AAAGTATTGC	TGATGTAGCT	ATAGAAGCTT	CATTTCACAC	AGAAAAATC	2040
	ACTTTGGTCA	ACAAGAATGC	TCAGATAATT	CTCAAACTCT	GCTTCAGTGC	AAAGTTTCAGA	2100
	CCTACTAAGC	AAAACAATCA	AGTGGCCATT	GTATATAACA	TCACACTTGA	TGCAGATGGA	2160
	TTTTTCAATC	GAGTAACTCC	CAGGGGGTTA	TTTAAAGAAA	ACAATGAAG	GTGCTGTCAG	2220
	AAGAATATGG	TAGTAAATCA	AGCACAGAGT	TGCCCCGAGC	ACATCATTTA	TATACAGGAG	2280
40	CCCTCTGATG	TGTGCAACTC	TTTGGATTGG	CGTGTGGACA	TCAGTCTGGA	AAACCCCTGGC	2340
	ACTAGCCCTG	CCCTTGAAGC	CTATTCTGAG	ACTGCCAAGG	TCTTCAGTAT	TCTTTCCAC	2400
	AAAGACTGTG	GTGAGGATGG	ACTTTGCATT	TCTGATCTAG	TCTAGATGT	CCGACAAATA	2460
	CCAGCTGCTC	AAGAACAACC	CTTTATTGTC	AGCAACCAAA	ACAAAGGTT	ACATTTTCA	2520
	GTAACACTGA	AAAAATAAAG	GGAAAGTGCA	TACAACACTG	GAATTGTTGT	TGATTTTCA	2580
45	GAAACTTGT	TTTTTGCATC	ATTCTCCCTA	CGGTTGATG	GGACAGAGT	AAACATGCCAG	2640
	GTGGCTGCAT	CTCAGAAAGT	TGTTGCTGTC	GATGTAGGCT	ACCTGCTTT	AAAGAGAGAA	2700
	CAACAGGTGA	CTTTTACTAT	TAACTTTGAC	TTCAATCTTC	AAAACTTCA	GAATCAGGCG	2760
	TCTCTCAGTT	TCCAGCCCTT	AAGTGAAAGC	CAAGAAGAAA	ACAAGGCTGA	TAATTTGGTC	2820
	AACTCTAAAA	TTCTCTCCTT	GTATGATGCT	GAAATTCAT	TAACAAGATC	TACCAACATA	2880
50	AAATTTTAT	AAATCTCTTC	GGATGGGAAT	GTTCCTTCAA	TCTGTGCACAG	TTTTTGAAGAT	2940
	GTGGTCCAA	AAATCTCTTC	CTCCCTGAAG	GTAACAACAG	GAAAGTGTCC	AGTAAGCATG	3000
	GCAACTGTAA	TCATCCATAT	CCCTCAGTAT	ACCAAGAAA	AGAACCCTAT	GATGTACCTA	3060
	ACTGGGGTGC	AAACAGACAA	GGCTGGTGAC	ATCAGTTGTA	ATGCAGATAT	CAATCCACTG	3120
	AAAAATAGAC	AAACATCTTC	TTCTGTATCT	TTCAAAAGTG	AAAATTTTCA	GCACAACAAA	3180
55	GAATTTAACT	CGAGAACTGC	TTCTGTAGT	AAATTTTCACT	GCTGGTTGAA	AGACGTTTCA	3240
	ATGAAGAGAG	AAATCTTTGT	TAAATGTGACT	ACCAAGAAAT	GGAAACGGGAC	TTTGCATCA	3300
	TCAACGTTCC	AGACAGTACA	GCTAACGGCA	GCTGCAGAAA	TCAACACCTA	TAACCCCTGAG	3360
	ATATATGTGA	TGAAGATAA	CACCTGTTACG	ATTCCCTGTA	TGATAATGAA	ACCTGATGAG	3420
	AAAGCCGAAG	TACCAACAGG	AGTTATATA	GGAAGTATAA	TTGCTGGAAT	CCTTTTGTCTG	3480
60	TAGCTCTGG	TTGCAATTTT	ATGGAAGCTC	GGCTTCTTCA	AAAGAAAATA	TGAAAAGATG	3540
	ACCAAAAATC	CAGATGAGAT	TGATGAGACC	ACAGAGCTCA	GTAGCTGAAC	CAGCAGACCT	3600
	ACCTGCAAGT	GGAAACGGCA	GCATCCAGC	CAGGGTTTGC	TGTTTGCCTG	CATGGATTTT	3660
	TTTTTAAATC	CCATATTTT	TTTATCATGT	CGTAGGTAAA	CTAACCTGCT	ATTTTAAAGAG	3720
	AAAACCTGAC	GTACGTTTGG	ATGAAGAAAT	TGTGGGGGCT	GGGGGAGGTG	CGGGGGGACG	3780
65	GTAGGGAAT	AATAGGGAAT	ATACCTATTT	TATATGATGG	GGGAAAAAAA	GTAACTCTTA	3840
	AACTGGCTGG	CCAGAGATTT	ACATTTCTAAT	TTGCATTGTC	TCAGAAACAT	GAAATGCTTC	3900
	CAAGCATGAC	AACCTTTTAA	GAAAAATATG	ATACTCTCAG	ATTTTAAAGG	GGAAAACTGT	3960
	TCTCTTTTAA	ATATTTGTCT	TTAAACAGCA	ACTACAGAG	TGGAAGTGCT	TGATATGTAA	4020
	GTACTTCCAC	TTGTGTATAT	TTTAAATGAAT	AITGATGTTA	ACAAGAGGGG	AAAAACAAAAC	4080
70	ACAGGTTTTT	TCAATTTATG	CTGCTCATCC	AAAGTTGCCA	CAGATGATAC	TTCCAAATGA	4140
	TAAATTTTAT	TATAACTAG	GTAAATTTG	TTGTTGGTTC	CTTTTATACC	ACGGCTGCC	4200
	CTTCCACACC	CCATCTTGCT	CTAATGATCA	AAACATGCTT	GAATAACTGA	GCITAGAGTA	4260
	TACCTCTCTAT	ATGTCATTTT	AAGTTAGGAG	AGGGGGOGAT	ATAGAGACTA	AGGCACAAAA	4320
	TTTGTGTTAA	AACTCAGAAAT	ATAACATTTA	TGTAATAATCC	CATCTGCTAG	AAGCCCATCC	4380
75	TGTGCCAGAG	GAAGGAAAG	GAGGAAATTT	CCTTTCTCTT	TTAGGAGGCA	CAACAGTTCT	4440
	CTTCTAGGAT	TGTTTGGCT	GACTGGCAGT	AACCTAGTGA	ATTTTGTAAA	GATGAGTAAT	4500
	TTCTTTGGCA	ACCTTCTCTC	TCCTTACTG	AACCACTCTC	CCACCTCTCT	GTGGTACCAT	4560
	TATTATAGAA	GGCCTCTACA	GCTGACTTTT	CTCTCCAGCG	GTCACAAAGT	ATCCCTCTCT	4620
80	TCCACCTTCA	TCCAAAGTTC	CCACTCTTTC	AGGACAGCTG	CTGTGCATTA	GATATAGGG	4680
	GGGAAAGTCA	TCTGTTTAAAT	TTACACACTT	GCATGAATTA	CTGTATATAA	ACTCCTTAAAC	4740
	TTCAGGGAGC	TATTTTCAAT	TAGTGCTAAA	CAAGTAAGAA	AAATAAGCTA	GAGTGAATTT	4800
	CTAAATGTGT	GAATGTAAAT	AATGTAAAGT	AAAACTCTCT	CAGGATTTTCA	4860	
	CCAGAAAGTTA	CAGATGAGGC	ACTGGAACCC	ACCAACCAAT	TAGCAGGTGC	ACCTTCTGTG	4920
	CTGCTCTGT	TTCTGAAGTA	CTTTTCTTTC	CACAAGAGTG	AATTTGACCT	AGGCAAGTTT	4980
	GTTCAAAAGG	TAGATCTGTA	GATGATTTGG	TCAGATTGGG	ATAAGGCCCA	GCAATCTGCA	5040



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 TTTTAAACAG CACCCCAATC ACTAGGATGC AGATGGACCA CACTTTGAGA AACACCAACC 5100  
 ATTTCTACTT TTTCACCTT ATTTCTCTG TTCCTGAGCC CCCACATTCT CTAGGAGAAA 5160  
 CTTAGATTAA AATTACAGCA CACTACATAT CTAAAGCTTT GACAGTCTCT TGACCTCTAT 5220  
 AAACCTCAGA GTCCCTCATT TAAATGGGA AGACTGAGCT GGAGTTCAGC AGTGATGCTT 5280  
 TTTAGTTTAA AAAGTCTATG ATCTGATCTG GACTTCTCTAT AATACAAATA CACAATCTCT 5340  
 CAAGAATTG ACTTGGAAAA G 5361

Seq ID NO: C124 DNA Sequence

Nucleic Acid Accession #: NM\_031460

Coding sequence: 103..1101

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 1 11 21 31 41 51  
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 20 ACGTGTCTGG ACCGCGCGGC GCTGGACTCG CTGATCCGGG ATGTCTCCA AGCATACAAA 360  
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 25 GGGGGCACTT GGCAGGATCC TGACAAGGCG CGGTGGCTGG CCGGCTCTGG CGCCCTCTTC 660  
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 30 CTGGAGACGC CAGGGAGGGT ATGTCTCTGC TGCCACCACT GCTCTAAGGA AGACTTCAG 960  
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 35 CTAGAGGCTG GGTGAGCTA TATGATTAAT TCTGCCAAT AGGGTATACA GAGACATGTC 1260  
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 40 GAAATAAACA TCTATGAAA 1519

Seq ID NO: C125 DNA Sequence

Nucleic Acid Accession #: NM\_004154

Coding sequence: 309..1295

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 CACGATGGGG AATTGTGCTC AGCACTTCAC GGACTGCAAG CGAGGCACCT GCTAACTCTT 420  
 55 GGATAACAAAG ACCCTGCGCA GAAGAACCAT GGCTTTGGAA GGCAGAGTTC AGGCTGAGGA 480  
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 65 GCGCGCGGCG TGCTGGGCTA GTGTGTGTAG CCGTGTGGCT GGCCTGAGCA ACCCAGTGCC 1020  
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 80 ACAAAAATAC AGTGTGACGT GTACTGTCAA AA 1832

Seq ID NO: C126 DNA Sequence

Nucleic Acid Accession #: NM\_007197

Coding sequence: 18..1763

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	TGATGGGGCA	CGAGAACCAG	CGCGAGGCAG	CCATCCAGTT	GCAAGAGTTC	GCGCGCTGG	240
	TGGAGTACGG	CTGCCACGGC	CACCTCCGCT	TCTTCTCTGT	CTCGCTGTAC	GCGCGATGT	300
	GCACCGAGCA	GGTCTCTACC	CCCATCCCGG	CCTGCGGGGT	CATGTGCGAG	CAGGCCCCGGC	360
	TCAAGTGTCT	CCCGATTATG	GAGCAGTTCA	ACTTCAAGTG	GCCCGACTCC	CTGGACTGCC	420
	GGAAATCTCC	CAACAAGAAC	GACCCCAACT	ACCTGTGCAT	GGAGGCGCCC	AACAACGGCT	480
10	CGGACGAGCG	CACCCGGGGC	TGGGGCTGT	TCCCGCGGCT	GTTCCGGCG	CAGCGGCCCC	540
	ACAGCGCGCA	GGAGCACCGG	CTGAAGGACG	GGGGCCCCGG	GCGCGGCGG	TGGCAACACC	600
	CGGGCAAGTT	CCACCAGCTG	GAGAAGAGCG	CGTCGTGCGC	GCCGCTCTGC	ACGCCCGGGG	660
	TGGACGTGTA	CTGGAGCGCG	GAGGACAAGC	GCTTCGCAGT	GSTCTGGCTG	GCCATCTGGG	720
	CGGTGCTGTG	CTTCTCTCC	AGCGCTTCA	CGGTGCTCAC	CTTCTCATC	GACCCGGCCC	780
15	GCTTCCGCTA	CCCGAGCGCG	CCCATCATCT	TCCTCTCCAT	GTGCTACTGC	GTCTACTCG	840
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	GCCAGCTCTA	TGTCATCCAG	GAGGAGCTGG	AGAGCACCGG	CTGCACGCTG	GTCTTCTGG	960
	TCCTCTACTA	CTTCGGCATG	GCCAGCTCGC	TGTGGTGGGT	GTCCTCAAG	CTCACTGGT	1020
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20	ACCTGGCAGC	CTGGGCCATG	CGGGCGGTGA	AGACCATCTT	GATCCTGGTC	ATGCGCAGGG	1140
	TGGCGGGGGA	CGAGCTCACC	GGGGTCTGCT	ACGTGGGCG	CATGAGCTGC	AAOGGCTCA	1200
	CCGGCTTCGT	GCTCATTTCC	CTGGCTGCT	ACCTGGTCAT	CGGCACGTC	TTCTTCTCT	1260
	CGGGCTTCGT	GGCCCTGTTT	CACATCCGGA	GGGTGATGAA	GACGGGCGG	GAGAACACGG	1320
	ACAAGCTGGA	GAGGCTCATG	GTGCGTATCG	GGCTCTTCTC	TGTGCTGTAC	ACCGTGCGGG	1380
25	CCACCTGTGT	GATCGGCTCG	TACTTTTACG	AACGCTTCAA	CATGGATTAC	TGGAAGATCC	1440
	TGGCGGCGCA	GCACAAGTGC	AAAATGAACA	ACCAGACTAA	AACGCTGGAC	TGCCTGATGG	1500
	CGGCTTCCAT	CCCGCGCGTG	GAGATCTTCA	TGGTGAAGAT	CTTTATGCTG	CTGGTGGTGG	1560
	GGATCACCG	CGGGATGTGG	ATTTGGACCT	CCAAGACTCT	GCAGTCTCTG	CAGCAGGTGT	1620
	GCAGCGCTAG	GTTAAAGAGC	AAGAGCCGGA	GAAACCGGCG	CAGCGTGATC	ACCAGCGGTG	1680
30	GGATTTACAA	AAAAGCCAG	CATCCCCAGA	AAACTCACCA	CGGAAATAT	GAGATCCCTG	1740
	CCCAGTCCGC	CACCTGCGTG	TGAACAGGGC	TGGAGGGAAG	GGCACAGGGG	CGCCCGGAGC	1800
	TAAGATGTGG	TGCTTTTCTT	GGTTGTGTTT	TTCTTTCTTC	TTCTTTCTTT	TTTTTTTTTT	1860
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	ACACTGAAG	GAAAAATGTA	CTTAAAGGGT	TTTGTTTTGT	TTTGGTTTTC	CAGCGAAGGG	1980
35	AAGCTCCTCC	AGTGAAGTAG	CCTCTTGTGT	AACTAAATTT	TGGTAAAGTA	GTTGATTTCAG	2040
	CCCTCAGAG	AAAACCTTTT	TTTAGAGCCC	TCCGTAATA	TACATCTGTG	TATTTAGATT	2100
	GGCTTTGCTA	CCCATTTACA	AATAAGAGGA	CAGATAACTG	CTTTGCAAT	TCAAGAGCCT	2160
	CCCTCGGGT	ACAAATGAG	CCATCCCGAG	GGCCACCCCG	CAGGAAGGCG	ACAGTGCTGG	2220
	GCGCATCCG	TGCAGAGGAA	AGACAGGACC	CGGGGCCCCG	CTCACACCCC	AGTGGATTTC	2280
40	GAGTTGCTTA	AAATAGACTC	TGGCTTTCAC	CAATAGTCTC	TCTGCAAGAC	AGAAACCTCC	2340
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	AAATAAAGAG	AGAAACAGT	ATTTGTCTAT	ATATAAGAGC	AAACAAAGAA	ATCTCCTAAC	2460
	AAAAGACTGA	AGAGGCCAG	CCCTCAGAAA	CCCTTCAGTG	CTACATTTTG	TGGCTTTTAA	2520
	ATGGAACCA	AGCCAAATGT	ATAGACGTTT	GGACTGATTT	GTGGAAGGGA	GGGGGGAAGA	2580
45	GGGAGAGGA	TCATTCAAAA	GTTACCCAAA	GGGCTTATTT	ACTCTTTCTA	TTGTTAAACA	2640
	AATGATTTCC	ACAAACAGAT	CAGGAAGCAC	TAGGTTGGCA	GAGACACTTT	GTCTAGTGTA	2700
	TTCTCTTAC	AGTGCCAGGA	AAGAGTGGTT	TCTGCGTGTG	TATATTGTA	ATATATGATA	2760
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	Nucleic Acid Accession #: NM_005761.1						
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	GGATGGGGCG	GCGCGGGGAG	CCCGAGCGCG	CGCAGGAACC	GCGCGCGCGG	CCGCGCGGGT	180
	CTCGGTGGCC	GCGCGGCTGA	GCGCGCGTGG	CGCGCGCGCG	CCCTGCGCGG	GGGCGGCCCC	240
60	CCAGCCCCCA	TGGAGGTCTC	CCGGAGGAA	GCGCGCGCGC	GCCCCCGCGG	CCCGCGAGCG	300
	CCACTGCCCC	TGCTGCGCTA	TCTGCTGGCA	CTGCGGCTGC	CGGCGCGGGG	CGGGAAGAG	360
	CCCGTGTGGC	GGTGGAGCA	AGCCATCGGA	GCCATCGCGG	CGAGCCAGGA	GGACGCGCTG	420
	TTTGTGGCGA	GCGGCAGCTG	CCTGGACCAG	CTGGACTACA	GCTTGGAGCA	CAGCCTCTCG	480
	CGCCTGTACC	GGGACCAAGC	GGGCAACTGC	ACAGAGCCGG	TCTCGCTGGC	GCCCCCGCGG	540
65	CGGCCCCGGC	CGGCGAGCAG	CTTCAGCAAG	CTGCTGCTGC	CCTACCGCGA	GGGGGCGGGC	600
	GGCCTCGGGG	GGCTGCTGCT	CACCGGCTGG	ACCTTCGACC	GGGGCGCTGC	CGAGGTGCGG	660
	CCCCTGGGCA	ACCTGAGCGG	CAACTCCCTG	CGCAACGGCA	CCGAGGTGGT	GTGCTGCCAC	720
	CGCAGGGGCT	CGACGGCGGG	CGTGGGTGAC	CGCGCGGGCC	GGAAACAAAG	CTGGTACCTG	780
	GCGGTGGCGG	AGACCTAGCT	GCTGCTGAG	CGGAGAGGG	CGAGCGGCTG	CAACCCCGCG	840
70	GCATCCGACC	ACGACACGGC	CATCGCGCTC	AAGGACAGGG	AGGGGCGCAG	CCTGGCCACG	900
	CAGGAGCTGG	GGCGCTTCAA	GCTGTGCGAG	GGCGGGGCA	GCTGCACTTG	CGTGGACGCC	960
	TTTCTCTGGA	ACGGCAGCAT	CTACTTCCCC	TACTACCCCT	ACAACCTATC	GAGCGGGCTG	1020
	GCCACCGGCT	GGCCAGCAT	GGCGCGCATC	GCGCAGAGCA	CGAGGTGCTT	GTTCCAGGGC	1080
	CAGGCATCCC	TGAGCTGCGG	CCACGGCCAC	CCGACGGGCC	GCGCGCTGCT	CCTCTCTCC	1140
75	AGCCTAGTGG	AGGCCCCGGA	CGTCTGGGCG	GGAGTGTTC	GCGCGGCGCG	TGAGAGGGGC	1200
	CAGGAGCGGC	GCTCCCCCAC	CACCAACGGC	CTCTGCTCTT	TCAGAAATGAG	TGAGATCCAG	1260
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	TCGTTTATG	GCACCGTGGT	AATGAACAGG	ACTGTTTAT	TCTTGGGGAC	TGGAGATGGC	1440
80	CAGTTACTTA	AGGTTATCT	TGGTGAGAA	TTGACTTCAA	ATTGTCCAGA	GTTTATCTAT	1500
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	AAGACTACAG	TGACTATGGT	GGGAAGCTTC	TCTCCAAGAC	ACTCAAAGTG	CATGGTGAAG	1860
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5	TTGGTTTCTT	GGAAATTTAT	AGACAGATTTC	AACTTTACCA	ACTGCTCATC	ATTAAAGAA	2040
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	CCCTTCCAG	CTTGCGACCC	TTCTGATTAT	GAGAGAAACC	AGGAACAGTG	TCCAGTGGCT	2160
	GTGAGAGA	CATCAGGAGG	AGGAAGACCC	AAGGAGAACA	AGGGGAACAG	AACCAACCAG	2220
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	AGCAACGTGA	TAGTAACGGG	AGCAAACTTT	ACCCGGGCAT	CGAACATCAC	AATGATCCTG	2340
10	AAAGGAACCA	GTACCTGTGA	TAAGGATGTG	ATACAGGTTA	GCCATGTGCT	AAATGACACC	2400
	CACATGAAT	TCTCTCTTCC	ATCAAGCCGG	AAAGAAATGA	AGGATGTGTG	TATCCAGTTT	2460
	GATGGTGGGA	ACTGCTCTTC	TGTGGGATCC	TTATCCTACA	TTGCTCTGCC	ACATTGTTC	2520
	CTTATATTTC	CTGCTACCCAC	CTGGATCAGT	GGTGGTCAAA	ATATAACCAT	GATGGGCAGA	2580
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	CTGCAGTATC	GGGAGGACCC	CAGATTACCG	GGGTATCGGG	TGGAATCCGA	GGTGGACACA	2820
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20	AGAAATCAAG	ATCTTACCAC	CATCCTTTTC	AAAATTAAAG	GCATCAAGAC	TGCAAGCACC	3000
	ATTGCCAACT	CTTCTAAGAA	AGTTCCGGTC	AAGCTGGGAA	ACCTGGAGCT	CTACGTCGAG	3060
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25	AGTCAACAAC	TAGAATTGCT	GGAAAAGCAG	CTCCGAAAG	AGATACGTGA	CGGCTTTGCT	3240
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	ACTGAAGTGA	TACTAACAAG	AGACGCCAAC	GACAAGAATG	AAAGTCTCAC	AGCTTTGGAT	3420
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30	AACCTTCTG	TGAAGGACAG	GTGCTGTGTT	GCCTCTCTCC	TAACCATTCG	ACTGCAAAAC	3540
	AAGCTGTGCT	AGCTGACCAG	CATCCTAGAG	GTGCTGACCA	GGGACTGTAG	GGAACAGTGT	3600
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	ACTGTGGCAT	TAAACGTCGT	CTTTGAAAAA	ATCCCGGAAA	ACGAGAGTGC	AGATGTCTGT	3900
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40	ATTCTTGAAG	ATGGAATCAC	CAAGCTAAAC	ACCAATGGCC	ACTATGAGAT	ATCAATGGA	4140
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45	AGCAGAGCTC	CATTGTCTAT	AAAATACTTT	TTTGACTTTT	TGGACGCCCA	GGCTGAAAAA	4440
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	CAGCAACTAG	GGAAAGGAAG	ACCAACTAAT	AAGCTTCTCT	ATGCCAAGGA	TATCCCAACC	4680
50	TACAAGAAAG	AAATGAAATC	TTATTACAAA	GCAATCAGGG	ATTTGCTCTC	ATTGTATCC	4740
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Seq ID NO: C128 DNA Sequence

Nucleic Acid Accession #: NM\_002185.1

Coding sequence: 23..1402

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	AGAACTGGAT	GACTACTCAT	TCTCATGCTA	TAGCCAGTTG	GAAGTGAATG	GATCGCAGCA	180
	TTCACTGACC	TGTGCTTTTG	AGGACCCAGA	TGTCAACACC	ACCAATCTGG	AATTGAAAT	240
	ATGTGGGGCC	CTGCTGGAGG	TAAAGTGCC	GAATTTCAAG	AAACTACAG	AGATATATTT	300
70	CATCGAGACA	AGAAATCTCT	TACTGATTGG	AAAGAGCAAT	ATATGTGTGA	AGGTTGGAGA	360
	AAAGAGTCTA	ACCTGCAGAAA	AAATAGACCT	AACCACTATA	GTAAACCTG	AGGCTCCTTT	420
	TGACCTGAGT	GTATCTATC	GGGAAGGAGC	CAATGACTTT	GTGGTGACAT	TTAATACATC	480
	ACACTTGCAA	AAAGAATATG	TAAAGATTTT	AATGCATGAT	GTAGCTTACC	GCCAGGAAAA	540
	GGATGAAAA	AAATGAGACG	ATGTGAATTT	ATCCAGCACA	AAGCTGACAC	TCCTGCAGAG	600
75	AAAGCTCCAA	CCGGCAGCAA	TGTATGAGAT	TAAAGTTGGA	TCCATCCCTG	ATCACTATTT	660
	TAAAGGCTTC	TGGAGTGAAT	GGAGTCCAG	TTATTACTTC	AGAACTCCAG	AGATCAATAA	720
	TAGCTCAGGG	GAGATGGATC	CTATCTTACT	AACCATCAGC	ATTTGAGTTT	TTTTCTCTGT	780
	GGCTCTGTTG	GTACTCTTGG	CCTGTGTGTT	ATGGAAAAAA	AGGATTAAAC	CTATCGTATG	840
	CCCGAGTCTC	CCCGATCATA	AGAAAGACTCT	GGAACATCTT	TGTAAGAAAC	CAAGAAAAAA	900
80	TTTAAATGTG	AGTTTCAATC	CTGAAAGTTT	CCTGAACTGC	CAGATTGATA	GGGTGGATGA	960
	CATTCAAGCT	AGAGATGAAG	TGGAAGGTTT	TCTGCAAGAT	ACGTTTCTCT	AGCAACTAGA	1020
	AGAACTCTGAG	AAGCAGAGGC	TTGGAGGGGA	TGTGCAGAGC	CCCAACTGCC	CATCTGAGGA	1080
	TGTAGTCGTC	ACTCCAGAAA	GCTTTGGAAG	AGATTCAATC	CTCACATGCC	TGGCTGGGAA	1140
	TGTCAGTGCA	TGTGACGCC	CTATTCTCTC	CTCTTCCAGG	TCCCTAGACT	GCAGGGAGAG	1200
	TGGCAAGAA	GGGCTCATG	TGTACCAGGA	CCTCTCTGTT	AGCCTTGGGA	CTACAAACAG	1260

5 CACGCTGCC CCTCCATTTT CTCTCCAATC TGAATCCTG ACATTGAACC CAGTTGCTCA 1320  
GGGTCAGCCC ATTCTTACTT CCTGGGATC AAATCAAGAA GAAGCATATG TCACCATGTC 1380  
CAGCTTCTAC CAAAACCAAGT GAAGTGTAAG AAACCCAGAC TGAACCTTACC GTGAGCGACA 1440  
AAGATGATTT AAAAGGGAAG TCTAGAGTTC CTAGTCTCCC TCACAGCACA GAGAAGACAA 1500  
AATTAGCAAA ACCCCACTAC ACAGTCTGCA AGATTCTGAA ACATTGCTTT GACCACTCTT 1560  
CCTGAGTTCA GTGGCACTCA ACATGAGTCA AGAGCATGCT GCTTCTACCA TGTGGATTG 1620  
GTCACAAGGT TTAAGGTGAC CCAATGATTG AGCTATTT 1658

10 Seq ID NO: C129 DNA Sequence  
Nucleic Acid Accession #: NM\_002722.1  
Coding sequence: 15..302

15 1 11 21 31 41 51  
| | | | |  
ACTCTGGACT CCGGATGGCT GCGCAGGCC TCTGCCTCTC CCGTCTGCTC CTGTCCACCT 60  
GCGTGGCTCT GTTACTACAG CCATGCTGG GTGCCAGGG AGCCCCACTG GAGCCAGTGT 120  
ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCAGTA TGCAGCTGAT CTCGTAGAT 180  
ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAGACA CAAAGAGGAC ACGTGGCCT 240  
TCTGGAGTG GGGTCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGAATTAT 300  
20 ATGCGACCT TCTGTCTCT ACGACTCCAT GAGCAGCGCC AGCCAGCTC TCCCTCTG 360  
ACCTTGGCT CTGGCCAAAG CTGTCTCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420  
AAGCC 425

25 Seq ID NO: C130 DNA Sequence  
Nucleic Acid Accession #: NM\_032545.1  
Coding sequence: 47..718

30 1 11 21 31 41 51  
| | | | |  
AAATGATCT TCAATGCACT AAGAGAAGGA GACTCTCAA CAAAAATGA CCTGGAGGCA 60  
CCATGTGAGG CTCTGTGTTA CGGTGAGTTT GGCAATACAG ATCATCAATT TGGGAAACAG 120  
CTATCAAGGA GAGAAACATA ACGGCGTAG AGAGGAAGTC ACCAAGTTG CCACTCAGAA 180  
GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCAATTC GGAGAGGTGA CTGGGAGCGC 240  
CGAGGGCTGG GGGCCGGAGG AGCCGCTCCC TACTCCCGG GCTTTCGGAG AGGGTGGCTC 300  
35 CGCGCGGCCG CGCTGCTGCA GGAAACGGCGG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG 360  
CCCGGCCAC TACCCGGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGGC 420  
CTGGAGCAC GGAGCGTGA CCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGCG 480  
CCTGCACTGC CTCCCCTCC AGACGCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540  
CCACGCTCAC GGGCCGAGCG CCGGGGGCGC GCCCAGCCTG CTACTCTTGC TGCCCTGCGC 600  
40 ACTCCTGCAC CGCCTCTGCG GCCCGGATGC GCCCGGCGAC CCTCGGTCCC TGGTCCCTTC 660  
CGTCTCCAG CGGGAGCGGC GCCCTGCGG AAGGCGGGA CTGGGCATC GCCTTTAATT 720  
TTCTATGTTG TAAATAATAG ATGTGTTTAG TTACCGTAA GCTGAAGCAC TGGGTGAATA 780  
TTTTTATTTG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840  
AAAAAA 846

45 Seq ID NO: C131 DNA Sequence  
Nucleic Acid Accession #: NM\_006533.1  
Coding sequence: 72..467

50 1 11 21 31 41 51  
| | | | |  
AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60  
CAGATGCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCTC 120  
TCTCCGACCG TGGTGTGACG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180  
55 CGGACCGAGA GTGACGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGGCC 240  
CCGACTGCGG ATTCTGTACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300  
AGGGCCGTTG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360  
CTGCTCGCCT GGGCTATTTC CCGAGTAGCA TTGTCCGAGA GGAACGAGAC CTGAAACCTG 420  
60 GCAAGTGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480  
CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAATATC AATCAGCCCA GTGCAAAAC 538

65 Seq ID NO: C132 DNA Sequence  
Nucleic Acid Accession #: AB064272  
Coding sequence: 1..708

70 1 11 21 31 41 51  
| | | | |  
ATGACACAAG TCACAGAAAA GTCCACAGAA CACCCAGAAA AGACCAAGTC AACCAAGAG 60  
AAAACACAA GAACCCAGAA AAGCCTAAG CTATACTCAG AGAAGACCAT ATGCACCAA 120  
GGGAAAAACA CACCACTCCC AGAAAAGCCT ACAGAAAACC TGGGSAACAC CACACTGACC 180  
ACTGAGACCA TAAAGCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC 240  
ACAAAGACTA TAAACCTTC AGTCAAGGTC ACAGAGACA AATCTCTCAC TACTACCTCT 300  
TCTATCTTAA ATAAACTGA AGTTACTCAT CAGGTGCCA CTGGTTCTTT CACCTCAT 360  
75 ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAAGCCA CAGGAAACGA GAGCCATCCA 420  
TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCAAGCTG GACAGATGGG AGAGAATGAT 480  
TCATTCCCTG CATGGGCCAT AGTTAATGTG GTCCCTGGTG CTGTGATTCT CCTCCTGGTG 540  
TTCTTGGCC TGATCTTCTT GGTCTCTAT ATGATGCGGA CACGCGCAG ACTAACCCAG 600  
AACACCCAGT ACAATGATGC AGAGGATGAG GGTGGCCCA ATTCTACCC GGTCTACCTG 660  
80 ATGGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGGTGA 708

Seq ID NO: C133 DNA Sequence  
Nucleic Acid Accession #: NM\_080870.1  
Coding sequence: 3..710

	1	11	21	31	41	51	
5	AGATGACACA	AGTCACAGAA	AAGTCCACAG	AACACCCAGA	AAAGACCACG	TCAACCCACG	60
	AGAAAAACCAC	AAGAACCCCA	GAAAAGCCCTA	OGCTATATCT	AGAGAGAGACC	ATATGCACCA	120
	AAGGGAAAAA	CACACCAGTC	CCAGAAAAGC	CTACAGAAAA	CCTGGGGAAC	ACCACACTGA	180
	CCACTGAGAC	CATAAAAGCC	CCAGTAAAGT	CCACAGAAAA	CCCAGAAAAA	ACAGCAGCAG	240
	TCACAAAGAC	TATAAAACCT	TCAGTCAAGG	TCACAGGAGA	CAAACTCTCT	ACTACTACCT	300
10	CTTCTCATCT	AAATAAAACT	GAAGTTACTC	ATCAGGTGCC	CACCTGGTTCT	TTCAACCTCA	360
	TTACATCTAG	AACGAAGCTG	AGTTCTATCA	CATCAGAAAC	CACAGGAAAC	GAGAGCCATC	420
	CATACCTCAA	TAAAGATGGC	TCACAGAAAG	GTATCCAAGC	TGGACAGATG	GGAGAGAAATG	480
	ATTCAATCCC	TGCATGGGCC	ATAGTTAATG	TGGTCCTGGT	GGCTGTGATT	CTCCTCCTGG	540
	TGTTCTTGG	CCTGATCTTC	TTGGTCTCCT	ATATGATGCG	GACACGCCGC	ACACTAACCC	600
15	AGAACACCCA	GTACAATGAT	GCAGAGGATG	AGGGTGGCCC	CAATTCTTAC	COGGTCTACC	660
	TGATGGAGCA	GCAGAATCTT	GGCATGGGCC	AGATCCCTTC	CCCAOCGTGA	TCTTGGAGTA	720
	GGCGCCACGC	CCTGGCTCTT	CCATGCTCTG	CCCTTTCTCT	GGATGAGGAA	COGGACTCAC	780
	AATTTCTATT	TCOGGGACTA	CAGGAAGGGC	AGAGAATACT	GACGGTTACC	AGTATTAACC	840
	CTTCATCTGT	TCTTGAACCT	GGTTGGGGAA	TGAGGTGATA	AGCAAGGAGG	GTGTAAAGTT	900
20	AGGGGACAAA	GAAGAAAGAA	TGAATAATAC	GAGCAGACAT	TCTCTGTAGA	AGGTAATGGT	960
	CTGAGAATGA	AAAGGTGTTT	GATGGACATG	TTGTGGGGGC	ACCAATGCAG	AACACTGCAC	1020
	TGAGTCTCAA	AGGAAGGACA	GGAGCCTTAT	AGGCAATGCC	CCAGACTGAC	TTGTGAGTGG	1080
	GGTTTATGGG	GAAAGGGAGG	GACTGAGGGC	AGAGTCTCTG	GGTTTCAGGA	CAGCATTATG	1140
	TTAATTCAT	TCACTATTAC	TTAAGAGTTT	GTGTGTAAC	AGGCTCATCT	CTGAGTTCTC	1200
25	AGGACCCCTG	CCCCCACCCT	CATTTTCTTA	ATGAAAAAAA	AAAACAAAA	AAACGGATCC	1260
	AAGAAGAAAA	GAGAATTTAT	TTCTTCTCC	ACTCTCTCCA	TGCCCTGGAG	AAAAAAAAGT	1320
	CCAGAAGAAA	TCATAAATAT	CTCTCATCTA	CATGGTTGCT	TCTCTTCTCT	CCCAATCCOC	1380
	TTAGTTTCTC	TAAATGTCTA	CAGTGGACGC	CCTGTTGGTT	TGGCTTGCCT	GGTTTGGGGT	1440
	GGACACGCAA	GGAGGGGATT	TTTATTGGC	CAGCAGTCTC	ACCCACTGAT	CTCCACCCCA	1500
30	GACCTTCCCT	GATTGGTGTG	TCAGCATTTA	TTTTCTCTGC	TCTTCCACCA	AAAGCCAGCT	1560
	GTAGCTTTAT	CTCGTAAAGG	TTACCCATCT	TCTCTACTGT	CCCAATTCTC	TCTCTCTGCT	1620
	CCTTCACCCC	AGATTCAAGT	TTTCTCTCTT	GTAGGCATTT	CATCTGTGTG	TGTTTCTCTG	1680
	ATTTTCTCTC	TCTCTTCTTA	TGGCCATTTC	ACCTTATTAC	TGATTGGGTA	GAGGGGAAAA	1740
35	AGGAGAATGA	TGATGATAGT	TTCTTCTGT	CTATTGACCT	TTTTTATAAT	AAAGTATAAC	1800
	ATGTT						1805

Seq ID NO: C134 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..10674

40	1	11	21	31	41	51	
	ATGTGGCCCTC	GCCTGGCCCTT	TTGTTGCTGG	GGTCTGGGCG	TCGTTTCGGG	CTGGGCGACC	60
45	TTTCAGCAGA	TGTCCCGCTC	GCGCAATTTT	AGCTTCCGCC	TCTTCCCGCA	GACCCGCGCC	120
	GGGGCCCCCG	GGAGTATCCC	OGCGCGCGCC	GCTCCTGGCG	ACGAAGCGCG	GGGGAGCAGA	180
	GTGGAGCGGC	TGGGCCAGGC	GTTCCGCGCA	CGCGTGCGGC	TGCTGCGGGA	GCTCAGCGAG	240
	CGCCTGGAGC	TTGTCTTCTT	GGTGGATGAT	TCGTCCAGCG	TGGGCGAAGT	CAACTTCCGC	300
	AGCGAGCTCA	TGTTGCTGCG	CAAGCTGCTG	TCGCACTTCC	COGTGGTGCC	CACGGCCACG	360
50	CGCGTGGCCA	TCTGACCTTT	CTGTCGAAG	AACTAAGTGG	TGCCGCGCGT	CGATTACATC	420
	TCCACCGGCC	GCGCGCGCCA	GCACAAGTGC	GCGCTGCTCC	TCCAAGAGAT	CCCTGCCATC	480
	TCCTACCGAG	GTGGCGGCAC	CTACACCAAG	GGCGCCTTCC	AGCAGCCGCG	GCAAAITCTT	540
	CTTCATGCTA	GAGAAAATCT	AACAAAAGTT	GTATTCTCTA	TCACTGATGG	ATATTCCAAT	600
	GGGGAGAGCC	CTAGACCAAT	TGCAGCGTCA	CTGGAGAGAT	CAGGAGTGA	GATCTTCACT	660
55	TTTGCCATAT	GGCAAGGGAA	CATTGAGAG	CTGAATGACA	TGGCTTCCAC	CCCAAAGGAG	720
	GAGCACTGTT	ACCTGCTACA	CAGTTTGTAA	GAATTTGAGG	CTTTAGCTCG	CCGGGCATG	780
	CATGAAGATC	TACCTTCTGG	GAGTTTATAT	CAAGATGATA	TGGTCCACTG	CTCATATCTT	840
	TGTGATGAAG	GCAAGGACTG	CTGTGACCGA	ATGGGAGACT	GCAAAITGTT	GACACACACA	900
	GGCCATTTTG	AGTGCATCTG	TGAAAAGGGG	TATTAAGGGA	AAGGTCTGCA	GTATGAATGC	960
60	ACAGCTTGCC	CATCGGGGAC	ATACAAACCT	GAAGGCTCAC	CAGGAGGAAT	CAGCAGTTGC	1020
	ATTCCATGTC	CTAGTGAARA	TCACACCTCT	CCACCTGGAA	GCACATCCCC	TGAAGACTGT	1080
	GTCTGCAGAG	AGGGATACAG	GGCATCTGGC	CAGACCTGTG	AACTTGTCCA	CTGCCCTGCC	1140
	CTGAAGCCCTC	COGAAAATGG	TTACTTTATC	CAAAACACTT	GCAACAACCA	CTTCAATGCA	1200
	GCCTGTGGGG	TCCGATGTCA	CCCTGGATT	GATCTTGTGG	GAAGCAGCAT	CATCTTATGT	1260
65	CTACCCAAATG	GTTTGTGGTC	CGGTTCAAG	AGCTACTGCA	GAGTAAGAAC	ATGTCTTCAT	1320
	CTCGCCACG	CGAAACATGG	CCACATCAGC	TGTTCTACAA	GGGAAATGTT	ATATAAGACA	1380
	ACATGTTTGG	TTGCCCTGTA	TGAAGGGTAC	AGACTAGAAG	GCACTGATAA	GCTTACTTGT	1440
	CAAGGAAACA	GCCAGTGGGA	TGGGCCAGAA	CCCCGGTGTG	TGGAGCGCCA	CTGTTCCACC	1500
70	TTTCAGATGC	CCAAAGATGT	CATCATATCC	CCCCACAAC	GTGGCAAGCA	GCCAGCCAAA	1560
	TTTGGGACGA	TCTGCTATGT	AAGTTGCCGC	CAAGGGTTCA	TTTTATCTGG	AGTCAAAGAA	1620
	ATGCTGAGAT	GTACCACTTC	TGGAAAATGG	AATGTGCGAG	TTTCCAGGAG	TGTGTGTAAG	1680
	GAGTGGAGGG	CTCCTCAAAAT	CACTGTCTCT	AAGGACATAG	AGGCTAAGAC	TCTGGAACAG	1740
	CAAGATTCTG	CCATGTTTAC	CTGGCAGATT	CCACAGCTTA	AAGACAATCT	TGGTGAAGAG	1800
	GTGTCACTCC	ACGTTTCTAT	AGCTTTCACC	CCACCTTAAC	TTTTCCCAAT	TGGAGATGTT	1860
75	GCTATGATAT	ACAGGCAAC	TGACCTATCC	GGCAACCCAG	CCAGCTGCAT	TTTCCATATC	1920
	AAGGTTATTG	ATGCAGAAC	ACCTGTCTAT	GACTGGTGCA	GATCTCCACC	TCCCGTCCAG	1980
	GTCTCGGAGA	AGGTACATGC	CGCAAGCTGG	GATGAGCCTC	AGTTCTCAGA	CAACTCAGGG	2040
	GCTGAATTGG	TCATTACCA	AAGTATATCA	CAAGGAGACC	TTTTCCCTCA	AGGGGAGACT	2100
	ATAGTACAGT	ATACAGCCAC	TGACCCCTCA	GGCAATAACA	GCACATGTGA	TATCCATATT	2160
80	GTCAATAAAG	GTCTCCCTTG	TGAAATTTCA	TTCAACCTGC	TAAATGGGGA	TTTTATATGC	2220
	ACTCCAGATA	ATACTGGAGT	CAACTGTACA	TAACTTGTCT	TGGAGGGCTA	TGATTTTACA	2280
	GAAGGCTCTA	CTGACAACTA	TTATTGTGCT	TATGAAGATG	GCGTCTGGAA	ACCAACATAT	2340
	ACCACTGAAT	GGCCAGACTG	TGCCAAAAAA	CGTTTTCGAA	ACCACGGGTT	CAAGTCTCTT	2400
	GAGATGTTCT	ACAAAGCAGC	TCGTTGTGAT	GACACAGATC	TGATGAAGAA	GTTTTCTGAA	2460
	GCATTTGAGA	CGACCTTGGG	AAAAATGGTC	CCATCATTTT	GTAGTGATGC	AGAGGACATT	2520

	GACTGCAGAC	TGGAGGAGAA	CCTGACCAA	AAATATTGCC	TAGAATATAA	TTATGACTAT	2580
	GAAAAATGGCT	TTGCAATTGG	ACCAGGTGGC	TGGGGTGCAG	CTAATAGGCT	GGATTACTCT	2640
	TACGATGACT	TCCTGGACAC	TGTGCAAGAA	ACAGCCACAA	GCATCGGCAA	TGCCAAGTCC	2700
5	TCACGGATTA	AAAGAAGTGC	CCCATTATCT	GACTATAAAA	TTAAGTTAAT	TTTTAACATC	2760
	ACAGCTAGTG	TGCCATTACC	CGATGAAAGA	AATGATACCC	TTGAATGGGA	AAATCAGCAA	2820
	CGACTCCTTC	AGACATTGGA	AACTATCACA	AATAAACTGA	AAAGGACTCT	CAACAAAGAC	2880
	CCCATGTATT	CCTTTAGCT	TGCATCAGAA	ATACTTATAG	COGACAGCAA	TTCAATTAGAA	2940
	ACAAAAAAGG	CTTCCCCTTC	CTGCAGACCA	GGCTCAGTGC	TGAGAGGGCG	TATGTGTGTC	3000
10	AATTGGCCTT	TGGGAACCTA	TTATAATCTG	GAACATTTC	CCTGTGAAAG	CTGCCGGATC	3060
	GGATCCTATC	AAGATGAAGA	AGGCAACTT	GAGTGCNAGC	TTTGCCCTC	TGGGATGTAC	3120
	ACGGAATATA	TCCATTCAAG	AAACATCTCT	GATTGTAAAG	CTCAGTGTAA	ACAAGGCACC	3180
	TACTCATACA	GTGGACTTGA	GACTTGTGAA	TCGTGTCCAC	TGGGCATTTA	TCAGCCAAAA	3240
	TTTGGTTCCG	GGAGCTGCCT	CTCGTGTCCA	GAACACACCT	CAACTGTGAA	AAGAGGAGCC	3300
	GTGAACATT	CTGCATGTGG	AGTTCCTTGT	CCAGAAGGAA	AATTCTCGCG	TTCTGGGTTA	3360
15	ATGCCCTGTC	ACCCATGTCC	TCGTGACTAT	TACCAACCTA	ATGCAGGGAA	GGCCTTCTGC	3420
	CTGGCCCTGTC	CCTTTTATGG	AACTACCCCA	TTGCTGSGTT	CCAGATCCAT	CACAGAATGT	3480
	TCAACTTATG	TTCTGAATAT	TACTATTTTC	GGTGGATTGG	GGCATCTGGA	GTGTGTTAAAT	3540
	TGTCCTTCTG	AGGTTTTC	TGAATGCTTC	TTAAACCTTT	GCCACAATAG	TGGAACCTGC	3600
	CAGCAACTTG	GGCGTGGTTA	TGTTTGTCTC	TGTCACCTTG	GATATACAGG	CTTAAAGTGT	3660
20	GAACACAGCA	TCGATGAGTG	CAGCCCACTG	CCTTGCCCTCA	ACAAATGGAGT	TTGTAAGGAC	3720
	CTAGTTGGGG	AAATTCATTG	TGAGTGCCTA	TCAGGTATACA	CAGGTACAGC	GTGTGAAGAA	3780
	AAATATAAATG	AGTGTAGCTG	CAGTCCCTTG	TTAAATAAAG	GAATCTGTGT	TGATGGTGTG	3840
	GCTGGCTATC	GTTCACATG	TGTGAAGGGA	TTGTAGGCC	TGCATTGTGA	AACAGAAGTC	3900
	AATGAATGCC	AGTCAAAACC	ATGCTTAAAT	AATGCAGTCT	GTGAAGACCA	GGTTGGGGGA	3960
25	TTCTTGTGCA	AATGCCCACT	TGGATTTTTG	GGTACCCGAT	GTGGAAGAAA	CGTCGATGAG	4020
	TGTCCTCAGT	AGCCATGCAA	AAATGGAGCT	ACCTGTAAAG	ACGGTGCCAA	TAGCTTCAGA	4080
	TGCCCTGTGTG	CAGCTGGCTT	CACAGGATCA	CACCTGTGAAT	TGAACATCAA	TGAATGTGAG	4140
	TCTAATCCAT	GTAGAAATCA	GGCCACCTGT	GTGGATGAAT	TAAATTCATA	CAGTTGTAAA	4200
	TGTCAGCCAG	GATTTTCAGG	CAAAAGGTGT	GAACAGAAAC	AGTCTACAGG	CTTTAACTCTG	4260
30	GATTTTGTGA	TTCTTGGCAT	CTATGGATAT	GTCAATGCTAG	ATGGCATGCT	CCCATCTCTC	4320
	CATGCTCTAA	CCTGTACCTT	CTGGATGAAA	TCCTCTGACG	ACATGAACCTA	TGGAACACCA	4380
	ATCTCCTATG	CAGTTGATAA	CGGCAGCGAC	AATACCTTGC	TCCTGACTGA	TTATAACGGC	4440
	TGGGTTCTTT	ATGTGAATGG	CAGGGAAAAG	ATAACAAACT	GTCCCTCGGT	GAATGATGGC	4500
	AGATGGGATC	ATATTGCAAT	CACCTGGACA	AGTGCCAATG	GCATCTGGAA	AGTCTATATC	4560
35	GATGGGAAAT	TATCTGAACG	TGGTGTGGC	CTCTCTGTTG	GTTCGCCCAT	ACCTGGSGTG	4620
	GGTGCGTTAG	TTCTGGGGCA	AGAGCAAGAC	AAAAAAGGAG	AGGGATTGAG	CCCACTGAG	4680
	TCTTTTGTGG	GCTCCATAAG	CCAGCTCAAC	CTCTGGGACT	ATGTCTCTGTC	TCACAGCAG	4740
	GTGAAGTCAC	TGGCTACCTC	CTGCCACAG	GAACCTCAGTA	AAGGAACGCT	GTTAGCATGG	4800
	CCTGATTTCT	TGTCAAGAAAT	TGTGGGGA	GTGAAGATCG	ATTCTAAGAG	CATATTTTGT	4860
40	TCTGATTTGCC	CACGCTTAGG	AGGGTCAGTG	CCTCATCTGA	GAACCTGATC	TGAAGATTTA	4920
	AAGCCAGGTT	CCAAAGTCAA	TCTGTTCTGT	GATCCAGGCT	TCCAGCTGGT	CGGGAACCTC	4980
	GTGCAGTACT	GTCTGAATCA	AGGACAGTGG	ACACAACCC	TTCTCTAGT	TGAACGCTAT	5040
	AGCTGTGGGG	TGCCACCTCC	TTTGGAGAAAT	GGCTTCCATT	CAGCCGATGA	CTTCTATGCT	5100
45	GGCAGCAGAC	TAACTACCA	GTGCAACAAAT	GGCTACTATC	TATTGGGTGA	CTCAAGGATG	5160
	TTCTGTACAG	ATAATGGGAG	CTGGAACGGC	GTTTCAACAT	CCTGCGCTGA	TGTCGATGAG	5220
	TGTGCAGTTG	GATCAGATTG	TAGTGAGCAT	GCTTCTTGCC	TGAACGTAGA	TGGATCCTAC	5280
	ATATGTTTAT	GTGTCCCACT	GTACACAGGA	GATGGGAAAA	ACTGTGCAGA	ACCTATAAAA	5340
	TTGAAGGCTC	CAGGAATATC	GGAAATATGG	CACCTCTCAG	GTGAGATTTA	TACAGTAGGT	5400
	GCOGAGTCA	CATTTTCTGT	TCAGGAAGGA	TACCACTTGA	TGGGAGTAAC	CAAAATCACA	5460
50	TGTTTGAATG	CTGGAGAAATG	GAATCATCTA	ATACCATATT	GTAAAGCTGT	TTCATGTGGT	5520
	AAACCGGCTA	TTCCAGAAAA	TGGTTGCATT	GAGGAGTTAG	CATTTACTTT	TGGCAGCAAA	5580
	GTGACATATA	GGTGAATATA	AGGATATACT	CTGGCGGGTG	ATAAAGAAATC	ATCCTGTCTT	5640
	GCTAACAGCT	TTTGGAGTCA	TTCCCTCCT	GTGTGTGAAC	CAGTGAAGTG	TTCTAGTCCG	5700
	GAATAATATA	ATAATGGAAA	ATATATTTTG	AGTGGGCTTA	CCTACCTTTC	TACTGTCATCA	5760
55	TATTCATGCG	ATACAGGATA	CAGCTTACAG	GGCCCTTCCA	TTATTGAATG	CAGCGCTTCT	5820
	GGCATCTGGG	ACAGAGCGCC	ACCTGCGCTG	CACCTGCTCT	TCTGTGGAGA	ACCACTGCGC	5880
	ATCAAGATG	CTGTCAATAC	GGGGAATAAC	TTCACTTTCA	GGAAACCGCT	CACCTTACCT	5940
	TGCAAGAAAG	GCTATACTCT	TGCTGGTCTT	GACACCAATG	AATGCGCTGGC	CGACGGCAAG	6000
	TGGAGTAGAA	GTGACCGACA	GTGCTGGCT	GTCTCTGTG	ATGAGCCACC	CATTTGGGAC	6060
60	CACGCGCTCT	CAGAGACTGC	CCATCGGCTC	TTTGGAGACA	TTGCATTCTA	CTACTGCTCT	6120
	GATGGTTACA	GCCTAGCAGA	CAATTCCCAG	CTTCTCTGCA	ATGCCAGGGG	CAAGTGGGTA	6180
	CCCCCAGAA	GTCAAGACAT	GCOCCTGTG	ATAGCTCATT	TCTGTGAAAA	ACCTCCATCG	6240
	GTTTCTTATA	GCATCTTGA	ATCTGTGAGC	AAAGCAAAAT	TTGCAGCTGG	CTCAGTTGTG	6300
	AGCTTTAAAT	GCATGGAAGG	CTTTGTACTG	AACACCTCAG	CAAAGATTGA	ATGTATGAGA	6360
65	GGTGGGCGT	GGAAACCTTC	CCCCATGTCC	ATCCAGTGCA	TCCCTGTGCG	GTGTGGAGAG	6420
	CCACCAAGCA	CTATGAATGG	CTATGCAAGT	GGATCAAAC	ACAGTTTGGG	AGCCATGGTG	6480
	GCTTACAGCT	GCAACAAGGG	GTTCTACATC	AAAGGGGAAA	AGAAGAGCAC	CTGCGAAGCC	6540
	ACAGGGCAGT	GGAGTAGTCC	TATACCGAAG	TGCCACCGGG	TATCTTGTGG	TGAACCACTC	6600
	AAGGTTGAGA	ATGGCTTTCT	GGAGCATACA	ACTGGCAGGA	TCTTTGAGAG	TGAAGTGAGG	6660
70	TATCAGTGTA	ACCGGGGCTA	TAAGTCAGTC	GGAGTCTCTG	TATTTGTCTG	CCAAGCCAAAT	6720
	CGCCACTGGC	ACAGTGAATC	CCCTCTGATG	TGTGTTCTCT	TCGACTGTGG	AAAACTTCCC	6780
	CCGATCCAGA	ATGGCTTCAAT	GAAGGAGAAA	AACTTTGAAG	TAGGGTCCAA	GGTTCAAGTT	6840
	TCTGTAAATG	AGGGTTATGA	GCTGTGTGTG	GACAGTTCTT	GGACATGTCA	GAATCTGGC	6900
	AAATGGAATA	AGAAATCAAA	TCCAAAGTGC	ATGCCCTGCC	AGTGCCCAAG	CGCCGCCCTC	6960
75	TTGGAAACCC	AGCTAGTATT	AAAGGAGTTG	ACCACCGAGG	TAGGAGTTGT	GACATTTTCC	7020
	TGTAAAGAA	GGCATGTCTC	GCAAGGCCCC	TCTGTCTGTA	AATGCTTGGC	ATCCAGCAAA	7080
	TGGAATGACT	CTTTCCTGTT	TTGTAAGATT	GTTCTTTGTA	CCCAACCTCC	CCTAATTTCC	7140
	TTTGGTGTCC	CCATTCCTTC	TTCTGCTCTT	CAFTTTGGAA	GTACTGTCAA	GTAATCTTGT	7200
80	GTAGGTGGGT	TTTTCTTAAG	AGGAAATCT	ACCACCTCT	GCCAACTCTA	TGGCACTGG	7260
	AGCTCTCCAC	TGCCAGAAATG	TGTTCCAGTA	GAATGTCCCC	AACCTGAGGA	AATCCCAAT	7320
	GGAAATCATG	ATGTGCAAGG	CCTTGCTAT	CTCAGCACAG	CTCTCTATAC	CTGCAAGCCA	7380
	GGCTTTGAAT	TGGTGGGAAA	TACTACCAAC	CTTTGTGGAG	AAAAATGTTA	CTGGCTTGG	7440
	GGAAACCAA	CATGTAAAGC	CATTGAGTGC	CTGAAACCCA	AGGAGATTTC	GAATGGCAAA	7500
	TTCTCTTACA	CGGACCTACA	CTATGGACAG	ACCGTTACCT	ACTCTTGCAA	CGAGGCTTT	7560

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 50

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CGGCTCGAAG GTCCCACTGC CTTGACCTGT TTAGAGACAG GTGATTGGGA TGTAGATGCC 7620
CCATCTTGCA ATGCCATCCA CTGTGATTCC CCACAACCCA TTGAAAATGG TTTTGTAGAA 7680
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Seq ID NO: C135 DNA Sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..390

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GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTTGGAG 180
CAGTGTCTGT ACAATGACGC CATGTGTGCC CTGAGCGAGA CCCGCCAATG TGGTCCCCCC 240
TGCACTCTCT GGCCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGSCCT CACAAAGCAT 300
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Seq ID NO: C136 DNA Sequence  
 Nucleic Acid Accession #: BC035671.1  
 Coding sequence: 126..1745

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GGGTCAATGT GCCCGGCGCC CGCGCGCGCG GCGCACTGGC GCGGGCTGCC GGGCGGGGCC 180
TCTTGGCTTT GCTGCTGCG GTCTCCGCC CGCTCGGCT GCAGCGGAG GAGCTGGGTG 240
ATGGCTGTGG ACACCTAGTG ACTTATCAGG ATAGTGGCAC AATGACATCT AAGAAATTATC 300
CGGGACCTTA CCCCAATCAC ACTGTTTGG AAAAGACAAT TACAGTACCA AAGGGGAAAA 360
GACTGATTTT GAGTGTGGGA GATTTGGATA TCGAATCCCA GACCTGTGCT TCTGACTATC 420
TTCTCTTAC CAGCTCTTCA GATCAATATG GTCCATCTG TGAAGTATG ACTGTTCCCA 480
AAGAACTCTT GTTGAACACA AGTGAAGTAA CGTCCGCTT TGAGAGTGA TCCACATTT 540
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25

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TGCTCAAAGC TGCCATCCAT GCAGGAATAA TTGCTGATGA ACTAGGTGGC CAGATCAGTG 780
TGCTTCAGCG CAAAGGGATC AGTCGATATG AAGGGATTCT GGCCAAATGGT GTTCTTTGGA 840
GGGATGGTTC CCTGTGAGAC AAGCGATTTT TGTTTACCTC CAATGGTTGC AGCAGATCCT 900
TGAGTTTGA ACCTGACGGG CAAATCAGAG CTTCTTCCTC ATGGCAGTCG GTCAATGAGA 960
GTGGAGACCA AGTCTACTGG TCTCCTGGCC AAGCCCGACT TCAGGACCAA GGCCCATCAT 1020
GGGCTTCGGG CGACAGTAGC AACAAACCACA AACCACGAGA GTGGCTGGAG ATCGATTGGS 1080
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ATTCAATTGGT GTGGCGCAAG ACAAGTCAAA GCACCACTGT TTCAACTAAG AAAGAAGATG 1440
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AGGTGCCCCC GGATGATGCT CAGAGATGAG GATCGGAACA CCATGTCTTT TCCCACCCCTA 1860
ACAAACAACA AGGGCAGTAA ATTAAAGTAC TCTTTGTAAG GTACAGTTAC CGATTAACTC 1920
AGAGATAAAA TATTTTCTTA AAAATATATT TCATTAAACA CCTATGCTGT CTCTATAAAA 1980
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2010

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Seq ID NO: C137 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1761

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GCTGCGGGCG GGGGCTCTCT GGCTTGTCTG CTGCGGCTCT CCGCCCGGCT CCGGCTGCAG 240
CGGGAGGAGC TGGGTGATGG CTGTGGACAC CTAGTGACTT ATCAGGATAG TGGCACAAATG 300
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GTACCAAAGG GGAAGAAGCT GATTCTGAGG TTGGGAGATT TGGATATCGA ATCCAGAAC 420
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AGTATGACTG TTCCCAAAGA ACTCTTGTG AACAACAGTG AAGTAACCGT CCGCTTTGAG 540
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GAGGCTCAGA AAACAGACTG TTGGAAGCAG ATTAATATC CCTTGCAGC ACATCAGTCA 1680
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ACAAGTGATA TGGCAGGTTA A 1761

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Seq ID NO: C138 DNA Sequence  
Nucleic Acid Accession #: PGENESH predicted  
Coding sequence: 1..2310

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GTTTGCGAAA AGACAATTAC AGTACCAAGG GGGAAAAGAC TGATTCTGAG GTTGGGAGAT 240
TTGGATATCG AATCCAGAC CTGTGCTTCT GACTATCTTC TCTTCAACAG CTCTTCAGAT 300
CAATATGGAA TGCAGAAGGA GGAGGAGACA GAAGTGCTTT GTCTTTCAGT GGTCTGGCGT 360
CAGAGAGTGG ACATTCCTGT GCAGCTGTTG CCCAGCTTCC TGGAAAGGTTG GAAGGTCAT 420
GCTGATGCAA AGGTTCCATA CTGTGAAAGT ATGACTGTTT CCAAAGAACT CTGTGTTGAA 480
ACAAGTGAAG TAAACGTCGG CTTTGAGAGT GGATCCACA TTTCTGGCCG GGGTTTTTTG 540
CTGACCTATG CGAGCAGGGA CCATCCAGAT TTAATAACAT GTTGGAAAG AGCTAGCCAT 600
TATTTGAAGA CAGAATACAG CAAATCTGTC CCAGCTGGTT GTAGAGAGCT AGCAGGAGAC 660
ATTTCTGGGA ATATGGTAGA TGATATAGA GATACCTCTT TATTGTGCAA AGCTGCCATC 720
CATGCAAGAA TATGCTGTA TGAAGTAGGT GGCCAGATCA GTGTGCTTCA GCGCAAGGG 780
ATCAGTCGAT ATGAAGGGAT TCTGGCCAAT GGTGTTCTTT CGAGGGATGG TTCCCTGTCA 840
GACAAGCGAT TTCTGTTTAC CTCCAATGGT TGCAGCAGAT CCTTGAGTTT TGAACCTGAC 900
GGGCAATCA GAGCTTCTTC CTCATGGCAG TCGGTCAATG AAGTGGAGA CCAAGTTTAC 960

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5 TGGTCTCCTG GCCAAGCCCG ACTTCAGGAC CAAGGCCCAT CATGGGCTTC GGGCGACAGT 1020  
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 GTGATGAATC TCAAAAACAA TAATTCTAAG TGAAGACCT ATAAAGGAAT TGTGAATAAT 1200  
 GAAGAAAAGG TGTTCAGGG TAACTCTAAC TTTGGGGACC CAGTGC AAAA CAATTTTCATC 1260  
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 ACACAAAAGT TAGATCTCAT CACAAGTGAT ATGGCAGATT ACCAGCAGCC CCTCATGATT 1800  
 15 GGCACCGGGA CAGTCAAGAG GAAGGGCTCC ACCTTCGGGC CCATGGACAC GGTATGCCGAG 1860  
 GAGGCAGGGG TGAGCACCGA TGCCGGCGGC CACTATGACT GCCCGCAGCG GGC CGGCGCG 1920  
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25 Seq ID NO: C139 DNA Sequence  
 Nucleic Acid Accession #: NM\_004616.2  
 Coding sequence: 180..893

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 35 TGGCAGGTGT GAGTGCCGTG ATAAATATT CTATGTTTAC CTTCACCTC TTGTCTTGGC 240  
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 CGACAGGTAT CCTAGGAGCT GTTTTCAAT CTAACTCTGA TCGCATTTGT AATGAAACTC 540  
 40 TCTATGAAAT CACAAGCTT TTGAGCGCCA CAGGGGAAAG TGAAAAACAA TTCCAGGAAG 600  
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 GCCAAAGCTA TAATGAAAA CAAGTTTACA AAGAGACCTG TATTTCTTTC ATAAAGACT 780  
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 45 TACTGGTTT GGTGTTTCT ATGCTCCTGT ATTGCCAGT CGGGAACAAA TGAATCTGTG 900  
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 AAATATGTAA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TTAATATGTC TCGGCTAGCT 1020  
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55 Seq ID NO: C140 DNA Sequence  
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Seq ID NO: C141 DNA Sequence  
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Coding sequence: 64..1524

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   GAGACCCGAG GTCCCGGGGG CAGCCCTGGA CGCGCCCTCT CTCTGCGGCG TCCCGACGGC 240
   GCGCCGCTT CCGGGACCA GAGCCTGGC CGCGCCCGCG GTGCAGGTGT TTGCAAGAGC 300
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   GTGGGTGGG ACCGGGAGAG CATGGGTGCC CTCAAGATGA TGGCCAGTGA GCCCTAGAG 780
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   GAAACCTTCT GTGCGCTGGA CCCCTGTGTG CTTGAACAC ACCAGTGCCA GCACGTCTGC 900
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   CAGCACATTT GTGTGAATGA CAGAACAGG TCCCATCATT GTGAATGCTA TGAGGGCTAC 1200
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30 GAATATGGAC AAATACATCG TTAAATTGCT CCAATTTCTC ACCTGAAAT GTGCACAGCT 1560
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   TAATTTGCCA TTATCTGTAT TAATGCTTGA ATATTACTGG ATAAATTGTA TGAAGATCTT 1680
   CTGCAGATC AGCATGATTT TTCCAGGAA ATACATATGC AGATACTTAT TAAGAGCAAA 1740
   CTTTAGTGTC TCTAAGTTAT GACTGTGAAA TGATTGGTAG GAAATAGAAT GAAAAGTTTA 1800
35 GTGTTCTTTT ATCTACTAAT TGAGCCATTT AATTTTAAA TTGTTATATT AGATAACCAT 1860
   ATTCACATTA GAACTTTAG GTCTAGTTTC TTTTGATAGT ATTATATAA TAAATCAATC 1920
   TTATTACTGA GAGTCAAAAT TGTACAAGT ATTTACACAT ACNACTTCAT ATAACTGAGA 1980
   TGAATGTAAT TTTGAACGT TTAACACTTT TTGTTTTTGG CTTATTTTGT TGGAGTATTA 2040
   TTGAAGATGT GATCAATAGA TTGTAATACA CATATCTAAA AATAGTTAAG ACAGATCAAG 2100
40 TGAACATGAT ATGTCATTT TTAATTCATT CTGGTCTTTG AAAGAAATGT ACTACTAAG 2160
   AGCACTAGTT GTGAATTTAG GGTGTTAAAC TTTTACCAG GTACAAAAT CCCAATTCA 2220
   CTTTATTATT TTGCTTCAGC ATCCAAGTGA CAAAGTTATA TATTTATAAA ATTGCTATAA 2280
   ATCGACAAAA TCTAATGTTG TCTTTTAAAT GTTAGTGATC CACTGCGCTC AGCCTCCCAA 2340
45 AGTGCTGGGA TTACAGGCTT GAAAGTCTAA CTTTTTITA CTTATATATT TGATACATAT 2400
   AATTTCTTTG GCTTTGAAAC TTGCAACTTT GAGAACAAAA CAGTCCCTTA AATTTTGAC 2460
   TGCTCAATTC TGTTTTCTGT TTGCATTGTC TTTAATATAA TAAAGTTAT TACCTTTACA 2520
   TATTATCATG TCTATTTTGG ATGACTCATC AATTTGTCT ATTAAAGATA TTCTCTTAAA 2580
   TTAAAAAAA AAAAAAAA 2599

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Seq ID NO: C142 DNA Sequence  
Nucleic Acid Accession #: NM\_016639.1  
Coding sequence: 40..429

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55 1      11      21      31      41      51
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   GCGCGGGGCG CAGACAGCGG CGGGCGCAGG ACGTGCACTA TGGCTCGGGG CTGCTGCGC 60
   CGGTTGCTGC GGTCTCTCGT GCTGGGGCTC TGGCTGGCGT TGCTGCGCTC CGTGGCCGGG 120
   GAGCAGCGCG CAGGACCGCG CCCCTGCTCC CGCGGCAGCT CCTGGAGCGC GGAAGCTGGC 180
60 AAGTGCATCG ACTGCGGTC TTGCAGGCGG CGACCGCACA CGACCTCTCG CCTGGGCTGC 240
   GCTGCAGCAGC CTCTGCCCCC CTTCGGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
   CTGACCTTCG TGCTGGGGCT GCTTCTGCGC TTTTGTGCTC GAGAGCATG CCGCAGGAGA 360
   GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGGAGAGG GCTGCCAGC TGTGGGCTG 420
65 ATCCAGTGAC AATGTGCCCG CTGCCAGCGG GGGCTCGCCC ACTCATCAT CATTATCCA 480
   TTCTAGAGCC AGTCTCTGCC TCCAGAGCG GCGGGAGGCC AAGCTCTCC AACCAAGG 540
   GGGGTGGGGG GGGGTGAATC ACCTCTGAGG CTTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
   AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GAGCCTCAC GCTGGCTCAC 660
   ACAAACAGC TGACACTGAC TAAGGAACCT CAGCATTTGC ACAGGGGAGG GGGGTGCCCT 720
70 CCTTCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGSCA GACTTGACAC TAGGCCCCAC 780
   TCACTCAGAT GTCTGAAAT TCCACCACGG GGGTCACCT GGGGGGTAG GACCTATTT 840
   TTAACACTAG GGGCTGGCCC ACTAGAGGG CTGGCCCTAA GATACAGACC CCCCACATC 900
   CCCAAGCGG GAGGAGATA TTTATTTGG GAGAGATTG GAGGGGAGG AGAATTTATT 960
   AATAAAGAA TCTTAACTT TAAAAAAA AAAAAAAA 998

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Seq ID NO: C143 DNA Sequence  
Nucleic Acid Accession #: NM\_001819  
Coding sequence: 113..2146

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80 1      11      21      31      41      51
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   CCAGGAGGCA CGCTGTTTT CCGGGGCGCG TCCATCGGCG CTCTCTCTG CGCCTGCTT 60
   CTCGGTCCA CGCGCATCT TCTTTTCGCG ACAGGGGCGG CCGAGCGGGG CCATGACGCC 120
   AACGCTGCTT CTACGCTCC TGGGAGCGGT GGGGCTGGGG GCTGTCAATT CCATGCCAGT 180
   GGATAACAGG AACCACATAT AAGGAATGTT GACTCGCTGC ATCATTGAGG TCCTCTCAAA 240

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5	TGCGTTGTG	AAGTCCAGCG	CTCCACCCAT	CACCCCTGAG	TGCCGCCAAG	TCCTGAAGAC	300
	GAGTAGAAAA	GACGTCAAAG	ACAAAGAGAC	AACTGAAAT	GAAAAACAA	AGTTTGAAGT	360
	AAGATTGTTA	AGAGACCCAG	CTGATGCCCTC	GGAAGCCAC	GAGTCTCCA	GCAGGGGAGA	420
	GGCAGGAGCC	CCAGGGGAGG	AGGACATCCA	AGGCCAACCA	AAGGCAGACA	CAGAGAAATG	480
	GGCAGAGGGA	GGCGGGCACA	GCCGAGAGCG	AGCGGATGAG	CCCCAGTGG	GCTCTATCC	540
	CTCCGACAGC	CAAGTCTCTG	AAGAAGTGAA	GACACGCCAT	TCTGAGAAGA	GCCAGAGAGA	600
	GGATGAGGAG	GAGGAGGAGG	GAGAGAACTA	TCAAAAAGGG	GAGCGAGGGG	AAGATAGCAG	660
	TGAAGAGAAA	CACCTTGAA	AGCCAGGAGA	GACACAAAC	GCTTTTCTCA	ATGAAAGAAA	720
	GCAGGCTTCA	GCTATAAAAA	AAGAGGAGTT	AGTGGCCAGA	TOGAAACAC	ATGCTGCCGG	780
10	GCATTCTCAG	GAGAAGACAC	ATAGCCGAGA	GAAGAGTAGC	CAGGAGAGTG	GAGAGGAGGC	840
	AGGGAGCCAG	GAGAATCACC	CCCAGGAGTC	TAAAGGCCAA	CCCCGAAGCC	AGGAAGAATC	900
	TGAGGAAGGT	GAGGAAGATG	CCACCTCTGA	GGTGGACAAA	CGACGCACGA	GGCCAGACA	960
	CCACCACGGG	AGGAGCAGGC	CCGACAGGTC	CTCTCAAGGA	GGGAGTCTTC	CCTCTGAGGA	1020
	AAAGGGACAC	CCCCAGGAGG	AATCTGAGGA	GTCAAACGTC	AGCATGGCCA	GTTTAGGGGA	1080
15	AAAGAGGGAC	CACCATTCAA	CCCCTACAG	GGCTTCAGAG	GAAGAACCTG	AATATGGAGA	1140
	AGAAATAAAG	GGTTATCCAG	GGCTCCAGGC	CCCTGAGGAC	CTGAGTGGG	AGCGCTATAG	1200
	GGGCAGAGGA	AGTGAAGAAT	ACAGGGCTCC	AAGACCTCAG	AGTGAGGAGA	GTTGGGATGA	1260
	GGAGGACAAG	AGAAACTACC	CCAGCTTAGA	GCTTGATAG	ATGGCACATG	GATATGGTGA	1320
	AGAAAGTGAG	GAAGAGAGGG	GCCTTGAGCC	GGGAAAGGGA	CGCCATCACA	GAGGCAGGGG	1380
20	AGGGGAGCCA	CGTGCTTATT	TCATGTCTGA	CACCAGAGAA	GAGAAAGGT	TCTTGGGTGA	1440
	AGGACACCAC	CGTGTCCAAG	AAAACCCAGT	GGACAAGGCA	AGGAGGCATC	CACAAGGTGC	1500
	TGGGAAGTAC	CTGGACAGAA	ATTATCTCAA	CTACGGTGAG	GAAGGAGCCC	CAGGGAAGTG	1560
	GCAGCAGCAG	GGAGACCTGC	AGGACACTAA	AGAAAACAGG	GAGGAAGCTA	GSTTTCAAGA	1620
25	TAAACAATAT	AGCTCCATC	ACACAGCTGA	AAAGAGGAAG	AGATTAGGGG	AACTGTTCAA	1680
	CCCATACTAC	GACCCCTCTC	AGTGGAAAGAG	CAGCCATTTT	GAAAGAAGAG	ACAACATGAA	1740
	TGACAAATTT	CTCGAGGGTG	AGGAGGAAAA	TGAGCTGACC	TTGAACGAGA	AGAATTTCTT	1800
	CCAGAAATAC	AACTATGACT	GGTGGGAGAA	AAAGCCCTTC	TCTGAGGATG	TGAATCGGGG	1860
	GTATGAGAAG	AGAAACCTCG	CCAGGGTCCC	CAAGCTGGAC	CTGAAAAGGC	AATATGACAG	1920
30	GGTGCCCACT	CTGGACCAGC	TCCTTCACCTA	CAGGAAGAG	TCAGCTGAGT	TCCAGACTT	1980
	CTATGATCTC	GAGGAGCCGG	TGAGCACCCA	CCAGGAGGCA	GAAATGAAA	AGGACAGGGC	2040
	TGACCAGACA	GTCTGACAG	AGGACGAGAA	AAAAGAACTC	GAAAACTTGG	CTGCAATGGA	2100
	TTTGAATCTG	CAGAAATAG	CTGAGAAATT	CAGCCAAAGG	GGCTGACTGT	CATTGGAGCG	2160
	GTGGGCACTG	TTAAGAAGCA	GCCATCACAT	GATCTGTTTT	TCACCCTTTC	ACTGAAAGAC	2220
35	ACCATTTATA	TACCCAGGGG	CAGAAAGTAG	AACTTACTAT	TCATTAATATG	TTTGACACAA	2280
	TTGGAATTGT	CTTTAATTTC	TGTCAGAAATG	CTATTGAAAA	TGTGAATTGC	ATGACTTGTG	2340
	GCATATTCTT	TTCTGCAAAA	TAGACATATT	AACATGCTTA	TGCAATGAC	TGTGCTACTG	2400
	TCCTTGGAAA	AATGTTTGTG	TCAGTTGGAA	ATAATAAAG	ATTCACCTGA	GACC	2454

Seq ID NO: C144 DNA Sequence  
Nucleic Acid Accession #: XM\_093082.1  
Coding sequence: 93..1988

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	CTTCTGTGG	TAGGGACCTC	TOCTCAGTAT	TTGAACTAA	CCAGCATCTG	ACAGATTTCG	60
	AATTTGTAAA	AAATACCCCTC	GAAGATTTCAG	GAATGAAGCT	TCTGTGTGAA	GGATTAAAC	120
	AGCCCAACTG	TGTATTACAG	ACATTGAGGT	GGTACCGGTG	CCTTATCTCT	TCTGCTTCTT	180
	GTGGGGCTCT	AGCAGCTGTT	CTTAGCACCA	GTCACTGGCT	CAGTGAAGTG	GAATTTAGTG	240
50	AGACAAAAT	GAAGCTTCA	GCTTTGAAAT	TGCTCTATGG	AGGCTTAAAA	GATCCAAATT	300
	GCAAAATTA	GAAGCTCAAC	TTGCAGTTTT	CTTTATCTGT	AACCGCTGCA	AAACTTCCAG	360
	TTGSAATGGT	TGGAATTTGT	TCTGGTTTCT	CGGGATCATT	GGTGCAATCT	CATTTTGGCT	420
	ACTGTGAGGA	CAGTTCTTTC	AAATGTGATC	TTTGTAAAGT	GCTCTGCGCT	TCCACAGAG	480
	TTGCTGTGTC	AAAGGATTGT	GGGAGTCCTA	AGTCCCTTCT	ATCAGAAAGG	CTGAACTGGG	540
55	CAGGAGACT	TGAGGAGTGG	GAGGAGGTTT	TGGGGTTGGG	GGTGCTTGTA	CAGCCCGGTG	600
	ACCCAGCATC	TCAGGGTGGG	GGGCATTGTG	AAAACATGAG	GTCTTTTAGA	GACTTTGGTG	660
	ACTTAGAAGT	CAAGGCAGAA	CCAAGCCTGA	GAAAAGGTGG	TATGGATCTC	CAGAGACCCA	720
	CCCTACAAGT	TGCTCTCTCT	TGCAAAATCT	TCTCCCTCAA	ACTATTCTCT	TTTATTGCAT	780
	TGCTTAATTC	TGCTGGTCAG	GTTAGTGTGG	TGCAAGTGAC	CATCCAGAGC	GGTTTCTGTA	840
60	AGTGACTGT	TGGATCTAAT	GTCACTCTCA	TCTGCATCTA	CACCAACACT	GTGGCCTCCC	900
	GAGAACAGCT	TTCCATCCAG	TGCTCTTTCT	TCCATAAGAA	GGAGATGGAG	CCAATTTCTT	960
	CTCCTTGGGA	GGAGGGGAG	TGGCCAGATG	TTGAGGCTGT	GAAGGGCACT	CTTGATGGAC	1020
	AGCAGGCTGA	ACTCCAGATT	TACTTTTCTC	AAGGTGGACA	AGCTGTAGCC	ATCGGGCAAT	1080
	TTAAAGATCG	AAATTACAGG	TCCAACGATC	CAGGTAATGC	ATCTATCACT	ATCTCGCATA	1140
65	TGCAGCCAGC	AGACAGTGGG	ATTACATCT	GCGATGTTAA	CAACCCCCCA	GACTTTCTCG	1200
	GCCAAACCA	AGGCATCCTC	AAGCTCAGTG	TGTTAGTGAA	ACCTTCTAAG	CCCTTTTGTA	1260
	GGTTTCAAGG	AAGACAGAA	ACTGGCCACA	CTATTTCCCT	TTCTGTCTCT	TCTGGGCTTG	1320
	GAACACCTTC	CCCTGTGTAC	TACTGGCATA	AACTTGAGGG	AAGAGACATC	GTGCCAGTGA	1380
	AAGAAACTTT	CAACCCAAAC	ACCGGATTT	TGGTCATTGG	AAATCTGACA	AATTTTGAAC	1440
70	AAGGTTATTA	CCAGTGTACT	GCCATCAACA	GACTTGGCAA	TAGTTCCTGC	GAAATCGATC	1500
	TCATTTCTTC	ACATCCAGAA	GTTGGAATCA	TTGTTGGGGC	CTTGATTGGT	AGCCTGGTAG	1560
	GTGCGCCCAT	CATCATCTCT	GTGTGTGCT	TGCAAGGAA	TAAGGCAAAA	GCAAGGCAA	1620
	AAGAAAGAAA	TTCTAAGACC	ATCGCGGAAC	TTGAGCCAA	GACAAAGATA	AAACCAAGGG	1680
	GAGAAAGCGA	AGCAATGCCA	AGAGAAGAGC	CTACCCAACT	AGAAGTAACT	CTACCATCTT	1740
75	CCATTATGTA	GACTGGCCCT	GATACCATCC	AAGAAACAGA	CTATGAGCCA	AAGCCTACTC	1800
	AGGAGCTCGT	CCAGAGCCTC	GCCCCAGGAT	CAGAGCCTAT	GGCAGTGCCT	GACCTTGACA	1860
	TCGAGTCTGA	GCTGGAGCCA	GAAACGCAGT	CGGAATTGGA	GCCAGAGCCA	GAGCCAGAGC	1920
	CAGAGTCAGA	GCCTGGGGTT	GTAGTTGAGC	CCTTAAGTGA	AGATGAAAAG	GGAGTGGTTA	1980
80	AGGCATAG						1988

Seq ID NO: C145 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1242

1 11 21 31 41 51

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	ATGGTGTTCG		CATTTTGGAA		GGTCTTTCTG		ATCCTAAGCT		GCCTTGCAGG		TCAGGTTAGT	60
	GTGGTGCAGG		TGACCATCCC		AGACGGTTTC		GTGAACGTGA		CTGTTGGATC		TAATGTCACT	120
	CTCATCTCGA		TCTACACCA		CACCTGTGGC		TCCCGAGAAC		AGCTTTCCAT		CCAGTGGTCT	180
	TTCTTCOCAT		AGAAGGAGAT		GGAGCCAAAT		TCTTCTCCTT		GGGAGGAGGG		GAGTGGCCA	240
	GATGTTGAGG		CTGTGAAGGG		CACCTCTGAT		GGACAGCAGG		CTGAATCCA		GATTTACTTT	300
	TCTCAAGGTG		GACAAGCTGT		AGCCATCGGG		CAATTTAAAG		ATCGAATTAC		AGGGTCCAAC	360
	GATCCAGGTA		ATGCATCTAT		CACATCTCTG		CATATGCAGC		CAGCAGACAG		TGGAATTTAC	420
	ATCTGCGATG		TTAACAAACC		CCCAGACTTT		CTCGGCCAAA		ACCAAGGCAT		CCTCAACGTC	480
	AGTGTGTTAG		TGAAACCTTC		TAAGCCCTTT		TGTAGCGTTC		AAGGAAGACC		AGAAACTGGC	540
	CACACTATTT		CCCTTTCTCG		TCTCTCTGCG		CTTGGAAAC		CTTCCCTGT		GTACTACTGG	600
	CATAAACTTG		AGGGAAGAGA		CATCGTGCCA		GTGAAAGAAA		ACTTCAACCC		AACCAACGGG	660
	ATTTTGTGTA		TGGAATACT		GACAAATTTT		GAACAAGGTT		ATTACCACTG		TACTGCCATC	720
	AACAGACTTG		GCAATAGTTC		CTGCGAAATC		GATCTCACTT		CTTCACATCC		AGAAGTTGGA	780
	ATCATTGTTG		GGGCTTGTAT		TGGTAGCCTG		GTAGGTGCCG		CCATCATCAT		CTCTGTGTGT	840
	TGCTTGGCAA		GGAATAAGGC		AAAAGCAAAG		GCAAAAGAAA		GAAATTTCTA		GACCATCGCG	900
	GAACCTTGAGC		CAATGACAAA		GATAAACCCA		AGGGGAGAAA		GCGAAGCAAT		GCCAGAGAGAA	960
	GACGCTACCC		AACTAGAAGT		AACCTTACCA		TCTTCCATTC		ATGAGACTGG		CCCTGATACC	1020
	ATCCAAGAAC		CAGACTATGA		GCCAAAGCCT		ACTCAGGAGC		CTGCCCCAGA		CCCTGCCCCA	1080
	GGATCAGAGC		CTATGGCAGT		GCCTGACCTT		GACATCGAGC		TGGAGCTGGA		GCCAGAAACG	1140
	CAGTGGGAAT		TGAGGCCAGA		GCCAGAGCCA		GAGCCAGAGT		CAGAGCCTGG		GGTGTAGTGT	1200
	GAGCCCTTAA		GTGAAGATGA		AAAGGGAGTG		GTTAAGGCAT		AG			1242

Seq ID NO: C146 DNA Sequence

Nucleic Acid Accession #: NM\_003020.1

Coding sequence: 29..664

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TGGCCTACTG	TTTTGGCTGG	CATCTGGATG	GACTCCAGCA	TTTGCTTACA	GCCCCGGGAC	120
CCCTGACCGG	GTCTCAGAAG	CAGATATCCA	GAGGCTGCTT	CATGGTGTTA	TGGAGCAATT	180
GGGCATTGCC	AGGCCCCGAG	TGGAATATCC	AGCTCACCAG	GCCATGAATC	TTGTGGGCCC	240
CCAGAGCATT	GARGGTGGAG	CTCATGAAGG	ACTTCAGCAT	TTGGGTCTTT	TTGGCAACAT	300
CCCCAACATC	GTGGCAGAGT	TGACTGGAGA	CAACATTCCCT	AAGGACTTTA	GTGAGGATCA	360
GGGGTACCCA	GACCCCTCCA	ATCCCTGTCC	TGTTGGAAAA	ACAGATGATG	GATGCTTAGA	420
AAACACCCCT	GACACTCCAG	AGTTCACTCG	AGAGTTCACG	TTGCACCAGC	ATCTCTTTGA	480
TCCGGAACAT	GACTATCCAG	GCTTGGGCAA	GTGGAACAAG	AAACTCCTTT	ACGAGAAGAT	540
GAGGGGAGGA	GAGAGACGAA	AGCGGAGGAG	TGTCATATCCA	TATCTACAAG	GACAGAGACT	600
GGATAATGTT	GTGCAAAAGA	AGTCTGTCCC	CCATTTTTC	GATGAGGATA	AGGATCCAGA	660
GTAAAGAGAA	GATGCTAGAC	GAAACCCAC	ATTACCTGTT	AGGCTCAGC	ATGGCTTAGT	720
TGCACGTGTA	AATGGAGTCC	CTGTGAATGA	CAGCATGTTT	CTTACATAGA	TAATTATGGA	780
TACAAAGCAG	CTGTATGTAG	ATAGTGTATT	GTCTTCACAC	CGATGATTCT	GCTTTTGTCT	840
AAATTAGAAT	AAGAGCTTTT	TTGTTTCTTG	GGTTTTTAAA	ATGTGAATCT	GCAATGATCA	900
TAAAAATTAA	AATGTGAATG	TCAACAATAA	AAAGCAAGAC	TATGAAAGGC	TCAGATTTCT	960
TGCAGTTTAA	AATGGTGTCT	GAGGTGTGAC	TATTTTGGCC	AAGTCTGTAG	AAAGCTGTCA	1020
TTTGATTTTG	ATTATGTAGT	TCATCCAGCC	CTTGGGCATT	GTTATACACC	AGTAAAGAG	1080
GCTGTACTCA	AGAGGAGGAG	CTGACACATT	TCACCTGGCT	GCCTCTTAAT	AAACATGAAT	1140
GCAAGCATTG	GC					1152

Seq ID NO: C147 DNA Sequence

Nucleic Acid Accession #: NM\_024021.2

Coding sequence: 144..806

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CTTTGGAACA	ACTTAAATAA	GTCAAATATA	CTTGGAGCTT	TAAAAATTAA	AAGGAGAGAG	120
ATTGAGCAC	CTTTTCTGCT	GCCATGACAA	OCATGCAAGG	AATGGAACAG	GCCATGCCAG	180
GGGCTGGCCC	TGGTGTGCCC	CAGCTGGGAA	ACATGGCTGT	CATACATTCA	CATCTGTGGA	240
AAGGATTGCA	AGAGAAGTTC	TTGAAGGGAG	AACCCAAAGT	CCTTGGGGTT	GTGCGATTC	300
TGACTGCCCT	GATGAGCCTT	AGCATGGGAA	TAACAATGAT	GTGTATGGCA	TCTAATACTT	360
ATGGAAGTAA	CCCTATTTC	GTGTATATCG	GGTACACAAT	TTGGGGTCA	GTAATGTTTA	420
TTATTTGAGG	ATCCTTGTC	ATTGCAGCAG	GAATTAGAAC	TACAAAGGC	CTGGTCCGAG	480
GTAGTCTAGG	AATGAATATC	ACCAGCTCTG	TACTGGCTGC	ATCAGGGATC	TTAATCAACA	540
CATTTAGCTT	GGCGTTTTAT	TCAATCCATC	ACCCCTACTG	TAACCTACTAT	GGCAACTCAA	600
ATAATTGTCA	TGGGACTATG	TCCATCTTAA	TGGGTCTGGA	TGGCATGGTG	CTCCTCTTAA	660
GTGTGCTGGA	ATTCTGCATT	GCTGTGTCCC	TCTCTGCTTT	TGGATGTAAA	GTGCTCTGTT	720
GTACCCCTGG	TGGGGTTGTG	TTAATTTCTG	CATCACATTC	TCACATGGCA	GAAACAGCAT	780
CTCCACACCC	ACTTAATGAG	GTTTGAGGCC	ACCAAAAGAT	CAACAGACAA	ATGCTOCAGA	840
AATCTATGCT	GACTGTGACA	CAAGAGCCTC	ACATGAGAAA	TTACCACTAT	CCAACTTCCA	900
TACTGATGTA	CTTGTGATA	TTATTATTAT	ATGTAATCCA	ATTATGAAC	GTGTGTGTAT	960
AGAGAGATAA	TAAATTCAAA	ATTATGTTCT	CATTTTTTTC	CCTGGAACCT	AATAACTCAT	1020
TTCACTGGCT	CTTTATCGAG	AGTACTAGAA	GTTAAATTA	TAAATTAATG	ATTTAATGAG	1080
GCAACAGCAC	TCTTAAAGTT	TTCACTCATC	ATAAGAACTT	TATATAAAGG	CATTACATG	1140
GCAAAATAGG	TTTGAAGACA	GAAAGACAAA	AAAAGATAT	TGTTAAATG	AGGCTCCCAT	1200
GCAAAACACA	TACCTCCCTC	CCATTTATTT	AACTTTTTTT	TTCTCTACCT	TATGGGGACC	1260
AAAGTCTTTT	TTCTTCTCAG	AAGTGGAGAT	GCATGGCCAT	CTCCCTCTCC	CTTTTCTCTT	1320
CTCCGTCTTT	TCTTTCCCCA	TAGAAAGTAC	CTTGAAGTAG	CACAGTCCGT	CCTTGCATGT	1380
GCAAGAGCTA	CACTTTGAGT	AAAAGTATAC	ATGGAGTAAA	AATCATATTA	AGCATCAGAT	1440
TCAACTTATA	TTTTCTATTT	CATCTTCTTC	CTTTCCTCTC	TCCCACTTTC	TACTGGGCAT	1500
AATTATATCT	TAAATATATA	TGGAAATGTG	CAACATATGG	TATTTGTTAA	ATACGTTTGT	1560
TTTTATTGCA	GAGCAAAAA	AAATCAAAT	AGAGCAATA	AAAAAATAA	AAAAAATAA	1619

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CCCCAAACGA TTGGTAAACT GCAGGTGTTT CCCGAGGCC CGCAGTGCTC CAAGGTGGAA 300
GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
AAGAAAGTCA TCCAGAAAAT TTGGACAGT GGAAACAAGA AAAAGTGAAT AACAAAAAAG 420
ACCATGCATC ATAAATTGTC CCAGTCTTCA GCGAGCAGT TTCTGGAGA TCCCTGGACC 480
CAGTAAGAAT AAGAAGGAAG GGTGGTTTT TTCCATTTT CTACATGGAT TCCCTACTTT 540
GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCCTTGG 660
CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT 720
TGAAGATAAC TATTGTATTT CTATCATACA TTCTTAAAG TCTTACCGAA AAGGCTGTGG 780
ATTTCGTATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTGTGTTCT 840
ACTCAGCTCT CTCATAAAAT AGGAAATATT TTAGTTCTGT TTCTTGGGG AATATGTTAC 900
TCITTAACCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACGGGTG TGTCATACCG 960
TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAAGG 1020
CTAATATATT TCCTTCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCATATAG GATGACTATA 1140
ATTCTGGTCA CTAATATATC ACTTTAGATA GATGAAGAAG CCAAAAAACA GATAAATTC 1200
TGATTGCTAA TTTACATAGA AATGTATTCT CTGGTTTTT TAAATAAAG CAAAAATTAAC 1260
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CATTTAGTTC TCMAAATATA TACAGATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
TTTAAAGGTT TTAACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500
TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAAATA AAAAAA 1547
  
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 Seq ID NO: C152 DNA Sequence  
 Nucleic Acid Accession #: NM\_005242.2  
 Coding sequence: 148..1341

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| | | | |
CGGCCCGCCC TGGGGAGGCG CGCAGCAGAG GCTCCGATTC GGGGCAGGTG AGAGGCTGAC 60
TTTCTCTCGG TCGCTCCAGT GGAGCTCTGA GTTTCGAATC GGTGGCGGCG GATTCGCCGC 120
GCGCCCGGCG TGGGGGCTTC CAGGAGGATG CGGAGCCCCA GCGCGGCGTG GCTGCTGGGG 180
GCGCCCATCC TGCTAGCAGC CTCTCTCTCC TGCAGTGGCA CCATCCAAGG AACCAATAGA 240
TCCTCTAAGG GAAGAAGCCT TATTGGTAAG GTTGATGGCA CATCCACGCT CACTGGAAAA 300
GGAGTTACAG TTGAAACAGT CTITTCGTGT GATGAGTTTT CTGCATCTGT CCTCACTGGA 360
AAACTGACCA CGGTCTTCTT TCCAATTGTC TACAATTTG TGTGTGTGGT GGGTTTGCCA 420
AGTAACGGCA TGGCCCTGTG GGTCTTTCTT TTCCGAACTA AGAAGAAGCA CCTGCTGTG 480
ATTTACATGG CCAATCTGGC CTGGCTGAC CTCTCTCTG TCATCTGGTT CCCCTTGAAG 540
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ATTGGCTTTT TCATGGAACA CATGTACTGT TCCATCTCT TCATGACCTG CCTCAGTGTG 660
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GAGCAGCTCT TGGTGGGAGA CATGTTCAAT TACTTCTCT CTCTGCGCAT TGGGGTCTTT 900
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CTCTCAACCC TTAACAGCTG CATCGACCCC TTGTCTTATT ACTTTGTTT ACATGATTTC 1200
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TGGAACTGTT TTAATGTTAT GAGGACGTGT CTGTTATTTC CTAATCAAAA AGGTCTCACC 1440
ACATAACCACC G 1451
  
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 Seq ID NO: C153 DNA Sequence  
 Nucleic Acid Accession #: NM\_003469.2  
 Coding sequence: 92..1945

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1 11 21 31 41 51
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TCOCAGTCTT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAGCTCA 300
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TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCTATGTA 600
TGAAGAGAAAT TCCAGGGATA ACCCCTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660
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5	CTCCAAGAGT	GGCTACCCCTA	AAACACCTGG	TGGTGTGGG	ACTGAGGCC	TACCAGACGG	1380
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	AGGCTCATCT	GAAGATGACC	TGCAGGAAGA	GGAACAAATT	GAGCAGGCCA	TCAAAGAGCA	1740
	TTTGAATCAA	GGCAGCTCTC	AGGAGACTGA	CAAGCTGGCC	CCGCTGAGCA	AAAGGTTCC	1800
10	TGTGGGGCCC	CCGAAGAATG	ATGATACCCC	AAATAGGCAG	TACTGGGATG	AAGATCTGTT	1860
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	TAATATCTTT	AAATGATGTA	CAGGCAGATG	AAACCAGGTC	ACTGGGAGT	CTGCTTCATT	2100
15	TCTCTGAGC	TGTTATCTTG	TGTATGGATA	TGTGTAATG	TTATGACTCC	TTGATAAAAA	2160
	ATTTATTATG	TCCATTATTC	AAGAAAGATA	TCTATGACTG	TGTTAATAG	TATATCTAAT	2220
	GGCTGTGGCA	TTGTTGATGC	TCACATATGA	TAAAAAAGTG	TCCTATAATT	CTATTGAAAG	2280
	TTTTTAATAT	TTATTGAATT	ATTTTGTAC	TGTCGTAGC	GTTTGTGGA	GTACTGGACC	2340
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30	GAGATCGCGG	GTCAGCTTTG	CAGTCGCTGC	CTTCTCGCGC	CTGACCATGC	ACCCCTGCAT	240
	CTTCTGCTGC	GGCAGAGCGG	AGCGCTTTAT	TTCTGGAGCT	GAGGGCTAAA	ACTTTTTTCA	300
	CTTTCTCTCT	CCTCAACATC	TGAATCATGC	CATGTGCCCA	GAGGAGCTGG	CTTGCAAACC	360
	TTTCCGRTGT	GGCTCAGCTC	CTTAACCTTG	GGGCGCTTTG	CTATGGGAGA	CAGCCTCAGC	420
	CAGGCCCGGT	TGCTTTCCCG	GACAGGAGGC	AAGAGCATTT	TATCAAGGGC	CTGCCAGAAT	480
35	ACCACGTGGT	GGGTCCAGTC	CGAGTAGATG	CCAGTGGGCA	TTTTTTGTCA	TATGGCTTGC	540
	ACTATCCCAT	CACAGTCAGC	AGGAGGAAGA	GAGATTGGA	TGGCTCAGAG	GACTGGGTGT	600
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	TTCTTTCCAA	TAGCTACATC	ATGGAGAAGA	GATATGGGAA	CCTCTCCCAT	GTTAAGATGA	720
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40	TTGGGACGCG	AGCCCTCAGT	GCCTGCCATG	GACTGACTGG	ATTTTCCCAA	CTACCACATG	840
	GAGACTTTTT	CATTGAACCC	GTGAAGAAGC	ATCCACTGGT	TGAGGGAGGG	TACCACCGCG	900
	ACATCGTTTA	CAGGAGGCG	AAAGTTCCAG	AAACCAAGGA	GCCAACTGT	GGATTAAAGG	960
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45	TGGTGGCGGA	CACAAGATG	ATTGAATACC	ATGGGAGTGA	GAATGTGGAG	TCCTACATCC	1140
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	GGTCCAGAGT	GACGAGAGG	TACATCACCC	GCTTCTTGA	CCGAGGCTGG	GGGTTCTGTC	1680
55	TTGATGACAT	ACCTAAAGAG	AAAGGCTTGA	AGTCCAAGGT	CATTGCCCTC	GGAGTGATCT	1740
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	TAGAAAACGT	CTGCCAGACA	CTGTGGTGCT	CGTGAAGGG	CTTTTGTGCG	TCTAAGCTGG	1860
	ACGCTGCTGC	AGATGGAAC	CAATGTGGTG	AGAAGAGATG	GTGTATGGCA	GGCAAGTGCA	1920
	TCACAGTGGG	GAGAAACCA	GAGAGCATTC	CTGAGGCTG	GGGCGCTGG	TCACCTGGT	1980
60	CCCACTGTTC	CAGGACCTGT	GGGGCTGGAG	TCCAGAGCGC	AGAGAGGCTC	TGCAACCAAC	2040
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65	TCATTGATGG	TACCCCTTGC	TTTGAAGCGG	GCAACAGCAG	AAATGTCTGT	ATTATATGCA	2340
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	GACAGAAAGA	GTGCCATGAA	AAGGCTTGT	CACCCAGGTG	GTGGGCGAGG	GAGTGGGAAG	3000
	CATGCTGGCG	GACATGGCGG	CCCAACGGGG	AGAAGAGCG	AACCGTCTG	TGCATCCAGA	3060
	CCATGTCTCT	TGACGAGCAG	GCTCTCCCGC	CCACAGACTG	CCAGCACCTG	CTGAAGCCCA	3120
	AGACCTCTCT	TCTCTCAAC	AGAGACATCC	TGTGCCCTC	GGACTGGACA	GTGGGCAACT	3180
80	GGAGTGAGTG	TTCTGTTTCC	TGTGGTGGTG	GAGTGGGAT	TGCGAGTGT	ACATGTGCCA	3240
	AGAACCATA	TGAACCTTGC	GATGTGACAA	GGAAACCCAA	CAGCCGAGCT	CTGTGTGGCC	3300
	TCCAGCAATG	CCCTTCTAGC	CGGAGAGTTC	TGAAACCAAA	CAAGGCACT	ATTTCCAATG	3360
	GAAAAAACCC	ACCAACACTA	AAGCCCGTCC	CTCCACCTAC	ATCCAGGCC	AGAAATGCTGA	3420
	CCACACCCAC	AGGCGCTGAG	TCTATGAGCA	CAAGCACTCC	AGCAATCAGC	AGCCCTAGTC	3480
	CTACCAACAGC	CTCCAAAGAA	GGAGACCTGG	GTGGGAAACA	GTGGCAAGAT	AGCTCAACCC	3540

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 5 TGGAGATTCA CAGTGGCTCA GGGGAAGAAA GAGAACAGCC TGAGGACAAA GATGAAAGCA 3840  
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 25 AAAGTGCCGA TTTACTTTGC ACTAAGGACA AACTGTGAGC CAGTTTCTGC CAGACACTGA 4980  
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Seq ID NO: C155 DNA Sequence  
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1 11 21 31 41 51  
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 CTAAAACTTC TGTGAAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTG 240  
 40 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300  
 ATCCACAAA TCAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360  
 GCCTTGATTA TACTGGCTTT GGGAGTATGT OGTAACGCTG AGGAAAACCT AATATATGAT 420  
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 45 CTGTTCAATG GGAAGTACTC AACCCGCGAA GTTGTCAACC ACTTCACTCC TGAATAATAA 600  
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 AACATCAGTA TTTATACAAA GTCACTGTGA GAAAAGATTG TGTCTGAGAA AAAAGAAAAA 780  
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Seq ID NO: C156 DNA Sequence  
 Nucleic Acid Accession #: NM\_004591  
 Coding sequence: 59..349

1 11 21 31 41 51  
 65 CACTCCCAA GAACGGGTA CTCAACACTG AGCAGATCTG TTCTTTGAGC TAAAAACCAT 60  
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 70 CGGCGAATCA GAAGCAGCAA GCAACTTGA CTGCTGTCTT GGATACACAG ACGGTATTCT 180  
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 75 TTTCTGGAAT GGAATTGGAC ATAGCCCAAG AACAGAAAGA ACCTTGTCTG GGTGGAGGT 420  
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 80 AAGATTATAT GGACTTTCTT GCAAGCAACA AGCTATTTT TAAAAAATC ATTTAACTAT 720  
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Seq ID NO: C157 DNA Sequence  
 Nucleic Acid Accession #: NM\_013271.1



Coding sequence: 27..809

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	AGACTGGCGC	TCCTCGCCGC	TTCCGGCGGT	CAGTGCCCGG	AGGTGAGGCG	GCGGGGGCGG	240
	TGCAGGAGCT	GGCGCGGGCG	CTGGGCGATC	TGCTGGAGGC	CGAACGTCAG	GAGCGGGGCG	300
10	GGGCGGAGGC	GCAGGAGGCT	GAGGATCAGC	AGGCGCGCGT	CCTGGCGCAG	CTGCTGCGCG	360
	TCTGGGGCGC	CCCCCGCAAC	TCTGATCCGG	CTCTGGGCCT	GGAACGACAG	CCCGACGCGC	420
	CTGCAGCGCA	GCTCGCTGCG	GCTCTGTCTC	GCGCCCGGCT	TGAACCTGCC	GCCCTAGCAG	480
	CCAGAGCTGT	CCCGCGCGCC	GTCCCGCGCG	CGGCGCTCCG	ACCCCGGCCC	CCGCTCTACG	540
	ACGACGGCCC	CGCGGGCCCC	GATGCTGAGG	AGGCAGGGCA	CGAGACACCC	GACGTGGACC	600
15	CCGAGCTGTT	GAGGTACTTG	CTGGGACGGA	TTCTTGGCGG	AAGCGCGGAC	TCCGAGGGGG	660
	TGGCAGCCCC	GCGCGCGCTC	CGCGGTGCGG	CGAACCAAGA	TGTGGGCTCT	GAGCTGCCCC	720
	CTGAGGGCGT	GCTGGGGGCG	CTGCTGCGTG	TGAACCGGCT	AGAGACCCCG	GCGCCCCAGG	780
	TGCTCTGCAG	CCGCTCTTGG	CCACCCTGAG	CACTGCCCCG	ATCCCGTGCA	CCCTGGGACC	840
	CAGAACTGCC	CCCGCATATC	CGCCACACAG	ACTTCTCCCC	GCCAGCAGCT	CCAGAGCAAC	900
20	TTACCCCGGC	CAGCCAGCCC	TCTCACCCGA	GGATCCCTAC	CCCCTGGCCC	ACAATAACAT	960
	GATCTGAGC						969

Seq ID NO: C158 DNA Sequence

Nucleic Acid Accession #: NM\_002245.2

Coding sequence: 183..1193

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	CGCGCTCCGG	CGGCTCTGCG	GCGTTGGCCT	TGGCTTTGGC	TTTGGCGGCG	GCGGTGGAGA	180
	AGATGCTGCA	GTCCTTGGCC	GGCAGCTCGT	GCGTGGCGCT	GGTGAGGCGG	CACCGCTGGG	240
	CTGGTGGCTT	GCGCTTCTTG	GTGCTGGGCT	ACTTGTCTTA	CCTGTCTTTC	GGCGCAGTGG	300
	TCTTCTCCTC	GGTGGAGCTG	CCCTATGAGG	ACCTGCTGCG	CCAGGAGCTG	CGCAAGCTGA	360
35	AGCGAGCGCT	CTTGGAGGAG	CACGAGTGCC	TGTCTGAGCA	GCAGCTGGAG	CAGTTCTGGG	420
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	GGAACTGGGA	CTTCACCTCC	GCGCTCTTCT	TGCCAGCAC	CGTGTCTTCC	ACCACAGGTT	540
	ATGGCCACAC	CGTGCCCTTG	TCAGATGGAG	GTAAGGCCTT	CTGCATCATC	TACTCCGTCA	600
40	TGGCATTCC	CTTCACCTTC	CTGTTCTCTA	CGGCTGTGGT	CCAGCGCATC	ACCGTGACAG	660
	TCACCCGCG	GCGGCTCCTC	TACTTCCACA	TCCGCTGGGG	CTTCTCCAAG	CAGGTGGTGG	720
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45	AATTCAGAGA	GCTCTATAAG	ATTGGGATCA	CGTGTACCTT	GCTACTTGGC	CTTATTGCCA	960
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	TCTATGTGAA	GAAGGACGAG	GACGAGGATC	AGGTGCACAT	CATAGAGCAT	GACCAACTGT	1080
	CTTCTCTCTC	GATCAGAGAC	CAGGCAGCTG	GCAATGAAAG	GGACCAAGAG	CAAAATGAGC	1140
	CTTTTGTGGC	CACCCAGTCA	TCTGCTGCGG	TGGATGGCCC	TGCAAAACCAT	TGAGCGTAGG	1200
50	ATTGTTGTC	TTATGCTAGA	GCAACAGGGT	CAGGGTGCAA	GGAAGAGGCT	TAAGTATGTT	1260
	CATTTTTATC	AGAAATGCAA	AGCGAAAATT	ATGTCACITT	AAGAAATAGC	TACTGTTTGC	1320
	AATGTCTTAT	TAAAAAACAA	CAAAAAAAGA	CACATGGAAC	AAAGAGCTGT	TGACCCGAGC	1380
	AGGATGTCTA	ATATGTGAGG	AAATGAGATG	TCCACCTAAA	ATTCAATATG	GACAAAATTA	1440
	TCTGAGCTTT	ACATAGGAGG	AGAATACTTG	AAGCAGTATG	CTGCTGTGGT	TAGAAGCAGA	1500
55	TTTTATACCT	TTAACTGGAA	ACTTTGGGGT	TTGCATTTAG	ATCATTTAGC	TGATGGCTAA	1560
	ATAGCAAAAT	TTATATTTAG	AAGCAAAAAA	AAAAAGCATA	GAGATGTGTT	TTATAAATAG	1620
	GTTTATGTGT	ACTGTGTTTG	ATGTACCCAC	CCAAATGAT	TATTTTGGGA	GAATCTAAGT	1680
	CAAACTCACT	ATTTATAATG	CATAGGTAAC	CATTAACTAT	GTACATATAA	AGTATAAATA	1740
	TGTTTATAT	CTGTATATAT	GGTTTAGGTC	ACCAGATCCT	AGTGTAGTTC	TGAAACTAAG	1800
60	ACTATAGATA	TTTTGTTTCT	TTTGATTTC	CTTTATACTA	AAGAATCCAG	AGTTGTGACA	1860
	ATAAAATAAG	GGGAATAATA	AACTTGAGAG	TGAATAACCA	T		1901

Seq ID NO: C159 DNA Sequence

Nucleic Acid Accession #: NM\_005472.1

Coding sequence: 93..404

	1	11	21	31	41	51	
65	AAAGGGAGCT	CTTGAAACTG	ATTGAGAGCC	CAOTGGATT	GCCAGCAGTT	TGAGCTTCTA	60
	CGAGTCTTTC	CCCAACCTCA	ATCCCTGTTG	CTATGGAGAC	TACCAATGGA	ACGGAGACCT	120
70	GGTATGAGAG	CCTGCATGCC	GTGCTGAAGG	CTCTAAATGC	CACCTTTCAC	AGCAATTTGC	180
	TCTGCGCGCC	AGGGCCAGGG	CTGGGGCCAG	ACAACCAGAC	TGAAGAGAGG	CGGGCCAGCC	240
	TACCTGGCCG	TGATGACAA	TCCTACATGT	ACATTCTCTT	TGTCATGTTT	CTATTGCTGT	300
	TAACTGTGGG	CAGCTCATC	CTGGGATACA	CCCGCTCCCG	CAAAGTGAGC	AAGCGTAGTG	360
75	ACCCCTATCA	TGTGTATATC	AAGAACCCTG	TGTCTATGAT	CTAACACGAG	AGGGCTGGGA	420
	CGGTGGAAGA	CCAAGACACC	TGGGGATTGC	GTCTGGGGCC	TCCAGAACTC	TGCTGTGGAC	480
	TGCATCAGGT	CT					492

Seq ID NO: C160 DNA Sequence

Nucleic Acid Accession #: NM\_005245.1

Coding sequence: 187..13959

	1	11	21	31	41	51	
80	CTGGGCGGCC	GGGCGCGGGG	AGAGGGGCGG	GGAGCGGCTC	GTGCGGCAGG	TACCATGCGG	60

	ACGCGCGAGC	CCGCGGAGGC	CCCGGCAGGC	CCGTCCCTGC	TCGGGGGGGC	GCTGAGACGG	120
	CGGTGAGCT	CCACGAGAGC	GCCGTGCGCA	CTTCGGGGCA	ACTTTGCGAT	TCCCGACAGT	180
	TAAGCAATGG	GGAGACATTT	GGCTTTGCTC	CTGCTTCTGC	TCCTTCTCTT	CCAACATTTT	240
5	GGAGCAGTGT	ATGGCAGGCC	ACGACTTGAA	CAGACTCCTC	TGCAGTTTAC	ACACCTCGAG	300
	TACAACGTCA	CCGTGCAGGA	GAACTCTGCA	GCTAAGACTT	ATGTGGGGCA	TCCTGTCAAG	360
	ATGGGTGTTT	ACATTACACA	TCCAGCGTGG	GAAGTAAGGT	ACAAAATTGT	TTCCGGAGAC	420
	AGTGAAAACC	TGTTCAAAGC	TGAAGAGTAC	ATTCTCGGAG	ACTTTTGCTT	TCTAAGAATA	480
	AGGACCAAAG	GAGGAAATAC	AGCTATTCTT	AATAGAGAAG	TGAAGGATCA	CTACACATTG	540
	ATAGTGAAG	CACTTGAAAA	AAATACTAAT	GTGGAGGGGC	GAACAAAGGT	CAGGGTGCAG	600
10	GTGCTGGATA	CAAATGACTT	GAGACCGTTA	TTCTCACCCA	CCTCATAACG	CGTTTCTTTA	660
	CCTGAAAAAC	CAGCTATAAG	GACCACTATC	GCAAGAGTCA	GCGCCACGGA	TGCAGACATA	720
	GGAAACCAAC	GGGAATTTTA	CTACAGTTTT	AAAGATCGAA	CAGATATGTT	TGCTATTTCAC	780
	CCAACCAAGT	GTGTGATAGT	GTTAACTGGT	AGACTTGATT	ACCTAGAGAC	CAAGCTCTAT	840
	GAGATGGAAA	TCTTCGCTGC	GGACCGTGGC	ATGAAGTTGT	ATGGGAGCAG	TGGCATCAGC	900
15	AGCATGGCCA	AGCTAAACGG	GCACATCGAA	CAGGCCAATG	AATGTGCTCC	GGTGATAACA	960
	GCAGTGACAT	TGTCAACATC	AGAAGCTGAC	AGGGACCCAG	CATATGCAAT	TGTGACAGTG	1020
	GATGACTGCG	ATCAGGGTGC	CAATGGTGAC	ATAGCATCTT	TAAGCATCGT	GGCAGGTGAC	1080
	CTTCTCCAGC	AGTTTAGAAC	AGTGAGGTCC	TTTCCAGGGA	GTAAGGAGTA	TAAAGTCAAA	1140
	GCCATCGGTG	ACATTGATTG	GGACAGTCAT	CCTTTCGGCT	ACAATCTCAC	ACTACAGGCT	1200
20	AAAGATAAAG	GAATCCGCCC	CCAGTTCTCT	TCTGTTAAAG	TCATTCACTG	GACTTCTCCA	1260
	CAGTTCAAAG	CCGGGCGAGT	CAAGTTTGAA	AAGGATGTTT	ACAGAGCAGA	AATAAGTGAA	1320
	TTTGCTCCTC	CCAACACACC	TGTGGTCATG	GTAAGGGCCA	TTCTGCTTAA	TTCCCATTTG	1380
	AGGTATGTTT	TAAAAGGAC	ACCTGAAAAA	GCTAAATTC	GTTTAAATTA	CAACACTGGT	1440
25	CTCATTTCTA	TTTTAGAAC	AGTTAAAAGA	CAGCAGGCG	CCCATTTTGA	ACTTGAAGTA	1500
	ACAACAAGTG	ACAGAAAAGC	GTCCACCAAG	GTCTTGGTGA	AAGTCTTAGG	TGCAAAATAGC	1560
	AATCCCCCTG	AATTTACCCA	GACAGCGTAC	AAAGCTGCTT	TTGATGAGAA	CGTGCCCAT	1620
	GGTACTACTG	TCAATGAGCT	GAGTGCCGTA	GACCTGATG	AGGGTGAGAA	TGGGTACGTG	1680
	ACATACAGTA	TGCCAAATTT	AAATCATGTG	CCGTTTGGCA	TTGACCATTT	CACGTGTGCC	1740
30	GTGAGTACGT	CAGAAAACTT	GGACTACGAA	CTGATGCTTC	GGGTTTATAC	TCTGAGGATT	1800
	CGTGCACTAG	ACTGGGGCTT	GCCGTACCGC	CGGGAAGTCG	AAGTCTTAGG	TGCAAAATAGC	1860
	CTCAATAACT	TGAATGACAA	CACACCTTTG	TTTGAGAAAA	TAAATTTGTA	AGGGACAATT	1920
	CCCAGAGATG	TAGGCGTGGG	AGAGCAAAAT	ACCACTGTTT	CTGCTATTGA	TGCAGATGAA	1980
	CTTCAGTTGG	TACAGTATCA	GATTGAAGCT	GGAAATGAAC	TGGATTGTTT	TAGTTTAAAC	2040
35	CCCAACTCGG	GGGTATTGTC	ATTAAAGCGA	TGCTTAATGG	ATGGCTTAGG	TGCCAAGGGT	2100
	TCTTTCCACA	GCTTGAAGAT	CACAGCTACA	GATGGAGAAA	ATTTTGCCAC	ACCAATATAT	2160
	ATCAACATAA	CAGTGGCTGC	CAGTCACAG	CTGGTAAACT	TGCAGTGTGA	AGAGACTGGT	2220
	GTTGCCAAAA	TGCTGGCAGA	GAAGCTCCTG	CAGGCAAAAT	AATTACACAA	CCAGGGAGAG	2280
	GTGGAGGATA	TTTTCTTCCA	TTCTCACTCT	GTCATGCTC	ACATACGCGA	GTTTAGAAGC	2340
40	ACTCTTCCGA	CTGGTATTCA	GGTAAAGGAA	AACACGCTTG	TGGGTTCCAG	TGTAATTTTC	2400
	ATGAATCCCA	CTGACCTTGA	CACCTGGCTT	AATGGAAGAA	TGGTCTATGC	TGTTTCTGGA	2460
	GGAAATGAGG	ATAGTTGCTT	CATGATTGAT	ATGGAAACAG	GAATGCTGAA	AATTTTATCT	2520
	CCTCTTGACC	GTGAAACAAC	AGACAAATAC	ACCTCGAATA	TTACCGTCTA	TGACCTTGGG	2580
	ATACCCCGAG	AGGCTCGGTG	CGCTCTTCTA	CATGTCGTGG	TTGTGATGTC	CAATGATAAT	2640
45	CCACCCGAGT	TTTACAGGAA	GAGCTATTTT	GTGGAAAGTA	GTGAAGACAA	GGAGGTACAT	2700
	AGTGAATACT	TCCAGGTTGA	AGCCACAGAT	AAAGACCTGG	GGCCCAACGG	ACACGTGAAC	2760
	TACTCAATTC	TTACAGACAC	AGACACATTT	TCAATTGACA	GCGTGACGGG	TGTTGTTAAC	2820
	ATCGCACGCC	CTCTGATACG	AGAGCTGACG	CATGAGCACT	CCTTAAAGAT	TGAGGCCAGG	2880
	GACCAAGCCA	GAGAAAGAGC	TCAGCTGTTC	TCCACTGTGC	TTGTGAAAGT	ATCACTAGAA	2940
50	GATGTTAATG	ACAACCCACC	TACATTTATT	CCACCTAATT	ATCGTGTGAA	AGTCCGAGAG	3000
	GATCTTCCAG	AAGGAACCGT	CATCATGTGG	TTAGAAGCCC	ACGATCCTGA	TTTAGTTCAG	3060
	TCGTGTCAGG	TGAGATACAG	CCTTCTGGAC	CACGGAGAAG	GAAACTTCGA	TGTGGATAAA	3120
	CTCAGTGGAG	CAGTTAGGAT	CGTCCAGCAG	TTGGACTTTG	AGAAGAAGCA	AGTGATATAAT	3180
	CTCAGTGGTA	GGGCTCAAGG	CAAGGGAAAG	CCAGTTTCTC	TGCTCTCTAC	TTGCTATGTT	3240
55	GAAGTTGAGG	TGGTGTATGT	GAATGAGAAC	CTGCACCCAC	CCGTGTTTTT	CAGCTTTGTG	3300
	GAAAAGGGGA	CAGTGAAGAA	AGATGCACCT	GTTGGTTTCAT	TGGTAATGAC	GGTGTCCGCT	3360
	CATGATGAGG	ACGCGGGAAG	AGATGGGGAG	ATCGATACCT	CCATTAGAGA	TGGCTCTGGC	3420
	GTTGGTGTTT	TCAAAATAGG	TGAAGAGACA	GGTGTCTATG	AGACGTGAGA	TGCACTGGAC	3480
	CGTGAATCGA	CCTCCCAITTA	TTGGCTAACA	GTCTTTGCAA	CCGATCAGGG	TGCTGTGCTT	3540
60	CTTTATCGT	TATAGAGAT	CTACATAGAG	GTGAGGATG	TCAATGACAA	TGCACACAG	3600
	ACATCAGAGC	CTGTTTATTA	CCCAGAAATC	ATGGAAAAAT	CTCCTAAAGA	TGTATCTGTG	3660
	GTCCAGATCG	AGGCATTGTA	TCCAGATTGG	AGCTCTAATG	ACAAGCTCAT	GTACAAAAAT	3720
	ACAAGTGGAA	ATCCACAAGG	ATTCTTTTCA	ATACATCCTA	AAACAGGTCT	CATCACAACT	3780
	ACGTCAAGGA	AGCTAGACCG	AGAACAGCAA	GATGAACACA	TATTAGAGGT	TACTGTGACA	3840
65	GACATGTGTA	GTCCCCCCAA	ATCAACCAT	GCAAGAGTCA	TTGTGAAAT	CCTGTATGAA	3900
	AATGACAACA	AACCTCAGTT	TCTGCAAAAG	TTCTACAAAA	TCAGACTCCC	TGAGCGGGAA	3960
	AAGCCAGACC	GAGAAAGAAA	TGCCAGACGG	GAGCGCTCT	ATCGGTCAT	AGCCACCGAC	4020
	AAGGATGAGG	GCCCCATATC	AGAAATCTCC	TACAGCATCG	AAGACGGGAA	TGAGCATGGC	4080
	AAATTTTTC	TGGAACCGAA	AACCTGGAGT	GTTTGTGCTA	AGAGGTTTTT	AGCAGCTGGA	4140
70	GAATATGATA	TTCTTTCAAT	TAAGGCAGTT	GACAAATGGT	GCCCTCAAAA	GTCATCAACC	4200
	ACCAGACTCC	ATATTGAATG	GATCTCCAAG	CCCAACAGT	CCCTGGAGCC	CATTTTCATT	4260
	GAAGAAATAT	TTTTTACCTT	TACTGTGATG	GAAAGTGACC	CCGTGCTCTA	CATGATTGGA	4320
	GTAATATCTG	TGGAGCCTCC	TGGCATACCC	CTTTGGTTTG	ACATCACTGG	TGGCAACTAC	4380
	GACAGTCAC	TGATGTGGA	CAAGGGAAC	GGAACCATCA	TTGTTGCCAA	ACCTCTTGAT	4440
75	GCAGAACAGA	AGTCAAACTA	CAACCTCACA	GTCCAGGCTA	CAGATGGAAC	CACCACTATC	4500
	CTCACTCAGG	TATTCATCAA	AGTAATAGAC	ACAAATGACC	ATCGTCTCA	GTTTCTCTAC	4560
	TCAAAGTATG	AAGTTGTTAT	TOCTGAAGAT	ACAGGCGCAG	AAACAGAAAT	TTTGCAAAATC	4620
	AGTGTGTGG	ATCAGGATGA	GAAAAACAAA	CTAATCTACA	CTCTGCAGAG	CAGTAGAGAT	4680
	CCACTGAGTC	TCAAGAAAT	TGCTCTTGAT	CCTGCAACCG	GCTCTCTCTA	TACTTCTGAG	4740
80	AAACTGAGAT	ATGAAGCTGT	TTCAACAGCA	CACCTCAAGG	TGATGTTACG	AGATCAAGAT	4800
	GTGCTGTGAA	AAAGCAACTT	TGCAAGGATT	GTGGTCAATG	TGAGCGACAC	GAATGACCAAC	4860
	GCOCCTGGT	TCAAGCTCTC	CTCCTACAAA	GGGCGGGTTT	ATGAATCGGC	AGCCGTTGGC	4920
	TCAAGTGTGT	TGCAAGGTGAC	GGCTCTGGAC	AAGGACAAAG	GGAAGAAATG	TGAAGTGTG	4980
	TACTCGATCG	AGTCAGGAAA	TATTGGAAT	ATTGGAAT	CTTTTATGAT	TGATCTCTGC	5040
	TTGGGCTCTA	TAAAACCTGC	CAAGAATA	GATCGAAGTA	ACCAAGCGGA	GTAATGATTA	5100

	ATGGTAAAG	CTACAGATAA	GGGCAGTCCA	CCAATGAGTG	AAATAACTTC	TGTGCGTATC	5160
	TTTGTACAAA	TTGCTGACAA	CGCCTCTCCG	AAGTTTACAT	CAAAAAGAATA	TTCTGTTGAA	5220
	CTTAGTGAAA	CTGTGACGAT	TGGGAGTTTC	GTGGGATG	TTACAGCCCA	TAGTCAATCA	5280
5	TCAGTGGTGT	ATGAAATAAA	AGATGGAAAT	ACAGGTGATG	CTTTTGATAT	TAATCCACAT	5340
	TCTGGAACATA	TCATCACTCA	GAAAGCCCTG	GACTTTGAAA	CTTTGCCCAT	TTACACATTG	5400
	ATAATACAAG	GAACATAACAT	GGCTGGTTTG	TCCACTAATA	CAACGGTTCT	AGTTCACTTG	5460
	CAGGATGAGA	ATGACAAACGC	GCCAGTTTTT	ATGCAGGCAG	AATATACAGG	ACTCATTAGT	5520
	GAATCAGCCT	CAATTAACAG	CGTGGTCCCTA	ACAGACAGGA	ATGTCCCACT	GGTGATTGCA	5580
10	GCAGCTGATG	CTGATAAAGA	CTCAAAATGCT	TTGCTTGAT	ATCACATTGT	TGAACCATCT	5640
	GTACACACAT	ATTTTGCTAT	TGATTCTAGC	ACTGGTGCTA	TTCATACAGT	ACTAAGTCTG	5700
	GACTATGAAG	AAACAAGTAT	TTTTCACTTT	ACCGTCCAAG	TGCATGACAT	GGGAACCCCA	5760
	CGTTTATTGG	CTGAGTATGC	AGCGAATGTA	ACAGTACATG	TAATTGACAT	TAATGACTGC	5820
	CCCCCTGTGT	TTGCCAAGCC	ATTATATGAA	GCATCTCTTT	TGTTACCAAC	ATACAAAGGA	5880
15	GTAAAGGTCA	TCACAGTAAA	TGCTACAGAT	GCTGATTCAA	GTGCATTCTC	ACAGTTGATT	5940
	TACTCCATCA	CCGAAGGCAA	CATCGGGGAG	AAGTTTCTTA	TGGACTACAA	GACTGGTGCT	6000
	CTCACTGTCC	AAAACAACAC	TCAGTTAAGA	AGCCGCTACG	AGCTAACCGT	TAGAGCTTCC	6060
	GATGGCAAGT	TTGCCGCGCT	TACCTCTGTC	AAAAITTAATG	TGAAAGAAAG	CAAGAGAAAT	6120
	CACCTAAAGT	TTACCCAGGA	TGTCTACTCT	GCGGTAGTGA	AAGAGAATTC	CAOCCAGGCC	6180
20	GAAACATTAG	CTGTCACTAC	TGCTATTGGG	AGTCCAATCA	ATGAGCCITT	GTTTTATCAC	6240
	ATCCTCAACC	CAGATCGCAG	ATTTAAATAA	AGCCGCACTT	CAGGGGTCTT	GTCAACCACT	6300
	GGCAGCGCCT	TCGATCGTGA	GCAGCAGGAG	GCGTTTGATG	TGGTTGTAGA	AGTGATAGAG	6360
	GAACATAAGC	CTTCTGCACT	GGCCCAAGTT	GTGTTGAAGG	TCATTGTAGA	AGACCAAAAT	6420
	GATAATGCGC	CGGTGTTTGT	CAACCTTCCC	TACTACGCCG	TTGTTAAAGT	GGACACTGAG	6480
25	GTGGGCCATG	TCATTGCGTA	TGTCACCTGCT	GTAGACAGAG	ACAGTGGCAG	AAACGGGGAA	6540
	GTGCATTACT	ACCTCAAGGA	ACATCATGAA	CACTTTCAAA	TTGGACCCCT	GGGTGAAAT	6600
	TCACGTGAAA	AGCAATTGGA	GCTTGACACC	TTAAATAAAG	AATATCTTGT	TACAGTGGTT	6660
	GCAAAAGATG	GAGGGAACCC	GGCCTTTTCA	GCGGAAGTTA	TGTTTCCGAT	CACGTGCTAG	6720
	AATAAAGCCA	TGCTGTGTTT	TGAAAAACCT	TTCTACAGTG	CAGAGATTGC	AGAGAGCATC	6780
30	CAGGTGCACA	GCCCTGTGGT	CCACGTGCGA	GCTAACAGCC	CGGAAGGCCCT	GAAAGTGTTC	6840
	TACAGCATCA	CCGTTCAGCA	CCCTTTCAGC	CAGTTCACTA	TTAACTTCAA	TACTGGAGTT	6900
	ATCAATGTCA	TAGTCTCTCT	GGACTTTGAG	GCCCAACCCG	CATATAAGCT	GAGCATACGC	6960
	GCAACTGACT	CCTTGACGGG	CGCTCATGCT	GAAGTATTGT	TGGACATCAT	AGTAGACGAC	7020
	ATCAATGATC	ACCTCTCTGT	GTTTGCTCAG	CAGTCTTATG	CGGTGACCCCT	GTCTGAGGCA	7080
35	TCGTGAATGT	GAACTGTCTG	TGTTCAAGTT	AGAGCCACCG	ATTCGTATTC	AGAACCAAAAT	7140
	AGAGGAATCT	CATACCCAGAT	GTTTGGGAAT	CACAGCAAGA	GTCAATGATCA	TTTTCATGTA	7200
	GACAGCAGCA	CTGSCCTCAT	CTCACTACTC	AGAACCCCTG	ATTACGAGCA	GTCCCGCGAG	7260
	CACACGATTT	TTGTGAGGGC	AGTTGATGGT	GGTATGCCCA	CGCTGAGCAG	TGATGTGATT	7320
	GTCAACGGTG	ACGTTACCGA	CCTCAATGGT	AATCCACCAC	TCTTTGAACA	ACAGATTAT	7380
40	GAAGCCAGAA	TTAGCGAGCA	CGCCCTCAT	GGGCATTTCG	TGACCTGTGT	AAAAGCCTAT	7440
	GATGCAGACA	GTTCAGACAT	AGACAAGTTG	CAGTATTCCT	TTCTGTCTGG	CAATGATCAT	7500
	AAACATTTTG	TCATTGACAG	TGCAACAGGG	ATTATCACCC	TCTCAAACCT	GCACCGGCAC	7560
	GCCCTGAAGC	CATTTTACAG	TCTTAACCTG	TCAGTGTCTG	ATGGAGTTTT	TAGAAGTTCC	7620
	ACCCAGGTTT	ATGTAACCTG	AATTGGAGGC	AATTGACACA	GTCCGTCTTT	CCTTCAGAAC	7680
45	GAATATGAAG	TGGAATCTAGC	TGAAAACGCT	CCCCATACATA	CCCTGTGTAT	GGAGGTGAAA	7740
	ACTACGGATG	GGGATCTGCG	TATTTATGGT	CACGTTACTT	ACCATATTGT	AAATGACTTT	7800
	GCCAAAGACA	GATTTTACAT	AAATGAGAGA	GGACAGATAT	TTACTTTTGA	AAAACCTGAT	7860
	CGAGAAACCC	CGGCGAGAGAA	AGTGATCTCA	GTCCGTTTAA	TGGCTAAGGA	TGCTGGAGGA	7920
	AAAGTTGCTT	TCGTGACCGT	GAATGTCTATC	CTTACAGATG	ACAAATGACAA	TGCACCAAA	7980
50	TTTCAGAGCAA	CCAAATACGA	AGTGAATATC	GGGTCCAGTG	CTGCTAAAGG	GACTTCAGTC	8040
	GTAAAGTCTG	CAAGTGATGC	CGATGAGGGC	TCCAATGCCG	ACATCACCTA	TGCCATTGAA	8100
	GCAGACTCTG	AAAGGTGATA	AGAGAATTTG	GAAATTAACA	AACTGTCCGG	CGTAATCACT	8160
	ACAAAGGAGA	GCCTCATTTG	CTTGGAAAAT	GAAATCTTCA	CTTCTCTTGT	TAGAGCTGTG	8220
	GATAATGGGT	CTCCATCAAA	AGAACTCTGT	GTTCTTGTCT	ATGTTAAAAAT	CCTTCCACCG	8280
55	GAAATGCAGC	TTCCAAATTT	TTCAAGAACCT	TTCTATACCT	TTACAGTGTC	AGAGGACGTG	8340
	CCTGTTGGAA	CAGAGATAGA	TCTCATCCGA	GCAGAACATA	GTGGGACTGT	TCTTTACAGC	8400
	CTGGTCAAG	GGAAATACCT	AGAAAGCAAT	AGGGATGAGT	CCTTTTGATG	TGACAGACAG	8460
	AGCGGGAGAC	TGAAGTTGGA	GAAAGTCTT	GATCATGAGA	CAACTAAGTG	GTATCAGTTT	8520
	TTCCATAGTG	CCAGGTGCGC	TCAAGATGAC	CATGAGATGG	TGGCTTCTGT	AGATGTTAGT	8580
60	ATCCAAGTGA	AAGATGCAAA	TGACAACAGC	CCGCTCTTTG	AATCTAGTCC	ATATGAGGCA	8640
	TTCAATTGTT	AAAACCTGCC	AGGGGGAAGT	AGAGTAATTC	AGATCAGGGC	ATCTGATGCT	8700
	GACTCAGGAA	CCAACGGCCA	AGTTATGTAT	AGCCTGGATC	AGTCACAAAG	TGTGGAAGTC	8760
	ATTGAATCCT	TTGCCATTAA	CATGGAAACA	GGCTGGATTA	CAACTTTAAA	GGAACTTGAC	8820
	CATGAAAAGA	GAGACATTTA	CCAGATTAAA	GTGGTTGCAT	CAGATCATGG	TGAAAAGATC	8880
65	CAGCTATCCT	CCACAGCCAT	TGTGGATGTT	ACCGTCAACG	ATGTCAACGA	TAGTCCACCA	8940
	CGATTCAAGG	CCGAGATCTA	TAAAGGGACT	GTGAGTGAGG	ATGACCCCCA	AGGTGGGGTG	9000
	ATTGCCATCT	TAAGTACCAC	GGATGCTGAT	TCTGAAGAGA	TCAACAGACA	AGTTACATAT	9060
	TTCAATACAG	GAGGGGATCC	TTTAGGACAG	TTTGGCGTTG	AACTATATCA	GAATGAATGG	9120
	AAGGTATATG	TGAAGAAACC	TCTAGACAGG	GAAAAAAGGG	ACAATTACCT	TCTTACTATC	9180
70	ACGGCAACTG	ATGGCACCTT	CTCATCAAAA	GCGATAGTTG	AAGTGAAGT	TCTGGATGCA	9240
	AATGACAACA	GTCCAGTTTG	TGAAAAGACT	TTATATTTCAG	ACACTATTCC	TGAAGAOGTC	9300
	CTTCTGGAAA	AATTGATCAT	GCAGATCTCT	GCTACAGACG	CAGACATCCG	CTCTAACGCT	9360
	GAAATTAATT	ACAGTTTATT	GGGTTCAGGT	GCAGAAAAAT	TCAACTATAA	TCCAGACACA	9420
	GGTGAATCTA	AAACGTCAAC	CCCCCTTGAT	CGTGAGGAGC	AAGCTGTTTA	TCATCTTCTC	9480
75	GTCAAGGCCA	CAGATGGAGG	AGGAAGATTG	TGCCAAGCCA	GTATTGTGCT	CAGCTAGAAA	9540
	GATGTGAAGC	ATAACGCCCC	CGAATTCTCT	GCGATCTCTT	ATGCCATCAC	CGTGTGTTGA	9600
	AACACAGAGC	CGGGAAGGCT	GCTGACAAGA	GTGCAGGCCA	CAGATGCGCA	CGCAGGATTA	9660
	AATCGGAAGA	TTTTATACCT	ACTGATTGAC	TCTGCTGATG	GGCAGTTCTC	CATTAAACGAA	9720
	TTATCTGGAA	TTATTCAGTT	AGAAAAACCT	TTGGACAGAG	AACTCCAGGC	AGTATACACC	9780
80	CTCTCTTTGA	AAGCTGTGGA	TCAAGGCTTG	CCAAGGAGGC	TGACTGCCAC	TGGCACTGTG	9840
	ATTGTATGAT	TTCTTGACAT	AAATGACAAC	CCCCCTGTGT	TTGAGTACCG	TGAATATGGT	9900
	GCCACCGTGT	CGGAGACAT	TCTTGTGGGA	ACTGAAGTTC	TTCAAGTGTG	TGCAGCAAGT	9960
	CGGGATATTG	AAGCAAAATGC	AGAAATCACCC	TACTCAATAA	TAAGTGGAAA	TGAACATGGG	10020
	AAATTCAGCA	TAGATTCTAA	AACAGGGGCC	GTATTTATCA	TTGAGAAATCT	GGATTATGAG	10080
	AGCTCTCATG	AGTATTACCT	AACAGTAGAG	CCCACTGATG	GAGGCACGCC	TTCACTGAGC	10140

	GACGTTGCCA	CTGTGAACGT	TAATGTAACA	GATATCAACG	ATAATACCCC	TGTGTTACGC	10200
	CAAGACACCT	ACACGACAGT	CATCAGTGAA	GATGCCGTTT	TTGAGCAGTC	TGTCATCAGC	10260
	GTATGCGCG	ATGATGCCGA	TGGACCTTCC	AACAGCCACA	TCCACTACTC	AAITATAGAT	10320
	GGCAACCAAG	GAAGCTCGTT	CACAATTGAC	CCCGTCAGGG	GAGAAGTCAA	AGTGACCAAA	10380
5	CTTCTCGACC	GAGAAACGAT	TTGAGGTTAC	ACGCTCAACG	TTCAAGCTTC	TGATAATGGC	10440
	AGTCCACCCA	GAGTCAACAC	GACGACCGTG	AACATCGATG	TGTCGAGTGT	CAATGACAAC	10500
	GCGCCGCTCT	TCTCCAGGGG	AAACTACAGT	GTCTATTATC	AGGAAAATAA	GCCAGTGGGC	10560
	TTGACGCTGC	TGCAGCTGGT	AGTAACAGAT	GAGGATTCTT	CCCTAACCGG	TCCACCCCTC	10620
	TTCTTTACTA	TTGTAACCTG	AAATGATGAG	AAGGCTTTTG	AAGTTAACCC	GCAAGGAGTC	10680
10	CTCCTGACAT	CATCTGCCAT	CAAGAGGAAG	GAGAAAGATC	ATTACTTACT	GCAGGTGAAG	10740
	GTGGCAGATA	ATGGAAGGCC	TCAGTTGTCA	TCTTTGACAT	ACATTGACAT	TAGGGTAATT	10800
	GAGGAGAGCA	TCTATCOGCC	TGCGATTTTG	CCCGTGAGAG	TTTTCATCAC	CTCTTCTGGA	10860
	GAAGAATACT	CAGGTGGCGT	CATTGGGAAG	ATCCATGCCA	CAGACCAGGA	CGTGTATGAT	10920
15	ACTCTAACCT	ACAGTCTCGA	CCCTCAGATG	GACAACTGT	TCTCTGTTTC	CAGCACAGGG	10980
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Nucleic Acid Accession #: NM\_014220.1  
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	TGGAGAGAGA	AATGATGCAT	CTTTTATTTT	TAAATGAAGT	AGATCAACAT	GGTGGAAACA	7380
75	AATGATAAAG	AACAGAAAAA	ATTTCAATAT	ATTACTAATA	ACTTTTTCCT	ATATAAATCC	7440
	TAAAATTCCT	ATAACATAGT	ATTTTACAGT	TTTATGAAGC	TTTCTATTGT	GACTTTTATG	7500
	GAATTAAGAG	ATGAAGAAGA	TGAGATATTT	TAGCAATTTAT	ATTTTTCAAA	ATTATATGTA	7560
80	TACTTAAAAA	TAAAGTAACT	TTATGC				7586

Seq ID NO: C163 DNA Sequence  
Nucleic Acid Accession #: NM\_000958  
Coding sequence: 389..1855

1 11 21 31 41 51  
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1301

5 CGGCACAGCC TCACACCTGA AGCTGTCTCT CCGCAGACG AGACCGGCGG GCACTGCAAA 60  
 GCTGGGACTC GTCTTTGAAG GAAAAAAT AGOGAGTAAG AAATCCAGCA CCATTCTTCA 120  
 CTGACCCATC CGCTGTCACC TCTGTCTTCC CAAGTTTTTG AAAGCTGGCA ACTCTGACCT 180  
 CGGTGTCCAA AAATCGACAG CCACTGAGAC CGGCTTTGAG AAGCGAAGA TTTGGCAGTT 240  
 TCCAGACTGA GCAGACAAG GTGAAAGCAG GTTGGAGGGG GGTCCAGGAC ATCTGAGGGC 300  
 TGACCTTGGG GGCTGTGTAG GCTGCCACCG CTGCTGCCGC TACAGACCCA GCCTTGCAT 360  
 CCAAGGCTGC GCACCGCCAG CCACTATCAT GTCCACTCCC GGGGTCAATT GTCGCGCTC 420  
 CTTGAGCCCC GACCGGCTGA ACAGCCCACT GACCATCCCG GCGGTGATGT TCATCTTCGG 480  
 GGTTGTGGGC AACCTGTGGG CATCGTGGT GCTGTGCAAG TCGCGCAAGG AGCAGAAGGA 540  
 10 GACGACCTTC TACAGCTGG TATGTGGGT GGCTGTCAAC GACCTGTGG GCATTGTGT 600  
 GGTGAGCCCG GTGACCATCG CCACTATCAT GAAGGGCCAA TGGCCCGGG GCCAGCCGCT 660  
 GTGCGAGTAC AGCACTTCA TTTCTGCTCT CTTGAGCCTG TCGGCTTCA GCATCATCTG 720  
 CGCATGAGT GTGAGCGCT ACCTGGCCAT CAACATGCC TATTCTTACA GCCACTACGT 780  
 15 GGACAAGCGA TTTGGCGGCC TCACGCTCTT TGCAGTCTAT GGTCCCAAG TGCTCTTTTG 840  
 CGCGCTGCCC AACATGGGTC TCGGTAGCTC GCGGCTGCAG TACCAGACA CCTGGTCTT 900  
 CATGCACTGG ACCACCAACG TGAAGGCGCA CGCGCGCTAC TCCTACATGT ACGGGGCTT 960  
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 CGCATGCAAC CGCAGTTCA TCGCGCGCAC CTGCTGGGCG ACCGAGCAGC ACCACGCGG 1080  
 20 CGCGCGCGCC TCGGTGTGCT CCGGGGGCCA CCGCGCTGCC TCCCAGCCT TCGCGCGCT 1140  
 CAGCGACTTT CGCGCGCGCC GGAGCTTCCG CGCATGCGCG GCGCGCGAGA TCCAGATGGT 1200  
 CATCTTACTC ATTGCCACCT CCTGTGTGT GCTCATCTGC TCCATCCCGC TCGTGTGTG 1260  
 AGTATTCTGC AACCACTTAT ATCAGCCAAG TTTGGAGCGA GAAGTCAGTA AAAATCCAGA 1320  
 TTTGCAAGCC ATCCGAATGT CTTCTGTGAA CCCCATCTTA GACCCCTGGA TATATATCT 1380  
 25 CCTGAGAAAG ACAGTGCTCA GTAAAGCAAT AGAGAAGATC AAATGCCTCT TCTGCCGCT 1440  
 TGGCGGGTCC CGCAGGGAGC GCTCCGGACA GCATGCTCA GACAGTCAA GGCATCTTC 1500  
 TGCCATGTCA GGCACCTCTC GCTCCTTCTA CTCGCGGAG CTGAAGGAGA TCAGCAGTAC 1560  
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 30 GAGGACTTTG CGAATATCAG AGACCTCAGA CTCTTCACAG GGTGAGGACT CAGAGAGTGT 1740  
 CTTACTGTGT GTGAGGGCTG GTGGAGCGCG CAGGGCTGGG CTTGCCCTTA AGGGGAGCTC 1800  
 CCTGCAAGTC ACATTTCCCA GTGAAACACT GAACCTATCA GAAATATGTA TATAATAGGC 1860  
 AAGGAAGGAA ATACAGTACT GTTCTTGAGC CCTTATAAAA TCCTGTGCAA TAGACACATA 1920  
 CATGTACAT TTAGCTGTGC TCAGAAGGGC TATCATCA 1958

Seq ID NO: C164 DNA Sequence  
 Nucleic Acid Accession #: NM\_002659.1  
 Coding sequence: 427..1434

40 1 11 21 31 41 51  
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 45 ATCAACAATC CATGAGTCAG GGCGAGGCCA GCGCCTTCA CACGAGCCGG CCGCGCCCG 240  
 GGAAGGAAGT TGTGGGCGGA GAGGTTCTGT ACGGGAGGAG GGGGAGGCGC CCAAGCATCT 300  
 GGGGCTGACT CGCTCTTTTC CAAAACGTCT GGGAGGAGTC CCGGGGCCA CAAACTGCC 360  
 TCCTTCTCTA GGCCAGAAAG AGAGAAGAGC TGCAGGGACC CCGCGCACAG GAGCTGCCCT 420  
 CGCGACATGG GTACCCGCGC GCTGCTGCGG CTGCTGCTGC TGTCCACAC CTGCGTCCA 480  
 50 GCCTCTTGGG GCGTGGGTG CATGCACTGT AAGACCAACG GGGATTGCCG TGTGGAAGAG 540  
 TGCGCCCTGG GACAGGACCT CTGAGGACC ACGATCGTGC GCTTGTGGGA AGAAGGAGAA 600  
 GAGCTGGAGC TGGTGAGAGA AAGCTGTACC CACTCAGAGA AGACCAACAG GACCTGAGC 660  
 TATCGAGTCT GCTTGAAGAT CACGAGCCTT ACGAGGTTG TGTGTGGGTT AGACTTGTG 720  
 AACCAGGAGC ACCTCTGGCG GGCTGTCACT TATTCCCGAA GCGGTTACCT CGAATGCATT 780  
 55 TCCTGTGGCT CATCAGACAT GAGCTGTGAG AGGGGCGGCG ACCAGAGCCT GCACTGCCG 840  
 AGCCCTGAAG AACAGTGCCT GGATGTGGTG ACCCACTGGA TCCAGGAAGG TGAAGAAGGG 900  
 CGTCCAAAGG ATGACCGCCA CCTCCGTGGC TGTGGCTACC TCCCGGCTG CCGGGCTCC 960  
 AATGGTTTCC ACAACAACGA CACCTTCCAC TTCTGAAAT GCTGCAACAC CACCAATATG 1020  
 AACGAGGGCC CAATCTGGA GCTTGAAAT CTGCGCAGA ATGGCGGCA GTGTTACAGC 1080  
 60 TGCAAGGGGA ACAGCACCCA TGGATGCTCC TCTGAAGAGA CTTTCTCTAT TGAATGCGA 1140  
 GGCCCCATGA ATCAATGTCT GGTAGCCACC GGCATCTACG AACCGAAAA CCAAGCTAT 1200  
 ATGGTAAGAG GCTGTGCAAC GCGCTCAATG TGCCAACATG CCCACCTGGG TGACGCTTC 1260  
 AGCATGAACC ACATGTAGT CTCTGCTGT ACTAAAGATG GCTGTAAACA CCCAGACCTG 1320  
 GATGTCCAGT ACGCGAGTGG GGCTGCTCCT CAGCCTGGCC CTGCCATCT CAGCCTCACC 1380  
 65 ATCACCTGTC TAATGACTGC CAGACTGTGG GGAGGCATCT TCCTCTGGAC CTAAACCTGA 1440  
 AATCCCCCTC TCTGCCCTGG CTGGATCCGG GGGACCCCTT TGCCCTTCCC TGGCTCCCA 1500  
 GCGCTACAGA CTTGCTGTGT GACCTCAGGC CAGTGTGCGG ACCTCTCTG GCTTCAGTT 1560  
 TCCAGCTAT GAAACAGCT ATCTCACAA GTTGTGTGAA GCAGAAGAGA AAAGCTGGAG 1620  
 70 GAAGGCGCTG GGCAATGGGA GAGCTCTGT TATTATTAAT ATTGTGCGG CTGTTGTGTT 1680  
 GTTGTATTA ATTAATATTC ATATTATTTA TTTTATACTT ACATAAAGAT TTTGTACCAG 1740  
 TGG 1743

Seq ID NO: C165 DNA Sequence  
 Nucleic Acid Accession #: AK027843.1  
 Coding sequence: 193..1731

75 1 11 21 31 41 51  
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 80 CTGTTACCAAG GGACAAATGC AATTTCAAAT TTAGCATTTG GTCTTCCAAG CAATAATGAA 180  
 TGTATTTCC AGATGTGATT TGAGAGTGA CAAGTGGATC CACTGGCATC TGTAAATTTG 240  
 CCTCCAACT TACTTGAGAA TTTAAGTCCA GAAGATTCTG TATTAGTTAG AAGAGCACAG 300  
 TTTACTTTCT TCAACAAAAC TGGACTTTTC CAGGATGTAG GACCCCAAAG AAAAATTTA 360  
 GTGAGTTATG TGATGGCGTG CAGTATTGGA AACATTACTA TCCAGAATCT GAAGGATCCT 420



5	TTTCAAAATA	AAATCAAAACA	TACAAGAAGT	CAGGAAGTGC	ATCATCCCAT	CTGTGCTTC	480
	TGGGATCTGA	ACAAAAACAA	AAGTTTGGGA	GGATGGAAACA	CGTCAGGATG	TGTTGCACAC	540
	AGAGATTGAG	ATGCAAGTGA	GACAGTCTGC	CTGTGTAACC	ACTTCACACA	CTTTGGAGTT	600
	CTGATGGACC	TTCCAGAAG	TGCTCACAG	TTAGATGCAA	GAACACTAA	AGTCTCACT	660
	TTTCATCAGCT	ATATTGGGTG	TGGAATATCT	GCTATTTTTT	CAGCAGCAAC	TCTCTGACA	720
	TATGTGTCTT	TTGAGAAATT	GCGAAGGGAT	TATCCCTCCA	AAATCTTGAT	GAACCTGAGC	780
	ACAGCCCTGC	TGTTCTCGAA	TCTCCTCTTC	CTCTAGATG	GCTGGATCAC	CTCCTTCAAT	840
	GTGGATGGAC	TTTGCAATGC	TGTTGCAATC	CTGTTGCATT	TCTTCTCTCT	GGCAACCTTT	900
10	ACCTGGATGG	GGCTAGAAGC	AATTCACATG	TACATTGCTC	TAGTTAAAGT	ATTTAACT	960
	TACATTGCTC	GATACATTCT	AAAATTCTGC	ATCATTGGCT	GGGTTTGGC	TGCCTTAGTG	1020
	GTGTGAGTTG	TTCTAGCGAG	CAGAAACAAC	AATGAAGTCT	ATGGAAAAGA	AAGTTATGGG	1080
	AAAGAAAAG	GTGATGAATT	CTGTTGGATT	CAAGATCCAG	TCATATTTTA	TGTGACCTGT	1140
	GCTGGGTATT	TTGGAGTCAT	GTTTTTCTG	AACATTGCCA	TGTTTATTGT	GGTAATGGTG	1200
15	CAGATCTGTG	GGAGGAATGG	CAAGAGAAGC	AACCGGACCC	TGAGAGAAGA	AGTGTAAAGG	1260
	AACCTGGCCA	GTGTGGTTAG	CTTGACCTTT	CTGTGGGCA	TGACATGGGG	TTTTGCATTC	1320
	TTTGCTGGGG	GACCCCTAAA	TATCCCTTTC	ATGTACCTCT	TCTCCATCTT	CAATTCAATTA	1380
	CAAGGCTTAT	TTATATTCAT	CTTCCACTGT	GCTATGAAGG	AGAATGTTCA	GAACAGTGG	1440
	CGGCGGCTATC	TCTGCTGTGG	TAGATTTCGG	TTAGCAGATA	ACTCAGATTG	GAGTAAGACA	1500
20	GCTACCAATA	TCATCAAGAA	AAGTTCTGAT	AATCTAGGAA	AATCTTTGTC	TTCAAGCTCC	1560
	ATTGGTTCCA	ACTCAACCTA	TCTTACATCC	AAATCTAAAT	CCAGCTCTAC	CACCTATTTC	1620
	AAAAGGAATA	GCCACACAGA	TAATGTCTCC	TATGAGCATT	CCTTCAACAA	AAGTGGATCA	1680
	CTCAGACAGT	GCTTCCATGG	ACAAGTCCTT	GTCAAACTG	GOCCATGCTG	ATGGAGATCA	1740
	AACATCAATC	ATCCCTGTCC	ATCAGGTCAT	TGATAAGGTC	AAGGGTTATT	GCAATGCTCA	1800
25	TTCAGACAAAC	TTCTATAAAA	ATATTATCAT	GTGAGACACC	TTGAGCCACA	GCACAAAGTT	1860
	TTAATGTCTT	TAGAAAAAAG	AAATCAATCT	GCAGAAATGT	GAAGATTGTC	AAGCAGTGTA	1920
	AACTGCAACT	AGTGAATGTA	ATGTGCTATT	ACCTAGGTAA	CTGCATATAT	ATAAGGAATG	1980
	TATTTTGTGA	AGAAAGCTTT	TGTGAAATTC	AGAATTTTTT	TTTTTAATAT	ATTCTTCCA	2040
	TGGAAGAGTT	GTATCACTA	AACTTCAGT	ACTGAGAGTA	ACATGACTCA	GTAGCCACAG	2100
30	AAGCTATGAT	TTGTAAAAATA	TATAATTGAA	TCAGAGTAAT	CATTAATGCAG	GGGAGACATT	2160
	CAAAATAGAG	ACAAAGGAGA	AGCAATGCTG	AGGAAGACCC	TAGATAGAGC	TCAATTTACT	2220
	CCACCTAATC	GTATATCTG	GATATACCCA	TTTTCTGCAT	CTTCTTCTC	AACATAAAC	2280
	TGTCCTTGCT	TTGAGACTTT	TAAGACATTT	CCTAAAGCAC	AAATAAAGC	CTCGTATTC	2340
	CCCATTTGAGA	GTTTTGTTC	AAGGAATATG	AAGTGAGACA	TATGGGTGAG	TCATAATAAT	2400
35	CAAAATAAAT	TATGAAGAGC	TGGGTCTGCA	ATAGCTAGTC	TAAAACTAC	TTGTGTGTC	2460
	GTCTCTGTGT	TATGATATAT	AAGAGCTGGA	GGAGGTCTGG	CAAGATAGAT	GGTGTATTAT	2520
	TTATGATATC	GGTGTGCTGA	TACAAACCTT	GCATACTATT	ATGCAGCTTA	CCTAATCTC	2580
	AGACTATTCT	GAGTAATGCT	TGCTTGCTAA	TGAATGTATA	GGAGACCACA	TTGTAATTGT	2640
	TCTTAGATGA	TGGAGTCCAT	GCAGTTTCTT	AGAAATGGGT	CTCAGTGCTG	GCTGTGCTTT	2700
40	TTACATTTTG	CTCTGGGTTA	TCTGGGAAGT	ATCAGGTTCT	GGGAGGCCAAC	AGCATTAAAT	2760
	GATAGAGAAA	GGAGACATTC	TGGCAAGGCC	AATCTGCTTA	AAGGCCAAGT	CCAGAACCTG	2820
	GAACCTAGAG	GCCTTTCTCT	CTGCCAGAAA	AACAGGTAGT	TTGCAGTCTG	AGATATGGGA	2880
	GAGCTTTTAG	GCTACACAGC	AACCAAGGGG	ACCTCTCACC	TTTTGCTGAG	CTTCAATCAG	2940
	GAGCTTATT	GCCTGGCTCC	AGCAGATGAT	GAGATAATGA	GGTAGTGGGT	TTTTTATTAC	3000
45	TGTTCCATTT	TGCAACATCC	TGCAACACCA	TCCTGGGAGA	CAAGAGCATT	ACCCAGCTTG	3060
	GCTTTCACGG	GGGAGGGTTG	TATTCAGT				3088

Seq ID NO: C166 DNA Sequence

Nucleic Acid Accession #: NM\_000574.1

Coding sequence: 66..1211

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	GGGCGCATGAC	CGTGGGCGG	CGGAGCGTGC	CCGCGGCGCT	GCCCTCTCTC	GGGAGCTGAC	120
55	CCCGGCTGCT	GCTGCTGGT	CTGTTGTGCC	TGCGGCGCGT	GTGGGGTGAC	TGTGGCCTTC	180
	CCCCAGATGT	ACCTAATGCC	CAGCCAGCTT	TGGAAGGCGG	TACAAATTTT	CCGAGGATA	240
	CTGTAAATAC	GTACAAATGT	GAAGAAAGCT	TTGTGAAAT	TCTGGCGAG	AAGGACTCAG	300
	TGATCTGCTT	TAAGGGCAGT	CAATGGTCTG	ATATTGAAGA	GTTCTGCAAT	OGTAGCTGCG	360
60	AGGTGCCAAC	AAGGCTAAAT	TCTGCATCCC	TCAACAGGCC	TTATATCACT	CAGAAATTAT	420
	TTCCAGTCCG	TACTGTTGTG	GAATATGAGT	GCGTCCAGG	TTACAGAAGA	GAACCTTCTC	480
	TATCACCAAA	ACTAACTTGC	CTTCAGAATT	TAAATGGTTC	CACAGCAGTC	GAATTTTGTA	540
	AAAAGAAATC	ATGCCCTAAT	CCGGAGAGAA	TACGAAATGG	TCAGATTGAT	GTACCAGGTG	600
	GCATATTATT	TGGTGCAACC	ATCTCCTTCT	CATGTAACAC	AGGGTACAAA	TTATTTGGCT	660
65	CGACTTCTAG	TTTTTGTCTT	ATTTCAAGCA	GCTCTGTCCA	GTGGAGTGAC	CCGTGCGCAG	720
	AGTGACAGAGA	AATTTATTGT	CCAGCACCAC	CACAAATTGA	CAATGGAATA	ATTCAAGGGG	780
	AACGTGACCA	TTATGGATAT	AGACAGTCTG	TAACTGATGC	ATGTAATAAA	GGATTCAACA	840
	TGATTGGAGA	GCACTCTATT	TATTGTACTG	TGAATAATGA	TGAAGGAGAG	TGGAGTGGCC	900
	CACCAACCTGA	ATGCAGAGGA	AAATCTCTAA	CTTCCAAGGT	CCCAACCAAC	GTTCAGAAAC	960
70	CTACCAACAGT	AAATGTTCCA	ACTACAGAAG	TCTCACCAAC	TTCTCAGAAA	ACCACCAACA	1020
	AAACCAACCA	ACCAATGCT	CAGCAACAC	GGAGTACACC	TGTTTCCAGG	ACAACCAAGC	1080
	ATTTTTCATGA	AACAAACCCA	AATAAAGGAA	GTGGAACCA	TTCAAGTACT	ACCGCTCTTC	1140
	TATCTGGGCA	CAGGTGTTTC	ACGTTGACAG	GTGTTGCTGG	GACGCTAGTA	ACCATGGGCT	1200
	TGCTGACTTA	GCCAAAGAAG	AGTTAAGAAG	AAAATACACA	CAAGTATACA	GACTGTCTCT	1260
75	AGTTTCTTAG	ACTTATCTGC	ATATTGGATA	AAATAAATGC	AATTGTGCTC	TTCAATTAGG	1320
	ATGCTTTTAT	TGCTTTTAA	ATGTTTAA	AATGTCAACA	GAGCAAGGAG	AAAAAAGGCA	1380
	GTCTCTGAAT	CACATCTTTA	GCACACCTAC	ACCTCTTGAA	AATAGAACAA	CTTGCAAGT	1440
	TGAGAGTGAT	TCCTTCTCTA	AAAGTGTAAG	AAAGCATAGA	GATTGTTGCG	TATTTAGAAT	1500
	GGGATCACGA	GGAAAGAGA	AGGAAAGTGA	TTTTTTTCCA	CAAGATCTGT	AATGTTATTT	1560
80	CCACTTATAA	AGGAATATAA	AAATGAAAAA	CATTATTGG	ATATCAAAAG	CAATATAAAA	1620
	CCCAATTTCAG	TCTCTTCTAA	GCAAAATTGC	TAAAGAGAGA	TGAACCAAT	TATAAAGTAA	1680
	TCTTTGGCTG	TAAAGCATTT	TCACTTTTCC	TGCGGGTTGG	CAAAATATTT	TAAAGGTAAA	1740
	ACATGCTGGT	GAACAGGGG	TGTTGATGGT	GATAAGGGAG	GAATATAGAA	TGAAGACTG	1800
	AATCTTCTCT	TGTTGACAAA	ATAGAGTTTG	GAAAAAGCCT	GTGAAAGGTG	TCTTCTTTGA	1860
	CTTAATGCTCT	TAAAGATAT	CCAGAGATAC	TACAATATTA	ACATAAGAAA	AGATTATATA	1920



TTATTCTCGA ATCGAGATGT CCATAGTCAA ATTTGTAAAT CTTATTCTTT TGTAATATTT 1980  
 ATTTATATTT ATTTATGACA GTGAACATTC TGATTTTACA TGTAACAA GAAAAGTTGA 2040  
 AGAAGATATG TGAAGAAAAA TGTATTTTTC CTAATAGAA ATAAATGATC CCATTTTTTG 2100  
 GT 2102

Seq ID NO: C167 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2651

10 1 11 21 31 41 51  
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 GAGCCCGAGC GCAGGATGTT GCTCAGGGTG GACTGCTCOG ACCTGGGGCT CTCGGAGCTG 180  
 15 CCTTCCAACC TCAGCGCTCT CACCTCCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240  
 CTGCTCCCGA ATCCCTCGCC CAGTCTCOG TTCTGGAGG AGTTACGTCT TGCGGGAAC 300  
 GCTCTGACAT ACATTCCCAA GGGAGCATTG ACTGGCCCTT ACAGTCTTAA AGTTCTTATG 360  
 CTGCAGAAAT ATCAGCTAAG ACAGTATCCC ACAGAAGCTC TGCAGAAATT GCGAAGCCTT 420  
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 20 CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACATGCGT TAAACAGAAAT CCCGCTCCAG 540  
 GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCTGAACAA AATACACCAC 600  
 ATACCAGACT ATGCCCTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAAT 660  
 AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT 720  
 25 TTAATTTACA TAACTTTGA TGAATTCCTC ACTGCAATTA GGACACTCTC CAACCTTAAA 780  
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 CCTGAACATA GAACACTGAC TCTGAATGGT GCTCACAAA TAACTGAATT TCCTGATTTA 900  
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 CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA 1020  
 30 GAAGATTACG CAGTCTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGAACCT AAGACATAAT 1080  
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 TTGGCTTGGG ACAAATATGC TATTATTCAC CCCAATGCAT TTTCCACTTT GCCATCCCCTA 1200  
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 TTAACCTACT TAAATTTAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC 1320  
 35 TTTCCAGAAC TCAAGTTTAT AGAAATGCCT TATGCTTACC AGTGTCTGTC ATTTGAGTGC 1380  
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 GACCTTCATA AGAAGATGC TGGAAATGTT CAGGCTCAAG ATGAACCTGA CCTTGAAGAT 1500  
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 CCAGGCCCTC TCAACCCCTG TGAACACCTG CTGTATGGCT GGCTGATCAG AATTGGAGTG 1620  
 40 TGAACCATAG CAGTCTGCGC ACTTACTTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA 1680  
 TCCCCTCTGT ACATTTCCCC CATTAAACTG TTAATTGGGG TCATGCGAGC AGTGAACATG 1740  
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 GCAACGATCG GTGCTCGGTG GGAGAAATGG GTTGGTTGCC ATGTCAATGG TTTTGTGTC 1860  
 ATTTTGTGCT CAGATCATC TGTTTCTCTG CTACTCTGG CAGCCCTGGA GCGTGGGTTT 1920  
 45 TCTGTGAAT ATTTCTGCAA ATTTGAAAGC AAAGCTCCAT TTTCTAGCCT GAAAGTAATC 1980  
 ATTTTGTCTCT GTGCCCTGCT GGCCCTGACC ATGGCCGAGC TTCCCTGCT GGTGGCAGC 2040  
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 50 GTAAACACA TTGCCCTGTT GCTCTTACAC AACTGCATCC TAAACTGCCC TGTGGCTTTT 2280  
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 CCTCACTTTA AGGAGGATCT GGTGAGCCTG AGAAAGCAA CCTACGTCTG GACAAGATCA 2460  
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 55 ACTCAAGCCT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCAGTTTCC 2580  
 GTGCCATCAC CAGCTTATCC AGTGACTGAG AGCTGCCATC TTTCTCTGT GGCATTGTGC 2640  
 CCATGCTTA A 2651

Seq ID NO: C168 DNA Sequence  
 Nucleic Acid Accession #: NM\_003667.2  
 Coding sequence: 49..2772

60 1 11 21 31 41 51  
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 65 CCCAGGCTCT GTGTGTTGCT GAGGGGCTGC CCCACACACT GTCAATTGCGA GCCCGACGCG 180  
 AGGATGTTGC TCAGGGTGGG CTGCTCCGAC CTGGGGCTCT CGGAGCTGCG TTCCACCTC 240  
 AGCGTCTTCA CCTCTACCT AGACCTCAGT ATGAACAACA TCAGTCAGCT GCTCCCGAAT 300  
 70 CCCCCTGCCC GTCTCCGCTT CCTGGAGGAG TTAGCTCTTG CGGGAACGCG TCTGCATAC 360  
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 CTGATGCTCA ACCACATCAG CTATGTGCC CCAAGCTGTT TCAGTGGCTC GCATTCCCTG 540  
 AGGCACTGTG GGCTGGATGA CAATGCGTTA ACAGAAATCC CCGTCCAGCG TTTTAGAAGT 600  
 75 TTATGGGCTT TGCAAGCCAT GACCTTGGCC CTGAACAAAA TACACCATAT ACCAGACTAT 660  
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 CTGGGAAGA AATGCTTTGA TGGGCTCCAC AGCCTAGAGA CTTTAGATTT AAATTACAAT 780  
 AACCTTGATG AATTCCCAC TGCAATTAGG ACACCTCTCA ACCTTAAAGA ACTAGGATTT 840  
 CATAGCAACA ATATCAGGTC GATACCTGAG AAAGCATTTG TAGGCAACCC TTCTCTTATT 900  
 80 ACAATACATT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA 960  
 CTGAACATAA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAATT TCCTGATTTA 1020  
 ACTGGAACCTG CAAACCTGGA GAGTCTGACT TTAACCTGGG CACAGATCTC ATCTCTTCTC 1080  
 CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA 1140  
 GAAATTTTAC CAGTTTCTTC AGTCTGCCAA AAGCTTCAGA AAATTGAACCT AAGACATAAT 1200  
 GAAATCTACG AAATTAAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATGCTGAAT 1260

5	TTGGCTTGGA	ACAAAATTGC	TATTATTAC	CCCAATGCAT	TTTCCACTTT	GCCATCCCTA	1320
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	TTAACTCACT	TAAATTTAAC	AGGAAATCAT	GCCTTACAGA	GCTTGATATC	ATCTGAAAAC	1440
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	TGTGAGAATG	CCTATAAGAT	TTCTAATCAA	TGGAATAAAG	GTGACAAACG	CAGTATGGAC	1560
	GACCTTCATA	AGAAAGATGC	TGGAATGTTT	CAGGCTCAAG	ATGAACGTGA	CCTTGAAGAT	1620
	TTCTGTCTTG	ACTTTGAGGA	AGACCTGAAA	GCCCTTCATT	CAGTGCAGTG	TTACCTTTCC	1680
	CCAGGCCCCC	TCAAAACCTG	TGAACACCTG	CTTGATGGCT	GGCTGATCAG	AATTGGAGTG	1740
10	TGGACCATAG	CAGTCTGGC	ACTTACTTGT	AATGCTTTGG	TGACTTCAAC	AGTTTTTACA	1800
	TCCCCTCTGT	ACATTTCCCC	CATTAAACTG	TTAATTGGGG	TCATCGCAGC	AGTGAACATG	1860
	CTCACGGGAG	TCTCCAGTGC	CGTGCTGGCT	GGTGTGGATG	CGTTCACTTT	TGGCAGCTTT	1920
	GCACGACATG	GTGCTGTGGT	GGAGAAATGG	GTTGGTTGCC	ATGTCAATTGG	TTTTTTGTCC	1980
	ATTTTGTGCT	CAGAAATCAT	TGTTTTCTGT	CTTACTCTGG	CAGCCCTGGA	GGGTGGGTTT	2040
15	TCTGTGAAAT	ATTCCTGAAA	ATTTGAAACG	AAAGCTCCAT	TTTCTAGCCT	GAAAGTAATC	2100
	ATTTTGTCT	GTGCCCTGCT	GGCCTTGACC	ATGGCCGAG	TTCCCCTGCT	GGGTGGCAGC	2160
	AAGTATGGGG	CCCTCCCTCT	CTGCCCTGCT	TTGCCCTTTG	GGGAGCCGAG	CACCATGGGC	2220
	TACATGCTAC	CGCTCATCTT	GCTCAATTCC	CTTGCTTTCC	TCATGATGAC	CATTGGCTAC	2280
	ACCAAGCTCT	ACTGCAATTT	GGACAAGGGA	GACCTGGAGA	ATATTGGGA	CTGCTCTATG	2340
20	GTAAACACCA	TTCCTCTGTT	GCTCTTCACC	AACCTGCATC	TAAACTGCC	TGTGGCTTTT	2400
	TTGTCTTCT	CTCTTTTAAT	AAACCTTACA	TTTATCAGTG	CTGAAGTAAT	TAAGTTTATC	2460
	CTTCTGGTGT	TAGTCCCACT	TCCTGCATGT	CTCAATCCCC	TTCTCTACAT	CTTGTTCAT	2520
	CCTCACTTTA	AGGAGATCT	GGTGAGCCTG	AGAAAGCAAA	CCTACGTCGT	GACAAGATCA	2580
	AAACACCCAA	GCTTGTATGT	AATTAATCT	GATGATGTGG	AAAAACAGTC	CTGTGACTCA	2640
25	ACTCAAGCCT	TGGTAACCTT	TACCAGCTCC	AGCATCACTT	ATGACCTGCC	TCCCAGTTCC	2700
	GTGCCATCAC	CAGCTTATCC	AGTGACTGAG	AGCTGCCATC	TTTCTCTGT	GGCATTGTCT	2760
	CCATGTCTCT	AATTAATATG	TGAAGGAAAA	TGTTTTCAAA	GGTTGAGAAC	CTGAAAATGT	2820
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Seq ID NO: C169 DNA Sequence  
Nucleic Acid Accession #: NM\_003506.1  
Coding sequence: 259..2379

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	ATCTTTGGAT	GGGGATCTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
	ATCAGGAATT	TGAAGAAAAA	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTTCTACCC	300
40	CTCCATAGAG	CGCTCATCT	CTTCACCTGT	GAACCAATTA	CTGTTCCCAG	ATGTATGAAA	360
	ATGGCCTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
	GCGGTGGAAA	TGGAGCATT	TCTTCTCTC	GCAAACTCTG	AATGTTCAAC	AAACATTGAA	480
	ACTTTCTCT	GCAAGACATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GTTTCCAGCT	540
	TGTGTAAGAC	TTTGTGAGAA	AGTATATTCT	GATTGCAAAA	AATTAATTGA	CACTTTGGG	600
45	ATCCGATGGC	CTGAGGAGCT	TGAATGTGAC	AGATTACAA	ACTGTGATGA	GACTGTTCT	660
	GTAACCTTTG	ATCCACACAC	AGAATTTCTT	GGTCTCTAGA	AGAAAACAGA	ACAAGTCCAA	720
	AGAGACATTG	GATTTTGGTG	TCCAAGGCAT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
	TTTCTGGGAA	TTGCGGAGT	TGCGCCTCCA	TGCCCCAACA	TGTATTTTAA	AAGTGATGAG	840
50	CTAGAGTTTG	CAAAAAGTTT	TATTGGAACA	GTTTCAATAT	TTTGTCTTTG	TGCAACTCTG	900
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	ATATATTACT	CTGTCTGTTA	CAGCATTGTA	TCTCTTATGT	ACTTCATTGG	ATTTTGTCTG	1020
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	CTAGGCTCTC	AAAAATAAGC	TTGACCCGTT	TTGTTCAATG	TTTTGTATTT	TTTCACAATG	1140
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65	GGAAGCAAAA	AGACATGCAC	AGAAATGGGCT	GGGTTTTTTA	AACGAAATCG	CAAGAGAGAT	1800
	CCAATCAGTG	AAAGTCGAAG	AGTACTACAG	GAATCATGTG	AGTTTTTCTT	AAAGCACAAT	1860
	TCTAAAGTTA	AACACAAAAA	GAAGCACTAT	AAACCAAGTT	CACACAAGCT	GAAGGTCAAT	1920
	TCCAATCCCA	TGGGAACCGC	CACAGGAGCT	ACAGCAAATC	ATGGCACTTC	TGCAGTAGCA	1980
	ATTACTAGCC	ATGATTACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAAC	CTCACCAGAA	2040
70	ACATCAATGA	GAGAGGTGAA	AGCGAGCGGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
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	AAGAGTGATA	TACTAGACAC	TGGCCTGGCA	CAGAGCAACA	ATTTGCAGGT	CCCCAGTTCT	2280
	TCAGAACCAA	GCAACCTCAA	AGGTTCCACA	TCTCTGCTTG	TTACCCAGGT	TTGAGGAGTG	2340
75	AGAAAAGAGC	AGGGAGGTGG	TTGTCTTCA	GATACTTGAA	GAACATTTTC	TCTCGTTACT	2400
	CAGAAGCAAA	TTTGTGTATC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
	TACGTTCTTC	TTTGTCACTT	AAAGTTGCAT	TGCCTACTGT	TATACTGAAA	AAAAATAGAGT	2520
	TCAAGATAAT	TATGACTCAT	TTCAACAAA	GGTTAATGAC	AACATATATC	CTGAAAACAG	2580
	AAATGTGACG	GTTAATAATA	TTTTTTTAAT	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
80	CCTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTTAAGATGT	ACTATGCTAT	2700
	TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCTTT	2760
	GTATCTTTT	ATATCATATT	GAAAAAAGC	TTATATGTAT	TTGAACTTTT	TTGAAATCCT	2820
	ATTCAAGTAT	TTTTATCATG	CTATTGTGAT	ATTTTAGACT	TTTGGTAGCT	TTTACACTGA	2880
	ATTTCTAGAA	AAATTGTAAA	ATAGTCTTCT	TTTATACGT	AAAAAAGAT	ATACCAAAAA	2940
	GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTTATTG	ATACCTTACC	ATCTAAAAATG	3000

5  
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 GGCCAAGTGC AATTGACTTC CCTTTTTTAA TGTTCATGA CCACCCATTG ATTGTATTAT 3240  
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Seq ID NO: C170 DNA Sequence  
 Nucleic Acid Accession #: NM\_000582  
 Coding sequence: 88..990

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 CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAAG 240  
 CAGAATCTCC TAGCCCCAGA GACCCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCCATG 300  
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 TTCACTCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGTTTAT 540  
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 GACGAGGACA TCACCTTACA CATGGAAGC GAGGAGTTGA ATGGTGCATA CAAGGCCATC 660  
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 GAAACGAGTC AGCTGATGA CCAAGTGTCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780  
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 CTTTCCAAAG TCAGCCGTGA ATCCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900  
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 TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTG 1440  
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Seq ID NO: C171 DNA Sequence  
 Nucleic Acid Accession #: NM\_002821  
 Coding sequence: 150..3362

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 CCTCAGCTCC TTCTCTAGAG CCGCGCGGGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC 180  
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 CTGTCCAGGA CACGGAGCGG CGTTTCGCCC AGGGCAGCAG CCTGAGCTTT GCAGCTGTGG 420  
 ACCGGCTGCA GAGCTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480  
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 GTCTCTAGCA TAGTGGGCTG TATTCTGTCT GCGCCACAG TGCTTTTGGC CAGGCTTGCA 780  
 GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840  
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 TGCCCTCCTG GCTGAAGAAG CCCCAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440  
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	GAGGGGCTTT	GCAGAAACGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCITGGGCTC	GGGCCCCGCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCCACGGTC	TAGCTGCAG	CCCATCACC	CGCTGGGAA	GAGTGAGTTT	GGGAGGTTG	2580
	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCTTGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAAGCTGAA	CCACGCCAAC	GTGGTGGCGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCCTG	AGGATTTCCA	2820
10	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAAACA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGGCGG	TAACTGCCTG	GTCACTGCC	AGAGACAAAT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCACTTCCG	CCAGGCCTGG	GTGCCGCTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGCAGG	3180
15	CAGATGATGA	AGTACTGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCTC	CAGCCGAGG	3240
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	CTTTTGACAT	TATATAAAC	GCCTTTTGTG	TATGACCAAC	GGCGGGCTTT	TATATGTAAT	4020
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Seq ID NO: C172 DNA Sequence

Nucleic Acid Accession #: NM\_002309.2

Coding sequence: 65..673

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	ATGTCAACA	AACCTCATGA	ACCAGATCAG	GAGCCAACTG	GCACAGCTCA	ATGGCAGTGC	240
	CAATGCCCTC	TTTATCTCT	ATTACACAGC	CCAGGGGGAG	CCGTTCCTCA	ACAACTTGGA	300
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45	GGCCAAAGCTG	GTGGAGCTGT	ACCGCATAGT	CGTGTACCTT	GGCACCTTCC	TGGGCAACAT	420
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	CACCGCCGAC	ATCCTGGGAG	GCCTCTTAG	CAACGTGCTG	TGCCGCTGT	GCAGCAAGTA	540
	CCAAGTGGGC	CATGTGGAGC	TGACCTACGG	CCCTGACACC	TGGGTAAAG	ATGTCTTCCA	600
	GAAGAAGAAG	CTGGGCTGTC	AACTCTGGG	GAAGTATAAG	CAGATCATCG	CGTGTGTGGC	660
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	TCCTGGTCC	CTACTCAACA	AAATATGATG	ATGGCTCCCG	ACACAAGGCG	CAGGGCCAGG	1860
70	GCTTAGCAGG	GCTTGGTCTG	GAAGTCAACA	ATGTTACAAG	TGGAATAAGC	TTACGGGTGA	1920
	AGCTCAGAGA	AGGGTCCGAT	CTGAGAGAAT	GGGGAGGCTT	GAGTGGGAGT	GGGGGGCTTT	1980
	GCTCCACCCC	CATCCCTTAC	TGTGACTTGC	TTTAGGCTGT	CAGGGTCCAG	GCTGCAGGGG	2040
	CTGGGCCAAT	TTGTGGGAGG	GCCGGGTGCC	TTTCTGTCTT	GCTTCCAGGG	GGCTGGTTCA	2100
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75	GCCCCCTGGA	GCAGTGGGCA	AGACAGTCC	TGTGGGCCAC	CCTGTCTCTG	TTTCTGTGTC	2220
	CCCATGCTGC	CTCTGAAATA	GCGCCCTGGA	ACAACTCTGC	CCCTGCACCC	AGCATGCTCC	2280
	GACACAGCAG	GGAAGCTTCT	CCTGTGGCCC	GGACACCCAT	AGACGGTGGG	GGGGCCCTGG	2340
	CTGGGCCAAT	CCCAAGGAAG	GTGGGGTAGA	CTGGGGGGAT	CAGCTGCCCA	TTGCTCCCAA	2400
	GAGGAGGAGA	GGGAGGCTGC	AGACGCCCTG	GACTCAGACC	AGGAAGCTGT	GGGCCCTCCT	2460
80	GCTCCACCCC	CATCCCACTC	CCACCCATGT	CTGGGCTCCC	AGGCAGGGAA	CCCGATCTCT	2520
	TCCTTTGTGC	TGGGGCCAGG	CGAGTGGAGA	AACGCCCTCC	AGTCTGAGAG	CAGGGGAGGG	2580
	AAGGAGGCG	CAGAGTTGGG	GCAGCTGCTC	AGAGCAGTGT	TCTGGCTTCT	TCTCAAAACC	2640
	TGAGCGGGCT	GCCGGCTCTC	AAGTTCTCTC	GACAAGATGA	TGGTACTAAT	TATGGTACTT	2700
	TTCACTCACT	TTGCACTTTT	CCCTGTGCT	CTCTAAGCAC	TTTACTGGA	TGGCGCGTGG	2760

5	GCAGTGTGCA GGCAGGTCT GAGGCCTGGG GTTGGGGTGG AGGGTGGCGC COGGAGTTGT 2820
	CCATCTGTGC ATCCCAACAG CAAGAOCAGG ATGTGGCTGT TGAGATGTGG GCCACACTCA 2880
	CCCTTGTCCA GGTATCAGGG ACTGCCCTTCT CCTTCCGTCT TCATCOGGCT TAGCTTGGGG 2940
	CTGGCTGCAT TCGCCAGGA TGGGCTTGA GAAAGACAAA CTGTCTGGA AACCCAGATT 3000
	GCTGATTCCA CCGGGGGGGC CCGGCTGACT CGCCCATCAC CTCATCTCCC TGTGGACTTG 3060
	GGAGCTCTGT GCCAGGCCA CCTTGGGGCC CTGGCTCTGA TFCGCTCTCC CACCCAGCCT 3120
	GGACTTGGCC CCATGGGACC CATCCTCAGT GCTCCCTCCA GATCCCGTCC GGCAGCTTGG 3180
	CGTCCACCTT GCACAGCATC ACTGAATCAC AGAGCCTTTG CGTGAAACAG CTCTGCCAGG 3240
10	CCGGAGCTGT GGTITCTCTT CCCTTTTAT CTGCTGGTGT GGACCAACC TGGGCTGGC 3300
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	TTTTTTTAAA AAGCACTGCT AGTTTACTTG TCTCTCTCC CATATGTCCC CATGTGCTC 3420
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15	CCCTGCAGAT GGTACAGATG TTCTTGCCTT AGAGTCATCT CTAGTTCCCC ACCTCAATCC 3600
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	TGATGAATGT ACCCTGTGGG GATGTTTCAT ACTGACAGAT TATTTTATT TATTCAATGT 3780
	CATATTTAAA ATATTTATTT TTTATACCAA ATGAATCACT TTTTTTTTAA AGAAAAAAA 3840
20	GAGAAATGAA TAAAGAACT ACTCTTCG 3868

Seq ID NO: C173 DNA Sequence  
Nucleic Acid Accession #: XM\_097508  
Coding sequence: 44..2788

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30	CACAGAGCTT	CAGCTCGGCC	TCTTCCACCA	CTGCGGCTCT	TTGGAGGAGC	TGGCTCTCTC	180
	TGGGAACCAT	CTCTCACACA	TCCCAGGACA	AGCATTTCTC	GGTCTCTACA	GCCTGAAAAAT	240
	CCTGATGCTG	CAGAACATC	AGCTGGGAGG	AATCCCGGCA	GAGGCGCTGT	GGGAGCTGCC	300
	GAGCTGTCAG	TGCTGCGGCC	TAGATGCCAA	CCTCATCTCC	CTGGTCCCGG	AGAGGAGCTT	360
	TGAGGGGCTG	TCCTCCCTCC	GGCACCTCTG	GCTGGAAGAC	AATGCACTCA	CGGAGATGCC	420
35	TGTCAAGGCC	CTCAACAACC	TCCTCTGCCCT	GCAGGCCATG	ACCCTGGCCC	TCAACGSCAT	480
	CAGCCACATC	CCGACTACG	CGTTCCAGAA	TCTCACCAGC	CTTGTGGTGC	TGCATTTGCA	540
	TAAACAACGC	ATCCAGCATC	TGGGAGCCCA	CAGCTTCGAG	GGGCTGCACA	ATCTGGAGAC	600
	ACTAGACCTG	AATTATAACA	AGCTGCAGGA	GTTCCTGTGT	GCCATCCGGA	CCCTGGGCGAG	660
	ACTGCAGGAA	CTGGGGTTCC	ATAACAACAA	CATCAAGGCC	ATCCCAAGAA	AGGCTTCTAT	720
40	GGGGAACCTT	CTGCTACAGA	CGATACACTT	TTATGATAAC	CCAATCCAGT	TTGTGGGAAG	780
	ATCGGCATTC	CAGTACCTGC	CTAAACTCCA	CACACTATCT	CTGAATGGTG	CCATGGACAT	840
	CCAGGAGTTT	CCAGATCTCA	AAGGCACCA	CAGCCTGGAG	ATCCTGACCC	TGACCCGCGC	900
	AGGCATCCGG	CTGCTCCCAT	CGGGGATGTG	CCACAGCTGT	CCCAGGCTCC	GAGTCTTGGA	960
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	CTCCCTGCAA	GCGCTGGATC	TTAGCTGGAA	CGGCATCCGG	TCCATCCACC	CCGAGGCTTT	1140
	CTCCACCTCG	CACTCCCTGG	TCAAGCTGGA	CCTGACAGAC	AACCAGCTGA	CCACACTGCC	1200
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50	GTGCTGTCCC	TATGGGATGT	GTGCCAGCTT	CTTCAAGGCC	TCTGGGCAGT	GGGAGGCTGA	1380
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	GTTTGTGTTG	GGTGCAGATT	CAGGCGCCAA	CACCTTGACT	GGCAATTCCT	GTGGCCTTCT	1740
	AGCCTCAGTC	GATGCCCTGA	CCTTGTGTC	GTCTCTGAG	TACGGAGCCC	GCTGGGAGAC	1800
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	GCTGTCTACT	CTGGCCGCGA	TGCAGTGAGC	CGCTTCGGTC	TCCTGTGTTC	GGGCTATGG	1920
60	GAGTTCCTCC	TCCTGGGCA	CGTTCGAGC	AGGGGTCTTA	GGCTGCTCTG	CACTGGCAGG	1980
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65	CATCTTGCGA	GACGGGCTCC	TCTACTGTCC	CGTGGCCTTC	CTCAGCTTTG	CCTCATGCT	2280
	GGGCTCTTTC	CTGTGCAAGC	CCGAGGCCGT	CAAGTCTGTC	CTGCTGGTGG	TGCTGCCCT	2340
	GCCTGCTGTC	CTCAACCCAC	TGCTGTACCT	GCTCTTCAAC	CCCCACTTCC	GGGATGACCT	2400
	TGGGCGGCTT	CGGCCCGCGC	CAGGGGACTC	AGGGCCCTTA	GCTATGTCTG	CGGCGGGGGA	2460
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70	CATTCTGAAA	GCTTCTGAAG	CTGGGCGGCC	CCCTGGGCTG	GAGACCTATG	GCTTCCCTC	2580
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	GAGGGCAGAG	GGATCTAAGC	CAGCAGGTGG	AGGCTTGTCA	GGGGGTGGCG	GCTTTCAGCC	2760
	CTCTGGCTTG	GCGTTTGTCT	CACACGTGTA	AATATCCCTC	CCCAATCTCT	TCTTCCCTC	2820
75	TCTTCCCTTT	CCTCTCTCCC	CTCOGGTGA	TGATGGCTGC	TTCTAAACA	AATACAACCA	2880
	AAACTCAGCA	GTGTGATCTA	TAGCAGGATG	GCCCAAGTCC	TGGCTCCACT	GATCACTCTT	2940
	CTCCTGTGAC	CATCAACCA	GGGTGCCCTT	TGGCCTGGCT	TTCOCTTGGC	CTTCTCAGC	3000
	TTCACTTGA	TACTGGGCTT	CTTCCTTGTG	ATGTCTGAAG	CTGTGGACCA	GAGACCTGGA	3060
	CTTTTGTCTG	CTTAAAGGAA	ATGAGGGAAG	TAAAGACAGT	GAAGGGGTGG	AGGGTTGATC	3120
80	AGGGCAGAGT	GGACAGGGAG	ACCTCACAGA	GAAAGGCTGT	GAAGGTGATT	TCCGSTGTGA	3180
	CTCATGGATA	GGATACAAA	TGTTGTTCCAT	GTACCATTA	TCTTGACATA	TGCCATGCAT	3240
	AAAGACTTCC	TATTAATAAA	AGCTTTGGAA	GAG			3273

Seq ID NO: C174 DNA Sequence  
Nucleic Acid Accession #: NM\_130849

Coding sequence: 101..2044

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TCTGCTGAGC CTGCTCAGCT CTGGCCAGGG CGCTCTGGAT CAAGAGGCTC TGGGCGGCGCT 240
GTTAAATACG CTGGCGGACC GTGTGCACTG CACCAACGGG CGGTGTGGAA AGTGCCCTGT 300
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35 CTGCTGCAAC GCGGGCTGT CCGTGCAGCA AGCACTGCTG CTGAACCTGG CCTCCGCGCT 1800
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Seq ID NO: C175 DNA Sequence

Nucleic Acid Accession #: NM\_018971

Coding sequence: 1..1128

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TGCTTGGCGG ACGGCTGCGG CGCGCTCGCC TGCTTCCCGG CGTCTATGCT GGGCGGCGCG 240
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60 CCGCGGCTCA GCGACGACTG GACCTTCCAC GGGCGGCGCG CCAAGCGCCA GCGCGCGGCC 720
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65 ACGGCTCGG TGTGGCTGAC CTTGCGGCG GCGCGCATCA ACCCGTCTGT GTGCTTCTCT 1020
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Seq ID NO: C176 DNA Sequence

Nucleic Acid Accession #: NM\_005631

Coding sequence: 290..2653

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GCCAGAGGGC CGGGCGCGCG GAGAGCTCCG GGGGGGCGCG GCGCCGGAAT CTCTGGGCGC 180
ACAGGTGCTC TAGGCGCGCT CCGCGGCGCG CGAGGTCTGT CGTGTGGCGG GGGGCGCTCG 240
AGGAGCAGGC GGGGCGCGCG GGGCTTTTGC TGAATTGGCG GGGTTGGCCA TGGCGGCTGC 300
78 CCGCCAGCG CGGGGCGCGG AGCTCCCGCT CCTGGGCTG CTGCTGCTGC TGCTGCTGGG 360
GGACCGCGGG CCGGGGCGCG CCTGAGAGCG GAACGCGACC GGGCTTGGCG CTGGAGCGCG 420
GGGCGGAGGC GCGAGGAGGA GCGCGCGGCT GACTGGCCCT CCGCGGCGCG TGAAGCACTG 480
CGGCGGCGCT GCGGCTGCG AGCGGCTGCG CTACAACTG TGCGTGGGCT CGGTGCTGCC 540
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5	CAAGCTCGTG	CTCTGGTGGG	GCCTCGGAA	TGCCCCCGC	TGCTGGGAG	TGATCCAGCC	660
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	TACCCCTCTGC	CAGGCCACCC	GAGGCCCTTG	TGCCATCGTG	GAGAGGGAGC	GGGGCTGGCC	780
	TGACTTCCCTG	CGCTGCACCT	CTGACCGCTT	CCCTGAAGGC	TGCACGAATG	AGGTGCAGAA	840
	CATCAAGTTC	AACAGTTCAG	GCCAGTGCGA	AGTGCCCTTG	GTTGGGACAG	ACAACCCCAA	900
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	GGCTGAGCAC	CAGGACATGC	ACAGCTACAT	CGCGGCTTC	GGGGCCGTCA	CGGGCCTCTG	1020
	CACGCTCTTC	ACCCTGGCCA	CATTGTGGC	TGACTGGCGG	AACTCGAATC	GCTACCCCTG	1080
10	TGTTATTCTC	TTCTACGTCA	ATGCGTGCTT	CTTTGTGGGC	AGCATTGGCT	GGCTGGCCCA	1140
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	CCTGATGGCT	GGTGTGGTTT	GGTTTGTGGT	CCTCACCTAT	GCCTGGCACA	CTTCTCTCAA	1320
	AGCCCTGGGC	ACCACCTACC	AGCCTCTCTC	GGGCAAGACC	TCCTACTTCC	ACCTGCTCAC	1380
15	CTGGTCACTC	CCCTTTGTCC	TCACGTGGGC	AATCCTTGCT	TGGGCGCAGG	TGGATGGGGA	1440
	CTCTGTGAGT	GGCATTGTGT	TTGTGGGCTA	CAAGAACTAC	CGATACCGTG	CGGGCTTCTG	1500
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20	CATTACCTTC	AGCTGCCACT	TCTACGACTT	CTTCAACGAG	GCTGAGTGGG	AGCGCAGCTT	1740
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25	GAAGAGCAAG	ATGATTGCCA	AGGCCCTTCTC	TAAGCGGCAC	GAGCTCCTGC	AGAACCAGG	2040
	CCAGGAGCTG	TCCTTCAGCA	TGCACACTGT	GTCCCAAGAG	GGGCCCGTGG	CGGGCTTGGC	2100
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	GATGGTGGCT	CGGAGGAGAG	CCATACTGCC	CCAGGATATT	TCTGTACACC	CTGTGGCAAC	2220
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	GCTGGGCGCG	CGCCTTGAGC	TTACCCCGCC	TGCCCTTGCC	CCAGTACCA	TTCTCTGACT	2400
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40	GTCTCTGTGT	CTGCCCTGCC	AGCTGCAGCC	TGGTTGGCAG	CATCTGTCTC	ATCGGGGCG	2940
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Seq ID NO: C177 DNA Sequence  
Nucleic Acid Accession #: AK094595  
Coding sequence: 1..2853

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65	AAGAACAAGC	CTGTGGAGCT	CCGCTGCCGC	GCCTTCCCG	CCACACAGAT	CTACTTCAAG	240
	TGCAACGGCG	AGTGGGTGAG	CCAGAACGAC	CAGTCAACAC	AGGAAGGCCT	GGATGAGGCC	300
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 Nucleic Acid Accession #: NM\_004625  
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 GGCTGGGTG CCTGCACTT ACCTGTGGGT CGCCCTGCCC TGCTACTGTC TCTACCTCGG 240  
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TCCTGCTGSC CGGCTTGTG TCCTGTTCG GCATCGGCTC GGTATCAAG CAACAGGACG 1560
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CCTGCTGTG GTGCAGCAAG GCGCGCGGG TGGCGGGGG CGCGGGGCGC ACGCGCGCGG 1920
GGGTGGCGCG GCGCGCGGG GCGCGGGGCG GCGGGGAGC CGCGGGGCGC GGGGGGCGG 1980
GCGCGCGCGG GGTCTCCTC TACAGCGAG CTAGCACTGG CTGACGTGG CGGTGGGCA 2040
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TGAAGCCTCC CAGACCCAGC CCGTTTCTCT CCATTGATGT GCGGGGAGCT CTTCCGCGCA 2340
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5 CGCGTTAATT TCTGTTGGCT GAGGAGGGTG GACTCTGCGG CGTTTCCAGA ACCCGAGATT 2400  
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 TGAACGAAA TCAAAATGTA GTTTTTCGAC CTTCGCCAAA GACGGTGTTC TTTCATGGAG 3060  
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 15 AGGCAGTAAT TCCCTTAGG CCTTGTATT TATCCTGCAT GGTATCACTA AAGGTTTCAA 3180  
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Seq ID NO: C182 DNA Sequence  
 Nucleic Acid Accession #: XM\_050625  
 Coding sequence: 222..1109

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 25 GCACCCAGCG AAGAGAGCGG GCGCCGGACA AGCTCGAACT CCGGCGCCCT GCGCTTCCCT 180  
 CGGCTCGGCT CCCTCTGCCC CCGGCGGGTC GCGCGCCAC GATGCTGCAG GCGCTTGGCT 240  
 CGCTGCTGCT GCTCTTCTCT GCGTGCCTCT GCTGCTGGG CTGCGGCGCGC GGGCTCTTCC 300  
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 TT 1382

Seq ID NO: C183 DNA Sequence  
 Nucleic Acid Accession #: NM\_001306.1  
 Coding sequence: 199..861

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 CGCCAGGCCC AGCGGCCCCG GCGCTCTGTC TCCCGCCACC CGGAGCCACC CGGTGGAGCG 180  
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 GACCTTCAGG CGGCCCGGCG CCTCATGCTG GTGGCCATCC TGCTGGCGGC CTTCGGGCTG 480  
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 TCCCGAGCAG CCAAGGCTTT GCGGGCGGGG CAGTGCAGTT CCGGGCCAGC GAGCCAACTT 1080  
 GCATGGACTG TGAACCTCA CCCTTCTGGA GCAGGGGGCC TGGGTGAGCG CCAATACTTG 1140  
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 Nucleic Acid Accession #: NM\_012449.1  
 Coding sequence: 66..1085

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 GGAGAAATTT AGAAGAAGAC GATTATTGTC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180

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AAAGACCTGT GCTTTTGCAT TTGCACCAAA CAGCCCATGC TGATGAATTT GACTGCCCCT 240
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CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420
CAATGGTTTC CATCACTCTC TTGGCATTGG TTACCTGCC AGGTGTGATA GCAGCAATTG 480
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GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC 660
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AGATTAGACA TGGTTGGGAA GACGTACCCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080
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Seq ID NO: C185 DNA Sequence  
Nucleic Acid Accession #: NM\_001775.1  
Coding sequence: 70..972

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CTCTCTCAGA GAGCCCAACT CTGTCTTGGC GTCACTATCC TGGTCTGTAT CCTGCTCGTG 180
GTGCTCGCGG TGGTGTGCCC GAGGTGGCGC CAGACGTGGA CGGCTCCGGG CACCACCAAG 240
CGCTTTCCCG AGACCTGCTT GCGCGATGCG GTCAAGTACA CTGAATTTCA TCCTGAGATG 300
AGACATGTAG ACTGCCAAAG TGTATGGGAT GCTTTCAAGG GTGCATTTAT TTCAAAACAT 360
CCTTGCAACA TTAAGTGAAG AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
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GTCCAGCGGG ACATGTTTAC CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC 540
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AAGGACTGCA GCAACAACCC TGTTCAGTA TTCTGGAAAA CGGTTTCCCG CAGGTTTGCA 660
GAAGCTGCCT GTGATGTGGT CCATGTGATG CTCATGGGAT CCGCAGTAA AATCTTTGAC 720
AAAAACAGCA CTTTTGGGAG TGTGGAAGTC CATAAATTGC AACCAGAGAA GGTTCAAGCA 780
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ACCATAAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT 900
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CATCATACAT GACTCAGCAT ACCTGCTGGT GCAGAGCTGA AGATTTTGA GGGTCCCTCA 1080
CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCAA AGTCTTAAA TAACTTATAT 1140
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Nucleic Acid Accession #: XM\_120513.2  
Coding sequence: 1..2208

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AGGACCCCAA AGCCCGGTAA ACACCGCGCG ACCACCCGGG CCAAGATCTT CAAGAGGTTT 180
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TACTCTGACG ACCCCGCCCC AACGACTAGC CCTCTCTCTG TGCAACCCCG AGAGTTTGGG 300
GTCACTCAGG GGGCGCCACG AGCTCGTTTC GGAAGCCGGA CCCCCTCCCG AGCCGACAGAA 360
GCCTCGAGTC CATCTCTGGG CATTTGGGAG GCAGCTCTGC AATCAGGAGC TCGGGCGGCA 420
GCCGCCCGCG CGGGGGCTCG GCGATGCCAG CCTCAGCGAC AGGCGCGCGC GCGCGCGGCC 480
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CATACATTAG AAAATATTTT ACTTGATTCC ACAGCTTCCC TGTGTAAATC TAGGCATCTA 1680
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CTTGAGGATG GCATCCGACG CCCCCTCCCT TTGAGTTGTG AGGCCTTGA AATGAGATTG 1860
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Seq ID NO: C187 DNA Sequence  
 Nucleic Acid Accession #: AB037745.1  
 Coding sequence: 26..1744

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Seq ID NO: C188 DNA Sequence

Nucleic Acid Accession #: NM\_014324.1

Coding sequence: 89..1237

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Nucleic Acid Accession #: XM\_091332.1

Coding sequence: 1..1401

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	AAAACTTTTA	CTAGCATTTA	GAGCTTTTCA	GAACATCCCC	ACTGTCTATG	GTCTCAGCAG	5100
	TGGAGACTGC	AAGTAAGGCT	TTTAATTTTA	GGAGGTTTTT	TTTTTTTTTT	TTTTTTCCCC	5160
15	TAAATGGTAT	GGCCAAAAGT	CAGAGTTAAA	ATATATATAG	TTAGATTCCA	ACTTCCTCCT	5220
	TCACCTCTAA	AATAGAAATC	AAACCCACTC	TTCATATATG	CTTCCAGAA	GGGCTTAAG	5280
	TACCAATCTC	TGCTTTGCAA	TGGGCACAA	CTTGGTCATG	TCTTGAGGCT	CTCTAAGAAA	5340
	AGAGAGGATC	TAGGATGGGA	GAGCTAGAAA	GTTGCTAACT	GGGAAGAAC	AGGCCCTGAG	5400
	GGGTGGGTCT	ACCAATCTGG	GAAGATTGGA	AAACAACTT	CTCGCAACTG	AAGGAAGGCT	5460
20	GAAGGCTGCT	GCAAGTCTAT	GAGTGACTTT	AGGATGAGCA	AAACATTGGG	CCACTTCCTA	5520
	ATGCCCTATG	TGTATAGTAC	CAGAAGCAAG	GTCTCAGACT	TACAGACCC	AGCTCTGTTC	5580
	CAAGGTGAGT	CTGAACCAAT	AGAAAGCAAA	CATGTGCAGA	TATCCAAACA	AGACTGCTCA	5640
	TGCAAGTGGG	GGCTGGCTAC	CCGTCTTAGG	CAGCAACAGC	AGAGCTCCAG	GGAGCTTATT	5700
	CAATATTATC	TGAGACTTGG	AAGACCCAGC	AGATGTTTAA	TGAAGTCACT	ATTTTGGCTC	5760
25	AAACCTCTCA	CTTCTCCCCC	TCCCCTCAAA	AAGCCCAACG	GTAACACAT	AAATGAAAGA	5820
	AAACCCACAG	AGGGGATGGG	AAATAAGAA	AATTCTCTCA	AGACTTCTCC	AGGCCCATGT	5880
	CACCTGGTCA	CGTGGTTTTT	ATGTGTATTA	GGATTGGGGG	ATGTGAAGAA	ATAAGTATCC	5940
	AGTACTTTAT	AACCAAGACA	ATTAAATGAT	ATTGGGGTAG	GGAAATGTTG	CCAGTTTGTG	6000
	TTAGTTTTCG	CATCACATTT	TCAACCCAGC	CTCACCTAGC	CCCAAGTAAT	CGGGCCGCCC	6060
30	GAAGAGGAGG	ACAGAGATGT	GCCAGAGTTG	ACCCAGTGTG	CGGATGATAA	CTACTGACGA	6120
	AAGAGTCATC	GACCTCAGTT	AGTGGTTGGA	TGTAGTCACA	TTAGTTTGCC	TCTCCCCATC	6180
	TTTGCTCTCC	TGGCAGGAG	AATATGCGGG	ACATGATGCT	AAGAGCCCTG	GGTAAATGTG	6240
	GTGAGAAATG	ACCGGTGCA	ATGCTACACA	TATGTGCTTC	TCAGTTGCGC	AAATGAACT	6300
	GCTTTGGGAG	ATTATCAGTA	GAAGAGTGT	TATCATATTG	GTGCTGAGTG	CTATGTGTGC	6360
35	TTATACAATT	TGTTCTTGTA	TTTAAATAAA	CTTTGAATAA	AAGAATAAAA	AAAAAATAAA	6420
	AAAAAATAA						6429

Seq ID NO: C192 DNA Sequence  
Nucleic Acid Accession #: NM\_006549.2  
Coding sequence: 824..2590

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45	CAACACAGAG	AGACCTGTGC	TCAAAACAAA	CAAAACAAAC	AACAAACAAA	CAAAACAAAG	120
	AAAAAATAAA	GGGAGTGGGC	CGGGCGCGGT	GACTCACACC	TGTAATCCCA	GCCTTTCCGG	180
	AGGCCAAGGC	GGGTGATGAT	CGAGGTGAGG	AATTCAGAT	TAGCCTGGAC	AACATGGTGA	240
	AACCCATCTC	CTACGAAATA	TACAAAAATT	AGCCAAATAT	GGTGCCCGGC	GCCTGTAATC	300
	CCAGCTACTC	GGGAGACTGA	GGCAGAGAAC	TGCTTGAACC	TGGGAGGCAG	AGGTTGCAGT	360
50	GATCCGAGAT	CGGTCTACTG	CATCTCCAGC	TGGGCGACAG	AGCGAGACTC	CGTTTCAGAA	420
	AAGAAAAATA	AAAAAAGGAG	TCCGGGTGGA	GCTCTCATTT	GCTCGTTGCA		480
	TGTGAGTGTG	CCTACGGGCT	AGAAATACCA	GAGAAGCACA	TCCGAAACGG	CTCGAAATCC	540
	ACCCAGTTAA	CTAGAGGGCT	TTGAACCTTT	TATTAACCTT	GAGGTTGACT	CTCTGTGCAA	600
	CTCGATTCCC	TTTTGGCTGT	TTGGCAGGGT	CAGTGAGACA	TCCCTGGGGT	CGCTCGACCC	660
55	CGTAGGACGG	TTCCAGGGAG	CCTCCAGGTC	TTGCTTTCTC	CTCTTCCCGG	CACAGTGCTG	720
	TTATCCAGCT	GGGGGATCCA	ACGCACACTT	AAGGCTCCAG	CAAAAGTGGT	CCGCTGCGGG	780
	ATGGGAGTGC	CCAGATGTGC	TGGATGAAGC	TGGGCGATGC	ACCATGTGAT	CATGTGTCTC	840
	TAGCCAGCCC	AGCAGCAACC	GGGCGCCCCC	CCAGGATGAG	CTGGGGGGCA	GGGGCAGCAG	900
	CAGCAGCGAA	AGCCAGAAGC	CCTGTGAGGC	CCTGCGGGGC	CTCTCATCTT	TGAGCATCCA	960
60	CCTGGGCGAT	GAGTCTCTCA	TTGTGGTCAC	CGAGTGTGAG	CCGGGCTGTG	CTGTGGACCT	1020
	CGGCTTGGCG	CGGGAACCGC	CCCTGGAGGC	CGATGGCCAA	GAGGTCCCCC	TTGACTCCTC	1080
	CGGCTCCAG	GGCGGGCCCC	ACCTCTCCGG	TCCGAGCTG	TCTCTGCAAG	AGCGGTCCCA	1140
	GGGTGGGCTG	GCAGCCGGTG	GCAGCCTGGA	CATGAACGGA	CGCTGCACTT	CGCCGTCCCT	1200
	GGCCTACTCA	CCCGTCAGCT	CCCGCAGTCT	CTCGCCCTGG	CTGCCCCGGC	GGCCGACAGT	1260
65	GGAGTCTCAC	CAGCTCTCCA	TCAAGGGTAT	GCAGGACTGT	GTGCACTGTA	ATCAGTATAC	1320
	CCTGAAGGAT	GAATTTGGA	AGGGCTCCTA	TGGTGTGCTC	AAGTTGGCCT	ACCAATGAAA	1380
	TGACAATACC	TACTATGCAA	TGAAGGTGCT	GTCCAAAAG	AAGCTGATCC	GGCAGGCCGG	1440
	CTTTCCACGT	CGCCCTCCAC	CCCGAGGCAC	CCGGCCAGCT	CCTGGAGGCT	GCATCCAGCC	1500
	CAGGGGCCCC	ATTGAGCAGG	TGTACCAGGA	AATTGCCATC	CTCAAGAAGC	TGGACCAACC	1560
70	CAATGTGGTG	AAGCTGGTGG	AGGTCTCTGA	TGAACCCAA	GAGGACCATC	TGTACATGGT	1620
	GTTGGAACCT	GTCAACCAAG	GGCCCGTGAT	GGAGTGCCCC	ACCCCTCAAC	CACCTCTGTA	1680
	AGACCAAGGC	CGTTTCTACT	TCCAGGATCT	GATCAAGGCG	ATCGAGTACT	TACACTACCA	1740
	GAAGATCATC	CACCGTGACA	TCAAACTTTC	CAACCTCTCT	GTCCGAGAAG	ATGGGCACAT	1800
	CAAGATCGCT	GACTTTGGTG	TGAGCAATGA	ATTCAAGGGC	AGTGACCGCG	TCCCTCTCAA	1860
75	CACCGTGGGC	ACGCCCGCCT	TCAATGGCACC	CGAGTGGCTC	TCTGAGACCC	GCAAGATCTT	1920
	CTCTGGGAAG	GCCTTGGATG	TTTGGGCCAT	GGGTGTGACA	CTATACTGCT	TGTCTTTGG	1980
	CCAGTGCCCA	TTTATGGAGC	AGCGGATCAT	GTGTTTACAC	AGTAAGATCA	AGAGTCAGGC	2040
	CCTGGAATTT	CCAGACCAAG	CCGACATAGC	TGAGGACTTG	AAGGACCTGA	TCAACCGTAT	2100
	GCTGGACAAG	AACCCCGAGT	CGAGGATCGT	GGTGCCGAGG	ATCAAGCTGC	ACCCCTGGGT	2160
80	CACGAGGCAT	GGGGCGGAGC	CGTTGCCGTC	GGAGGATGAG	AACGCAAGCG	TGGTGAAGT	2220
	GACTGAAGAG	TAGATCGATA	ACTCAGTCAA	ACACATTTCC	AGCTTGCAAA	CGGTGATCCT	2280
	GGTGAAGACC	ATGATAGCTA	AACGCTCCTT	TGGGAACCCA	TTCAGAGGCA	GCCGGGCGGA	2340
	GGAAACGCTC	CTGTGAGGCG	CTGGAAACTT	GCTCACCAAA	AAACCAACCA	GGGAATGTGA	2400
	GTCCCTGTCT	GAGCTCAAGG	AAGCAAGGCA	GCGAAGACAA	CCTCCAGGGC	ACCGACCCGC	2460
	CCCCCGTGGG	GGAGGAGGAA	GTGCTCTTGT	GAGAGGCAGT	CCCTGCGTGG	AAAGTTGCTG	2520

5	GGCCCCCGCC	CCCGGCTCCC	CCGCAACGCT	GCATCCACTG	CGGCGGAGG	AGGCCATGGA	2580
	GCCCCAGTAG	CTGCCTGGAT	CGCTCGACCT	GGCATGCGCG	CCGCGTGGCC	TCTGGGGGGC	2640
	TGCTGCACCG	CGTTTCCATA	GCAGCATGTC	CTACGGAAAC	CCAGCACGTC	TGTAGAGCCT	2700
	CGATCGTCAT	CTCTGGTTAT	TGTGTTTTC	CTTTGTTGTT	TAAAGGGGA	CAAAAAAAA	2760
	AAAAAAGGA	CTTGACTCCA	TGACGTGGAC	CGTGGCGGCT	GGCTGGCTGG	ACAGGCGGGT	2820
	GTGAGGAGTT	GCAGACCCAA	ACCCACGTGC	ATTTTGGGAA	ATTGCTTTT	AAAAGATTTT	2880
	TATGCCAAAA	ATCCTTCATT	GTGATTTTCA	GAACCACTGC	AGATATACCA	AGTGACTGTG	2940
	TGTGGGGTTT	GACAACTGTG	GAAAGGCGAG	CAGAAAATC	CGGGGGCTG	AGGCCATGGA	3000
10	GGTGGTTGCT	GCATTTGAGA	GGGAGTAGGG	GGCTAGATGT	GGCTCCTAGT	GCAAAACGGA	3060
	AACCATGGCA	CCTTCCAGAG	CCGTGGTCTC	AAGGAGTCAG	AGCAGGGCTG	GCCCTCAGTA	3120
	GCTGCAGGGA	GCITTTGATG	AACCTATTTC	TAAGAAGGAT	TTTTAAATTT	TTTATGGGTA	3180
	GAATTTAGT	CAGGAAAAA	GAAAGGCTT	GAAATTTAAT	AAGTGTGCT	GGAAGGGGAT	3240
	TTTCCAGGC	TGGAAGGGTA	TTCAGCAGCT	GTGGTGGGGA	AACATTTCTC	CTGAAAGACT	3300
15	GAACGTGTTT	CTTCATGACA	GCTGCTCAAA	GCAGGTTTCT	GAGATAGCTG	ACCGAGCTCT	3360
	GGTAAATCTC	TTTGTCAAAT	TACGAAACT	TCAGGGTGAA	ATCCTATGCT	TTCAATGTACA	3420
	TTACATGGCT	TAAGATTAAA	CAAAAAACAT	TTTCAAGTCT	CTAACTAGAG	TGAATCTAG	3480
	AGCACAGTAG	TTCAAGAACT	ATTTAGAGCT	TCCAGGATAT	ATTTACAGC	TTCAAGCATG	3540
	TGATCAGTTA	GAGCCGATGA	AACCTATGCC	CGCCTGTATA	TATATTAGCA	GCTTAGCTAG	3600
20	TTCAATAACT	GTTATTCTA	AAGACTGCTA	AGGTTTGTG	TTCAATTTAA	ATCCTAGCTG	3660
	ATTGTTGTGG	TCAATGAAAT	ACCCAGTTTC	TGAAGGGCCA	GGTGGGAAAT	GCTTTCACCTG	3720
	GACCAACACA	CAAAATGATCA	TCCTGAGGAT	CTGAGCTTCC	CTAGACTCCA	CACAATAACC	3780
	TTGGGGCACC	CTTTTAGAGA	AGACTGTGGA	AACCCACAGC	ACTCGTTGGG	GTATGAGGAA	3840
	ACCAAGGCTT	GGCACAGGAA	GTTCCTCTT	GTAGCTAAAA	GTCCAGAAAG	AAAGGGTTCA	3900
25	TCCTTTGAC	TTCCACTGGA	TATTGGGAAG	TTTGGTTGAG	GTCAAGTGT	GACTCCTTCC	3960
	AGAGCCACAG	GTAGGGGAGT	GTGAAGTTGA	GGGGGAGGAA	AGCTGGAAGG	ACTCTGCCCT	4020
	GGGAGATTCC	CAGCTCTGCT	TTCCAGCGCT	TGGTGGAAATC	TGGGCTGGGG	AAAGACGGCA	4080
	CCGGGAAACT	GCTCTTCCCT	ATTGTTTCCA	TCTGATCAGC	TGTGGTGTGA	GGACTTCTCA	4140
	GACAAAGGCA	AGGCTCGTG	CCCTGCCCCA	GCCCATTCAT	GGAGCCCTGG	GCTTCTTGG	4200
30	CTTCCATAGA	TCCTAAGCTC	TTGACTGTAG	TTTAGCCAGA	CTTGTTTTGC	TATCTTATAA	4260
	GCAGTTCAGA	ATTAGGGAAT	GCTGGTTTTC	AAGAGCAAAG	GACAGGTAGT	CTAGAGAGGG	4320
	TCGTCTGGCC	TGCTTGTCTG	GTCTTTGTAA	CCCAGCACTT	CCTCTTGCCC	TCCTGGCTTT	4380
	ATGTTTATGG	GAGAGGACTC	AATAGCTCCA	CCCTTCTGG	CACCAAGTGG	GGCTTGGTTA	4440
	GTTTGCAATA	AGCACCTTGC	AGAGGTTAAA	GCCAGCGGGT	CCCTAGTCTT	AGGCCACGCC	4500
35	TGCTTGTGTG	GGCTCTGGCC	TGGCTTGGTG	GCTGGCCAG	GGGGCAGCAG	TGCTTAGAGC	4560
	TTCTGACGGG	CTTCTCTTGT	TTACACAGCT	GCATCAGACA	ATGCCATTTC	TCCCCACACC	4620
	GGAACTTCC	ATCTAAGATT	TCTTCCAGGG	AATGCCAGCA	ATCAGGCAGC	ACCCAGCTGT	4680
	GGGGCAGTGT	GGGTGGGGGA	GACCCACATT	GATGACTTTT	TTTTTTTCTT	TAAATGAAGA	4740
	AACACCAAG	AAAGCTGTGG	AAAGGACCTG	CCCCACATGA	AAAGGATAAG	CCAAGATGGC	4800
40	TGTAAACACA	GAGCATTGGA	GCTGCCACTC	TTGGAGCACA	TTGATTTTTC	AAAAGCCAGC	4860
	TCTGTACAGA	AAGGAGGTGC	TGTTATGACA	GCTCTTCCAG	TGGGCAAGAA	GGACGCCCAT	4920
	AATTTCTTCC	ATTGCTAGCT	CATCTGTGGG	ACCAATTGGG	TGTAAGCAAC	CTGTGGCCCTG	4980
	CACCTGTGGC	CTCGAAGGAA	GCACAAACCC	TCCATCCACT	TCCCATTTCC	CTGCCCCCTT	5040
	TCCACCTCCC	CCTTCCATCC	CACCAGCTGC	CAGTGGCTCC	CAGAAAGCCT	TATTAGAGCC	5100
45	CTTGTGATGA	CTTGGGGCTG	CGGAGGCCCT	TCCCTACTGG	TCTGGCCCTT	CCTGAGAGGC	5160
	AGGTCTTCCG	CTTCTCAGAG	CITTCCTGAA	CAAGGAGAAAT	GCCTGTGCAG	GTGGACACAC	5220
	AGGCCTGGCC	TGTCGCTCTC	ACTTGTCTTC	CAGCGGGGAG	CTTCAAGTTG	CCGAGTGGAA	5280
	GAACCATGAC	CTCCACTTGC	TTCCAAAGTG	CTAGGGAAGT	TTCAAGGTAC	GCTGGTTCCC	5340
	CTCTCCAGCT	GGAGGCCGAG	TTTCTGGGGA	CTGCAGATTT	TTCTACTCTG	TGATCGATTTC	5400
50	AATGCCCGAT	GCTTCTGTTT	CATTCCCGAC	CCTTCTACT	ATGCATTTTC	CTTTTATCAG	5460
	GTGTATAAAG	TTAAATAGTG	TGTATTATC	ACTAAAAAGT	ACATGAACCT	AAGAGACAAC	5520
	TAAGCCTTTC	GTGTTTTTCC	ACAGGTGTTT	AAGCTTCTCT	GTACAGTTGA	AATAAACAGA	5580
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Seq ID NO: C193 DNA Sequence  
Nucleic Acid Accession #: NM\_018646  
Coding sequence: 217..2394

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	GGGCGGGCCC	TTGGGGGGGC	TGATGTGGCC	CCAAGGCTGA	GTCCCGTCAG	GGTCTGGGCT	180
	CGGCCTCAGG	CCCCCAAGGA	GCCGGCCCTA	CACCCCATGG	GTTTGTCACT	GCCCAAGGAG	240
65	AAAGGGCTAA	TTCTCTGCC	ATGGAGCAAG	TTCTGCAGAT	GGTTCCAGAG	ACGGGAGTCC	300
	TGGGCCCAAG	TCAGAGATGA	GCAGAACCTG	CTGCAGCAGA	AGAGGATCTG	GGAGTCTCCT	360
	CTCCTTCTAG	CTGCCAAAGA	TAATGATGTC	CAGGCCCTGA	ACAAGTTGCT	CAAGTATGAG	420
	GATTGCAAGG	TGCACAGAG	AGGAGCCATG	GGGGAACAG	CGCTACACAT	AGCAGCCCTC	480
	TATGACAACC	TGGAGGCCGC	CATGGTCTG	ATGGAGGCTG	CCCGGAGCT	GCTCTTTGAG	540
70	CCCATGACAT	CTGAGCTCTA	TGAGGGTCAG	ACTGCACATG	ACATCGCTGT	TGTGAACCCAG	600
	AACATGAACC	TGGTGGGAGC	CCTGCTTGCC	CGCAGGGCCA	GTGCTCTGTC	CAGAGCCACA	660
	GGCACTGGCT	TCCGCGGTAG	TCCCTGCAAC	CTCATCTACT	TTGGGGAGCA	CCCTTTGTCC	720
	TTTGTGCTCT	GTGTGAACAG	TGAGGAGATC	GTGCGGCTGC	TCATTGAGCA	TGGAGCTGAC	780
	ATCCGGGCCC	AGGACTCCCT	GGGAAACACA	GTGTTACACA	TCTCTATCTT	CCAGCCCAAC	840
75	AAAACCTTTG	CCTGCCAGAT	GTACAACCTG	TTGCTGTCTT	ACGACAGACA	TGGGGACCAC	900
	CTGCAGCCCC	TGGACCTCGT	GCCCAATCAC	CAGGGTCTCA	CCCCTTTCAA	GCTGGCTGGA	960
	GTGGAGGGTA	ACACTGTGAT	GTTTCAGCAC	CTGATGCAGA	AGCGGAAGCA	CACCCAGTGG	1020
	ACGTATGGAC	CACCTGACCT	GACTCTCTAT	GACCTCACAG	AGATCGACTC	CTCAGGGGAT	1080
80	GAGCATGCTC	GTCTGGAAC	TATCATCAAC	ACCAAGAACG	GGGAGGCTCG	CCAGATCCTG	1140
	GACCAGAGCG	CGGTGAAGGA	GCTGGTGAGC	CTCAAGTGGG	AGCGGTACGG	GCGGCCGTAC	1200
	TTCTGTCATG	TGGGTGCCAT	ATATCTGCTG	TACATCATCT	GCTTCACCAT	GTGCTGCATC	1260
	TACCGGCCCC	TCAAGCCCCG	GACCAATAAC	CGCACGAGCC	CCCGGACCAA	CACCCCTTTA	1320
	CAGCAGAAGC	TACTTCAGGA	AGCCTACATG	AOCCTTAAGG	ACGATATCCG	GCTGGTCCGG	1380
	GAGCTGGTGA	CTGTCAITGG	GGCTATCATC	ATCCTGCTGG	TAGAGGTTCC	AGACATCTTC	1440
	AGAATGGGGG	TCACTCGCTT	CTTTGGACAG	ACCAATCTTG	GGGGCCCAT	CCATGTCTCT	1500

5 ATCATCACTT ATGCTTTCAT GGTGCTGGTG ACCATGGTGA TGCGGCTCAT CAGTGCCAGC 1560  
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 GCCCAGGAT TCCAGATGCT AGGCCCTTTC ACCATCATGA TTCAGAAAGT GATTTTGGC 1680  
 GACCTGATGC GATTCTGCTG GCTGATGGCT GTGGTCACTC TGGGCTTTGC TTCAGCCTTC 1740  
 TATATCATCT TCCAGACAGA GGACCCCGAG GAGCTAGGCC ACTTCTACGA CTACCCCATG 1800  
 GCCCTGTTCA GCACCTTCGA GCTGTTCTTT ACCATCATCG ATGGCCAGC CAACTACAAC 1860  
 GTGACCTGTC CCTTCATGTA CAGCATCACT TATGCTGCCT TTGCCATCAT CGCCCACTG 1920  
 CTGATGCTCA ACCTCTCAT TGCCATGATG GCGGACACTC ACTGGCGAGT GGCCCATGAG 1980  
 CGGGATGAGC TGTGAGGGGC CCAGATTGTG GCCACCAAGG TGATGCTGGA GGGGAAGCTG 2040  
 10 CCTCGCTGCC TGTGGGCTCG CTCGGGATC TGCGGAGCGG AGTATGGCCT GGGAGACCGC 2100  
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 20 GGCAGAGGAA GCCCAGGCA AGCACGGGGC TGGCAGGGC TGAGGAACCT TCCTGTGGCC 2640  
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 TGCTTGGGCG CTCGGTCTCC ACCCAGGGT CATAAGTGGG GAGAGAGCCC TTCAGGCGG 2760  
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 AAGGCTCTG GGGGTGGGAA GTGGGCTAG GTCTTGCCAA CTCATCTTC AATAAGTGC 2880  
 25 TTTTCGATC CCTGAAAAA AAAAAA AAAAAA 2918

Seq ID NO: C194 DNA Sequence  
 Nucleic Acid Accession #: NM\_021910.1  
 Coding sequence: 260..601

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 CCGGGCCGAG CGCTCTGACA TGCAAGAAGT GACCTGGGC CTGCTTGTGT TCCTGGCAGG 300  
 CTTTCTGTCT CTGGAAGCCA ATGACCTAGA AGATAAAAC AGTCCTTTCT ACTATGACTG 360  
 GCACAGCCTC CAGGTTGGCG GGTCTCATCTG CGCTGGGTTT CTGTGGCCCA TGGGCATCAT 420  
 40 CATGCTCATG AGTGAATGGA GGAGCTCGGG GGAGCAGGCG GGCAGGGGCT GGGGCTCCCC 480  
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 TGCACAGAAA CTTGAATCCC AGGATGGAAT TCTTCTCTCT CTGCTGGGAC TCCTTTGCAT 720  
 45 GGCAGGGCTC CATCTACCT CTCGCAAGAG GGTCTCTTTG TTCAATTTTT TTTAATCTAA 780  
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 CTGCTTGTCT GGAAAAGGCC ACAGGCTGT TCCCTTGTGG CTTGGGACAT GGCAAGGCC 960  
 CGCCCTCTGC CTCTCAGCC ATGGGACCTC ATATGCAATT TGGGATTTAC TAGTAGCCAA 1020  
 50 AAGGAATGAA AGAGAGCTCT AACAGATGG AACACTGGAA CATTCCAGTG GACCTTGGAC 1080  
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 55 CCCAATACCT AATAAGGCAT GCGAAATGTT CTCATGAAT ACCCACAAC ACGCTTAAAA 1380  
 CTCAAAACAC CCAAAATAT CTCTCCAAT GTCTGAGAC ATGAACCCAA AAAGAGACCC 1440  
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Seq ID NO: C195 DNA Sequence  
 Nucleic Acid Accession #: NM\_005971.2  
 Coding sequence: 176..439

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 65 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACCA GGCAGCGGTT TCACCCAGTC 180  
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 CCTAGAAGAT AAAAACATGC CTTTCTACTA TGACTGGCAC AGCTCCAGG TTGGCGGGCT 300  
 CATCTGCGCT GGGGTTCTGT GGGCAGTGG CATCATCATC GTCATGAGTG CAAAATGCAA 360  
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 75 CAATTTTTTT TAATCTAAAA TGATTGTGCC TCTGCCCAAG CAGCTGGAG ACTTCTATG 660  
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 CAGAGGCTGG CTTAGGCTCT GCTTGTGGG AAAAGCCAC AGGCTGTGTC CCTTGTGGCT 780  
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 GGATTTACTA GTAGCCAAAA GGAATGAAAG AGAGCTCTAA CCAGATGGAA CACTGGAACA 900  
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 TCACCTTTAT ACAGATCTTT TCCAAATACC CAAATATCCC TGCAAGCCCG TTAATAAATT 1080  
 CCTATGTCTA CCTTAAATAA CATACATGTA CCACATAGTG TGAGAACTTC CAACAAGCCT 1140  
 CAAAGTCCCT TGAGACTCCC CAATACCTAA TAAGGCATGC GAAATGTCT CATGAACACT 1200  
 CCCACACAC GCCTAAACT CAAACACCC AAAAATATCT CCTCAATGT CTGAGACAT 1260

GAACCCAAAA AGAGACCCAC AATAAACTCG TGACTTGTCC CCTC

1304

Seq ID NO: C196 DNA Sequence

Nucleic Acid Accession #: NM\_004961.2

Coding sequence: 55..1575

5

	1	11	21	31	41	51	
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	TCCAAAGTTC	TTCCAGTCCT	CCTAGGCCATC	TTATTGATCC	TCCAGTCGAG	GGTCGAGGGA	120
	CCTCAGACTG	AATCAAAGAA	TGAAGCCTCT	TCCCGTGATG	TTGTCTATGG	CCCCAGCCCC	180
	CAGCCTCTGG	AAAATCAGCT	CCTCTCTGAG	GAACAAAGT	CAACTGAGAC	TGAGACTGGG	240
	AGCAGAGTTG	GCAAACTGCC	AGAAGCCTCT	CGCATCCTGA	ACACTATCCT	GAGTAATTAT	300
15	GACCACAAA	TGCGCCCTGG	CATTGGAGAG	AAGCCCACTG	TGGTCACTGT	TGAGATCGCC	360
	GTCAACAGCG	TTGGTCTCT	CTCTATCCTA	GACATGGAAT	ACACCATTGA	CATCATCTTC	420
	TCCAGACCT	GGTACGACGA	AOSCTCTGT	TACAACGACA	CCTTTGAGTC	TCTTGTCTG	480
	AATGGCAATG	TGGTGGACCA	GCTATGGATC	COGACACCT	TTTTTAGGAA	TTCTAAGAGG	540
	ACCCACGAGC	ATGAGATCAC	CATGCCCAAC	CAGATGGTCC	GCATCTACAA	GGATGGCAAG	600
	GTGTTGTACA	CAATTAGGAT	GACCATTGAT	GCCGGATGCT	CACCTCCAT	GCTCAGATT	660
20	CCAATGGAAT	CTCACTCTTG	CCCTCTATCT	TTCTCTAGCT	TTTCTATCC	TGAGATGAG	720
	ATGATCTACA	AGTGGGAAAA	TTTCAAGCTT	GAATCAATG	AGAAGAATC	CTGGAGGCTC	780
	TTCCAGTTTG	ATTTTACAGG	AGTGAGCAAC	AAAACTGAAA	TAATCACAA	CCAGTTGGT	840
	GACTTCATGG	TGATGACGAT	TTTCTTCAAT	GTGAGCAGGC	GGTTTGGCTA	TGTTGCCTTT	900
25	CAAAACTATG	TCCCTCTTTC	CGTGACCAAG	ATGCTCTCCT	GGGTTCCTTT	TTGGATCAAG	960
	ACAGAGTCTG	CTCCAGCCCG	GACCTCTCTA	GGGATCACCT	CTGTTCTGAC	CATGACCAAG	1020
	TTGGGCACCT	TTTCTCGTAA	GAATTTCCCG	CGTGTCTCCT	ATATCACAGC	CTTGGATTTC	1080
	TATATCGCCA	TCTGCTTCGT	CTTCTGCTTC	TGCGCTCTGT	TGGAGTTTGC	TGTGCTCAAC	1140
	TTCTCTGATCT	ACAACAGAGC	AAAAGCCCAT	GCTTCTCCTA	AACTCCGCCA	TCTCTGATTC	1200
	AATAGCCGAT	CCCATGCCCC	TACCGTGCA	CGTTCCCGAG	CCTGTGCCCG	CCACATCAG	1260
30	GAAGCTTTTG	TGTGCCAGAT	TGTCACCATT	GAGGGAAGTG	ATGGAGAGGA	GCGCCCGTCT	1320
	TGCTCAGCCC	AGCAGCCCCC	TAGCCCAAGT	AGCCCTGAGG	GTCCCGCAG	CCTCTGCTCC	1380
	AAGCTGGCCT	GCTGTGAGTG	GTGCAAGCGT	TTTAAGAAGT	ACTTCTGCAT	GGTCCCGAT	1440
	TGTAGAGGCA	GTACCTGGCA	CGAGGGCCGC	CTCTGCATCC	ATGTCTACCG	CCTGATAAAC	1500
	TACTCGAGAG	TTGTTTTCCT	AGTGACTTTC	TTCTTCTTCA	ATGTGCTCTA	CTGGCTTGT	1560
35	TGCTTAACT	TGTAGGTACC	AGCTGGTACC	CTGTGGGGCA	ACCTCTCCAG	TTCCCCAGGA	1620
	GGTCCAGGCC	CCTTGCCAA	GGAGTTGGGG	GAAGAGCAGC	GCAGCAGCAG	GAGCGACTAG	1680
	AGTTTTCCT	GCCCCATTCC	CCAAACAGAA	GCTTGACAGG	GGTTTGTCTT	TGCTGCCCT	1740
	CTCCCTTACC	TGGCCCATTC	ACTGAGTCTT	CTCAGCAGAC	CATTTCAAAT	TATTAATAAA	1800
	TGGGCCACCT	CCCTCTTCTT	CAAGGAGCAT	CGGTGATGCT	CAGTGTTCAA	AACCACAGCC	1860
40	ACTTAGTGAT	CAGCTCCCTA	AAACCATGCC	TAAGTACAGG	GGGATTAGCT	ATCTTCCAAC	1920
	AATGCTGACC	ACACAGCAAT	TACTGCATTT	TTCCAGAGC	CCACTATTGC	CTTTGTAGTG	1980
	CTTTGGGCC	AGTTCTGGCC	TCAGCCCTCA	AGTGCACCGA	CTAGTTGCTT	GCCTATACCT	2040
	GGCACTCAT	TAAGATGCTG	GGCAGCAGTA	TAACAGGAGG	AAGAGATCCC	TCTCCTTTGG	2100
45	TCAGATTATT	ATGTTCTCAG	TTCTCTCTCC	CTGCTACCCC	TTTCTCTGCA	GATAGATAGA	2160
	CAGTGGCAAT	ATCCCTTTAG	GAAGAGGGGG	GGGCAGCAG	AGAGCCTATT	TGGGACAGCA	2220
	TTCTCTCTCT	TCTGCTGCTG	TGACATCTCC	CTCTCCTTGC	TGGCTCCATC	TTTCTCTGTC	2280
	ACTACCAATT	CAATGCCCTT	CATCCAATGG	GTATCTATT	TTGTGTGTGA	TTATAGTAAC	2340
	TACTCCCTGC	TTTATATGCC	ACCCTCTTCC	TTCTCTTTGA	CCCCGTGAC	TCTTTCTGTA	2400
50	ACTTTCCAG	TGACTTCCCT	TAGCCCTGAC	CCAGGCACCTA	GGCCTTGGTG	ACTTCTCTGG	2460
	GCCAGAAAC	TAAGGAAACT	CGGCTTTGCA	ACAGGCATTA	CTCGCCATTG	ATTGGTGCCC	2520
	ACCCAGGGCA	CAGTGTCCGA	GTTCTATCAC	TTGCTTGACC	CCTGGACCCA	TAAACCACTG	2580
	CAGCTGTATA	CCCGGGGCAC	TCTAACCATC	ACAATCAATC	AATCAAATTC	CCTTAAATTT	2640
	GTATGGCACT	GGAACTTTGG	CAAAGCACTT	TTGACAAAGT	GTGTCTGATT	GGAGCTTCAT	2700
55	GATAGCCTTG	TGACATCTTT	AGGGCAGGAT	TCTTATCCCC	ATTTTGCGAG	TGAAAACCTT	2760
	GAGTCACAGA	TTTCTGTGGG	ACTGTGGATC	TCACTGGAAG	CTATCCAAAG	GCCCACTGTC	2820
	ACCTTCTAGA	CCACATGATA	GGGCTAGACA	GCTCAGTTCA	CCATGATTCT	CTTCTGTAC	2880
	CTCTGCTGGC	ACACCACTGG	CAAGGCCAGC	AATGGCCAGC	TCTCTTTTGA	TCAATTTCTG	2940
	GGCCTGAGGT	GCTCAGACTG	CCCCCAAGAT	CAAATCTCTC	CTGGCTGTAG	TAACCCAGTG	3000
60	GAATGAATTT	GGACATGCCC	CAATGCTTCT	ATATGCTAAG	TGAAATCTGT	GTCTGTAATT	3060
	TGTTGGGGGG	TGGATAGGGT	GGGGTCTCCA	TCTACTTTT	GTCAACATCA	TCTGAAATGG	3120
	GGAAATATGT	AAATAATAT	ATCAGCAAAG	CAAAAAGAAA	AAAAAAA		3168

Seq ID NO: C197 DNA Sequence

Nucleic Acid Accession #: NM\_021984.1

Coding sequence: 572..1753

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	CAGAGAAGTG	CTCAAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCAAGCGG	180
	GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
	CAGTGCCTCC	CAGCAAGAGC	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TGAGGGGACC	300
75	TCAGACTGAA	TCAAAGAATG	AAGCCTCTTC	CCGTGATGTT	GTCTATGGCC	CCCAGCCCCA	360
	GCCTCTGAAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
	CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCTGTA	GTAATTATGA	480
	CCACAAACTG	GCCCTTGCCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTTG	AGATCTCGGT	540
	CAACAGCCTT	GCTCCTCTCT	CTATCCTAGA	CATGGAATAC	ACCATGTACA	TCACTTCTTC	600
80	CCAGACCTGG	TACGACGAAC	GCCTCTGTTA	CAACGACACC	TTTGAGTCTC	TTGTTCTGAA	660
	TGGCAATGTG	TGGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTAGGAATT	CTAAGAGGAC	720
	CCACGAGCAT	GAGATCACCA	TGCCCAACCA	GATGGTCCGC	ATCTACAAGG	ATGGCAAGGT	780
	GTTGTACACA	ATTAGGATGA	CCATTGATGC	OGGATGTCTA	CTCCACATGC	TCAGATTTC	840
	AATGGATTCT	CAGCTTGGCC	CTCTATCTTT	CTCTAGCTTT	TCCTATCCTG	AGAATGAGAT	900
	GATCTACAAG	TGGGAAAATT	TCAAGCTTGA	AATCAATGAG	AAGAACTCCT	GGAAGCTCTT	960

5 CCAAGTTGGAT TTTACAGGAG TGAGCAACAA AACTGAAATA ATCACAAACC CAGTTGGTGA 1020  
 CTTCATGGTC ATGACGATTT TCTTCAATGT GAGCAGGCGG TTTGGCTATG TTGCTTTTCA 1080  
 AAACATATGCT CCTTCTTCCG TGACCAACGAT GCTCTCCTGG GTTTCCTTTT GGATCAAGAC 1140  
 AGAGTCTGCT CCTCTCTAGG GATCACCTCT GTTCTGACCA TGACCAAGTT 1200  
 GGGCACCTTT TCTCGTAAGA ATTTCCCGCG TGTCTCCTAT ATCACAGCCT TGGATTCTTA 1260  
 TATCGCCATC TGCTTCGTCT TCTGCTTCTG CGCTCTGTGG GAGTTTGTCT TGCTCAACTT 1320  
 CCTGATCTAC AACAGACAA AAGCCCATGC TTCTCCTAAA CTCCGCCATC CTGATATCAA 1380  
 TAGCCGTGCC CATGCCGTA CCGGTGCAAG TTCCCGAGCC TGTGCCGCC AACATCAGGA 1440  
 AGCTTTTGTG TGCCAGATTG TCACCACTGA GGGAAAGTAT GGAGAGGAGC GCCCGTCTTG 1500  
 10 CTACGCCAGC CAGCCCCCTA GCCCAGGTAG CCTGAGGGT CCCCGCAGCC TCTGCTCCAA 1560  
 GCTGGCCTGC TGTGAGTGGT GCAAGCGTTT TAAGAAGTAC TTCTGCATGG TCCCGATTTG 1620  
 TGAGGGCAGT ACCTGGCAGC AGGCCCSCTT CTGCATCCAT GTCTACCGCC TGGATAACTA 1680  
 CTCGAGAGTT GTTTTCCAG TGACTTTCTT CTCTTCAAT GTGCTCTACT GGCCTGTTTG 1740  
 CCTTAACCTG TAGGTACCGA CTGGTACCTT GTGGGGCAAC CTCTCCAGTT CCCAGGAGG 1800  
 15 TCCAAGCCCC TTGCCAAGGG AGTTGGGGGA AAGCAGCAGC AGCAGCAGGA GGCATAGAG 1860  
 TTTTCCCTGC CCCATTCCCC AAACAGAAAG TTGCAGAGGG TTTGTCTTTG CTGCCCTCT 1920  
 CCCCTACCTG GCCCAATCAC TGAGTTTCTT CAGCAGACCA TTTCAAATTA TTAATAAATG 1980  
 GGCCACCTCC CTCTTCTTCA AGGAGCATCC GTGATGCTCA GTGTTCAAAA CCACAGCCAC 2040  
 20 TAGTGATCA TCCCTTAAAG ACCATGCTTA AGTACAGGCG GATTAGCTAT TTCCCAACAA 2100  
 TGCTGACCA CAGACAAATTA CTGCATTTT CCAGAAGCCC ACTATTGCCT TTGCAGTGCT 2160  
 TTCGGCCAG TTCTGGCCTC AGCCTCAAAG TGCACCGACT AGTTGCTTGC CTATACCTGG 2220  
 CACCTCATT TAAGTCTGGG CAGCAGTATA ACAGGAGGAA GAGATCCCTC TCCTTTGGTC 2280  
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 25 CTGGCATTAT CCGCTTAAAG AGAGGGGGGG GCAGCAAGAG AGCCTATTG GGACAGCATT 2400  
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 30 CCAGGGCACA CTGTGGAGT TCTATCACTT GCTTGACCCC TGGACCCATA AACCACTCCA 2760  
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 ATGGCACTGG AACTTTGGCA AAGCACTTTT GACAAAGTGT GTCTGATTGG AGCTTCATGA 2880  
 TAGCCTGTG ACATCTTAG GGCAGGATTC TTATCCCCAT TTGTCAGATG AAAACCTGA 2940  
 35 GTACAGATT TCTGTGGGAC TGTGGATCTC ACTGGAAGCT ATCCAAGAGC CCACTGTAC 3000  
 CTTCTAGACC ACATGATAGG GCTAGACAGC TCAGTTCAAC ATGATTCTCT TCTGTACCT 3060  
 CTGTGCGCAC ACCAGTGGCA AGGCCAGAA TGGGACCTC TCTTTAGCTC AATTTCTGGG 3120  
 CCTGAGGTGC TCAGACTGCC CCAAGATCA AATCTCTCT GCGTGTAGTA ACCCAGTGA 3180  
 ATGAATTTGG ACATGCCCA ATGCTTCTAT ATGCTAAGTG AAATCTGTGT CTGTAATTTG 3240  
 40 TTGGGGGTG GATAGGGTGG GGTCTCCATC TACTTTTTGT CACCATCATC TGAATGGGG 3300  
 AAATATGTA ATAAATATAT CAGCAAGG 3329

Seq ID NO: C198 DNA Sequence  
 Nucleic Acid Accession #: NM\_021987.1  
 Coding sequence: 572..1657

45 1 11 21 31 41 51  
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 50 TCCAAAGTTC TTCCAGTCCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120  
 CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAATAT GACCACAGCG 180  
 GTGTAAGAA AGGCAAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTGT 240  
 CACTGCTCC CAGCAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300  
 TCAGACTGAA TCAAGAAGT AAGCCTCTTC CGGTGATGTT GTCTATGGCC CCCAGCCCCA 360  
 55 GCCTCTGAAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420  
 CAGAGTTGGC AAACCTCCAG AAGCCTCTCG CATCCTGAAC ACTATCCTGA GTAATTATGA 480  
 CCACAACTG CGCCCTGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTTG AGATCTCCGT 540  
 CAACAGCCTT GGTCTCTCT CTATCCTAGA CATGGAATAC ACCATTGACA TCATCTTCTC 600  
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 60 CCGCATCTAC AAGGATGGCA AGGTGTTGTA CACAATTAGG ATGACCATG ATGCCGATG 720  
 CTCACTCCAC ATGCTCAGAT TTCCAATGGA TTCTCACTCT TGCCCTCTAT CTTTCTCTAG 780  
 CTTTCTCTAT CCTGAGAATG AGATGATCTA CAAGTGGGAA AATTTCAAGC TTGAAATCAA 840  
 TGAGAAGAAC TCCTGGAAGC TCTTCCAGTT TGATTTTACA GGAGTGAGCA ACAAACCTGA 900  
 AATAATCACA ACCCCAGTTG GTGACTTCAT GGTCAATGAC ATTTTCTTCA ATGTGAGCAG 960  
 65 GGGTTTGGC TATGTTGCC TTTCAAACTA TGTCCCTTCT TCGTGACCA CGATGCTCTC 1020  
 CTGGGTTTCC TTTTGGATCA AGACAGAGTC TGCTCCAGCC CGGAOCTCTC TAGGGATCAC 1080  
 CTCTGTCTG ACCATGACCA GTTGGGCAC CTTTCTCGT AAGAAATTCC CGGTGTCTC 1140  
 CTATATCACA GCCTTGGATT TCTATATCGC CATCTGCTTC GTCTTCTGCT TCTGCGCTCT 1200  
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 TGATGGAGAG GAGCGCCCGT CTGTCTCAGC CCAGCAGCCC CTTAGCCAG GTAGCCCTGA 1440  
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 GTACTTCTGC ATGCTCCCGG ATTGTGAGGG CAGTACCTGG CAGCAGGSCC GOCCTGTGAT 1560  
 75 CCAATGCTAC CGCCTGGATA ACTACTCGAG AGTTGTTTTC CCAGTGACTT TCTTCTCTT 1620  
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 CAACCTCTCC AGTTCCCGAG GAGGTCCAAG CCCCTTGCCA AGGGAGTTGG GGGAAAGCAG 1740  
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5	CCTTTCTCTG	CAGATAGATA	GACACTGGCA	TTATCCCTTT	AGGAAGAGGG	GGGGGCAGCA	2280
	AGAGAGCCTA	TTTGGGACAG	CATTCTCTCT	TCTCTGCTGC	TGTGACATCT	CCCTCTCCTT	2340
	GCTGGCTCCA	TCCTTGGTCT	GCCTACCAA	TTCAATGCC	TTCAATCCAAT	GGGTATCTAT	2400
	TTTTGTGTGT	GATTATAGTA	ACTACTCCCT	GCTTTATATG	CCACCTCTTT	CCTTCTCTTT	2460
	GACCCCTGTG	ACTCTTTCTG	TAACCTTTCC	AGTGACTTCC	CCTAGCCCTG	ACCAGGCACT	2520
	AGGCCCTGGT	GACTTCTCTG	GGCCAAGAAA	CTAAGGAAAC	TCGGCTTTGC	AACAGGCATT	2580
	ACTCGCCATT	GATTGGTGCC	CACCCAGGGC	ACACTGTGGG	AGTTCTATCA	CTTGCTTGAC	2640
	CCCTGGACCC	ATAAACCACT	CCACTGTTAT	ACCCGGGGCA	CTCTAACCAT	CACAATCAAT	2700
10	CAATCAAAAT	CCCTTAAAT	TGTATGGCAC	TGGAACTTTG	GCAAAGCACT	TTTGACAAGT	2760
	TGTGTCTGAT	TGGAGCTTCA	TGATAGCCTT	GTGACATCTT	TAGGGCAGGA	TTCTTATCCC	2820
	CATTTTGGAG	ATGAAAACCC	TGAGTCACAG	ATTTCTGTGG	GACTGTGGAT	CTCACTGGAA	2880
	GCTATCCAA	AGCCCACTGT	CACCTTCTAG	ACCACATGAT	AGGGCTAGAC	AGCTCAGTTC	2940
	ACCATGATTC	TCCTCTGTCA	CCTCTGCTGG	CACACCACTG	GCAAGGCCCA	GAATGGCGAC	3000
15	CTCTCTTTAG	CTCAATTTCT	GGGCTGAGG	TGCTCAGACT	GCCCCAAGA	TCAAATCTCT	3060
	CCTGGCTGTA	GTAACCCAGT	GGAATGAAT	TGGACATGCC	CCAATGCTTC	TATATGCTAA	3120
	GTGAAATCTG	TGCTCTGAAT	TGTTGGGGG	GTGGATAGGG	TGGGGTCTCC	ATCTACTTTT	3180
	TGTCACCATC	ATCTGAAATG	GGGAAATATG	TAAATAAATA	TATCAGCAAA	GC	3232

Seq ID NO: C199 DNA Sequence  
Nucleic Acid Accession #: NM\_021990.1  
Coding sequence: 1309..2490

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	GCCAGAGCGT	GAGCGGCGAC	CTCCGCGCAG	GTGGTGGGCG	CGGTCTCCGC	GGAAATGTTG	60
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	CAGAGAGTGT	CTCAAAATCA	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCAAGCGG	180
	GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAA	CCCCCTTTGT	240
30	CACCTGCCCTC	CAGCAAAAGG	AGCACTATCC	GGACTTCTAA	CACCATCGGT	GAGTTTCATA	300
	CCTTGGCAGA	TGGCCTTTAA	CATTTTGTGT	TAATTCAAAT	ATCTCTACTA	ATCTTCTCT	360
	TTTTCTTGGC	TGTGGTGCAT	GGCTGTGGAG	CTCAGGGTGG	ACTCCTGTGG	GGCAGCCAGT	420
	TCCTGGATGG	CTGTCTGTGG	GTGGAGGACT	CCTGCCCTTC	CTGTTTAGAC	ACCCACAAAG	480
	GCTGCTCTTT	AGCCTCTCTC	CCTTCATCCC	CTTCCCCTGC	CCCCAGTGCA	ACGAGTATTA	540
35	CACAACCAAC	AAAACCGCAA	AATATTCCCA	CAATTTTCTG	GTCTCTCTCG	GGAGAGGCCG	600
	CTCTGGCTTT	TCCTCTCAGC	CCTGGCCCTC	TGCTGTCTCC	TCACTCCTGG	TTGGTGTGG	660
	TCAGGCTGAC	TAGAGGCCAA	GGCGACCAAC	ACTAGGCAAA	CGCGGCCAGC	GCCTCAGACT	720
	AAATGGCCCTC	TTCTATTCCAC	GTGTAACATT	CTTTTAAAT	CTAGGTCTTG	GTTTTGTGTA	780
	TTTTTTCTTA	AATAAAGAG	TGATCATAAA	AGAGGGACAG	CATAGAAAGT	CCCCAAAGAG	840
40	CAGCAAGGTT	TTAAAGAAAT	TCACAAGCCT	AATCTGTAC	TGCTTTATA	TTTGCTATTA	900
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	GAGGCACTAG	CTGGGGCCCC	TACAGAGTGC	AGGGCAGAGC	TTCAATTTTC	GTTTGAATGT	1020
	TCTAGGCTCG	AGGGACCTCA	GACTGAATCA	AAGAATGAAG	CCTCTCCCG	TGATGTGTGC	1080
	TATGGCCCCC	AGCCCCAGCC	CTGGAAAAAT	CAGCTCCTCT	CTGAGGAAC	AAAGTCAACT	1140
45	GAGACTGAGA	CTGGGAGCAG	AGTTGGCAAA	CTGCCAGAA	CCTCTCGCAT	CCTGAACACT	1200
	ATCCTGAGTA	ATTATGACCA	CRAACTGGGC	CCTGGCATTG	GAGAGAAGCC	CAGTGTGGTC	1260
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	ATTGACATCA	TCTCTCCCA	GACCTGGTAC	GAAGAACGCC	TCTGTTCATA	CGACACCTTT	1380
	GAGTCTCTTG	TCTGAATGG	CAATGTGGTG	AGCCAGCTAT	GGATCCCGGA	CACCTTTTTT	1440
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	ACAAACCCAG	TTGGTGACTT	CATGGTCAAT	ACGATTTTCT	TCAATGTGAG	CAGGCGGTTT	1800
	GGCTATGTTG	CCTTTTCAAAA	CTATGTCCCT	TCTTCGGTGA	CCAGATGCT	CTCCTGGGTT	1860
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	CTGACCATCA	CCAGGTGGG	CACCTTTTCT	CGTAAGAAAT	TCCCGGTGT	CTCTATATC	1980
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	TTTGTCTGTC	TCACCTTCT	GATCTACAA	CAGACAAAAG	CCCATGCTTC	TCCTAAACTC	2100
	CGCCATCTCT	GTATCAATAG	CGGTGCCAT	GCCGTACCC	GTGCAGCTTC	CCGAGCCTGT	2160
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	GAGGAGCGCC	CGTCTTGCTC	AGCCAGCAG	CCCTTAGCC	CAGGTAGCC	TGAGGGTCCC	2280
	CGCAGCTCT	GCTCCAGCT	GGCTTGTGT	GAGTGGTGCA	AGCGTTTAA	GAAGTACTTC	2340
65	TGCTAGGTCC	CCGATTTGTA	GGGAGTACC	TGGCAGCAGG	GCCGCTCTG	CATCCATGTC	2400
	TACCGCCTGG	ATAACTACTC	GAGAGTTGTT	TTCOCAGTGA	CTTCTTCT	CTTCAATGTG	2460
	CTCTACTGGC	TTGTTTGCTT	TAACTTGTAG	GTACCAGCTG	GTACCTGTG	GGGCAACCTC	2520
	TCCAGTTCCC	CAGGAGTCCC	AAGCCCTTGG	CCAAGGGAGT	TGGGGGAAAG	CAGCAGCAGC	2580
	AGCAGGAGCG	ACTAGAGTTT	TTCTGCCCC	ATTTCCCAAA	CAGAAGCTTG	CAGAGGGTTT	2640
70	GTCTTTGCTG	CCCCCTCTCC	CTACCTGGCC	CAITCACTGA	GTTTTCTCAG	CAGACCATTT	2700
	CAAAATTAATA	ATAAATGGGC	CACCTCCCTC	TTCTTCAAGG	AGCATCCGTG	ATGCTCAGTG	2760
	TTCAAAACCA	CAGCCACTTA	GTGATCAGCT	CCCTAAAACC	ATGCTAAGT	ACAGCGGAT	2820
	TAGCTATCTT	CCAACAATGC	TGACCAACAG	ACAATTACTG	CATTTTCCA	GAAGCCCACT	2880
	ATTGCTTTTG	CAGTGTCTTC	GGCCCTCAGC	CTCAAAGTGC	ACCGACTAGT	ACCGACTAGT	2940
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	ATCCCTTCTC	TTTGGTACAG	TTAATATGTT	CTCAGTTCTC	TCTCCTGTCT	ACCCCTTTCT	3060
	CTGCAGATAG	ATAGACACTG	GCAITATCCC	TTTAGGAAGA	GGGGGGGCA	GCAAGAGAGC	3120
	CTATTTGGGA	CAGCATTCCT	CTCTCTCTGC	TGCTGTGACA	TCTCCTCTC	CTTGTCTGGT	3180
80	CCATCTTTGG	TCTGCACTAC	CAATTCATG	CCCTTCATCC	AATGGGTATC	TATTTTGTG	3240
	TGTGATTATA	GTAACACTCT	CCTGCTTTAT	ATGCCACCTT	CTTCTCTCTC	TTTGACCCCT	3300
	GTGACTCTTT	CTGTAACTTT	CCAGTGACT	TCCCTAGCC	CTGACCAAGC	ACTAGGCCTT	3360
	GGTGACTTCC	TGGGGCCAA	AACTAAGGA	AACCTGGCTT	TGCAACAGGC	ATTACTGCC	3420
	ATTGATTTGT	GCCACCCAG	GGCACACTGT	CGGAGTTCTA	TCACTTGCTT	GACCCCTGGA	3480
	CCCATAAAC	AGTCCACTGT	TATACCCGGG	GCACTCTAAC	CATCACAATC	AATCAATCAA	3540
	ATTCCTTTAA	ATTGTATAGG	CACGTGAAC	TTGGCAAGC	ACTTTTGACA	AGTTGTGTCT	3600

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GATTGGAGCT TCATGATAGC CTGTGACAT CTTTAGGGCA GGATTCTTAT CCCCATTTTG 3660
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Seq ID NO: C200 DNA Sequence  
Nucleic Acid Accession #: NM\_021819.1  
Coding sequence: 39..1619

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CTCCTCTAGC CAGGTTTGAG TACAAGCTCA GCTTCAAAGG CCCAAGGCTG GCATTCGGCT 180
GGGCTGGAAT ACCCTTCTGG AGCCATCATG GAGACGCCAT CCTGGGCTG GAGGAAGTGC 240
GGCTGACGCC ATCCATGAGG AACCGGAGTG GCGCGGTGTG GAGCAGGGCC TCTGTCCCT 300
TCTCTGCCCT GGAAGTAGAG GTGCAATGA GGGTGACGGG ACTGGGGCGC CGGGGAGCCC 360
ACGGCATGGC CGTGTGTATC ACCCGGGGCA GGGGCCATGT AGGCTCTGTC CTTGGGGGGC 420
TGGCTTCTGT GAGCGGCATC GGGATCTTCT TTGACTCTCC GGCAGAGGAT ACTCAGGACA 480
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GAGCTAGCCA AGGGCTGGGC TCCTGTCTAT GGGACTTCCG GAACCGGCCA CACCCCTTCA 600
GAGCAGGGAT CACTTACTGG GGGCAGAGGC TGCGCATGTC CTGGAACAGT GGCCTCACTC 660
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TGACCTTCAG CTTGAGTGAG CCCAGGCCAG AGGTTCCCTC TCAGCCCTTC CTGGAGATGC 840
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GGGAGGATGT AACTCCAAAA TCAGACTCTG AAGCTCAAGG AGAAGGGGAA AGGCTCTTTG 960
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AGCAGCTGGC CCAGGCTGAG AGACAATGGA AGAAGCAGCT GGGGCCCCCA GGCCAAGCCA 1080
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Seq ID NO: C201 DNA Sequence  
Nucleic Acid Accession #: XM\_117036.1  
Coding sequence: 25..495

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GGCCCTGGG GGCTGTTCCG ACCACACAGG TGCCCGAGGG AGGCAGGGCA GGGCCCGGTG 240
GGACCCAGCC CGAAACGCA GGTGTGTGCC CAGTTTGA CAAGGCTGCT GGTGTGGGTG 300
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TGTCACGGCC ACAGCGGGCG CACCGTGGGT GGCTCTGTTT CTTGAAACG TCCAGAACAG 420
GCAGCCCGCG AGACAGGGAG GGGCCAGCG GTGCCAGGG GAAGTGGGA TGGGAATGAG 480
TGCGGATGGG GCTGAGGTTT TTCTGTAAGG ATGAATGCTC TGAAGCTGTG AATAGACACA 540
CGGAACCTGT CAGCTTCACT GGTGAACCGT GTGGGAGTGT AATCCATCTC AACAGAGCTG 600
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Seq ID NO: C202 DNA Sequence  
Nucleic Acid Accession #: XM\_167803.2  
Coding sequence: 1162..1488

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GAGGCGCAGC ACCCGAGGCG CTGCTGGAGC TGGGAGAGAG TGTGGTGGGA AGTCTTGAGC 240
GGAGGAGGGG ATCTGCCCTT CTCCACTCTT CTCTTGGATC CGCCTCGGTT TCCTGTCCCC 300
CCACCAACCG CTGCCCCGCG GGAAGACCGC CCAGTGAGCC AGCCCCCACC TTCCAGGCGC 360
CTTGGCCCTG GGGATCCAA CCACTTGTAT CGAGTGGGCG GGGCAACGGC TCCCATTTT 420
TCCCGAGGCC CGCCACAGA GCTCTTAGCC AATCCTATGC AGAGAGCATC TCCTGGCAGG 480
GGTCTCTTCC CAACCAAGAC CCACCCAGGC ACATTAGCGA CCAGGCTTGG GCTTCCCCAG 540
CGCCCCACCA CCACCAAGTG CAGGTGGAGC TCTGGGATGC TATGTTGGGG CGGCAAGCGG 600
TGGCCGAGG GCGGGTAGG CTAGCAAGG AGGTAAAGGT GGTATGGAT GGGGGGGGG 660
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AGTGTAAATTA CGGAATCCGT ACTGCAAGGC CCACCTGCCC CTCCCCCACA GAGCCTCCAG 960
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GGCTTCGTCT GCCATCTTTG TGGGTGCCCT AGACTTAGTC CTTATCTTGT CCTGGTTTCC 1080
TTTCTTGTGA CCATCTCCCC ATGAAAGTGC TGTACAAATT CCACCCGCC CAGGACCCCC 1140
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CCAGGGGGGC TCCCGGAGC CCCAGGGGTG GGGATTGGTG GCCACTGTTT GTATGTTCTT 1260
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Seq ID NO: C203 DNA Sequence  
Nucleic Acid Accession #: NM\_024780.1  
Coding sequence: 31..1023

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ACCTCATGTG GCCAGGACAT CTACCGGCTC CTCTGTATGG ATTTTGTGTT CTCTTTAGTC 240
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TGATGACTCT TTTGTAACCC AGACACCAAT CAAATAAGGG GAGGAGACGA AAATGGAATG 1080
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AGTACCGTAG CCAATGAGAT TTATCCGAGA CGCGATTATT GCTAATTTGA AATTTTCCCA 1740
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Seq ID NO: C204 Protein Sequence  
Protein Accession #: Eos sequence

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CAGTGAGAA GAAAGCTTGC AGGAGGCAGG AGATGCTGTC CGATGACCAC GTGAATGAAA 240
TCATCATACA GGTGAGAAAT GTTCTCTCTG GGGTCCAAAG CCACCCATCC TCAAATCAGA 300
TTTTTCAGA AAAGGTGCTG CTAGACTCAA GCATCAACAT GGTTTTGTCA ATATCTGACA 360
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TGCGGTTTTC AACATCTTTG AATGAGTCSA TGTCTCAGAC CCTTCATAGC CTAGAATGCA 480
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GATCCAAGAA CAGCCTGTG GAAATTCGTA ATTCCATCAG CCTGTGGCAG AAGAOCCTGA 780
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GGAACAGCGG GGCATCTTAC AACATGCAGC TGGCCTACAT CTTCAATATC GGAGCATGCT 1080
TGACCACCTG CTCTCTCAGT TTGCTGTTC GCATGGCCAA GTATTTCOOG AACCAACTTC 1140
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TCCTTCTGAT GATTTTGTG TTCTCTTTAG TCAATTCCTT CCTGGGGAG TTTCTGAGGA 1740
GAATCATTTG GATGCAACTG ATCACAAGTC TTGGCCTTCA GGAGTTTGAC ATTGCCAGGA 1800
ACGTTCTAGA ACTGATCTAT GCACAAACTC TGGTGTGGAT TGGCATCTTC TTCTGCCCCC 1860
TGCTGCCCTT TATCCAAATG ATTATGCTTT TCATCATGTT CTACTCCAAA AATATCAGCC 1920
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ACCTAGGAAG AGATAACTAG GGAATAATGT ATATTATCTT CAAGAAGTGT GTGCAGGAAT 2820
GATTGTTTCT TAGAAATCTC TCCTGCCAGA CTGCCAAGG TTAGAAACT 2880
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CCTCTGAATT GTAGAACCTG CATTATTTG TGAATTTGAA CTAAAGACAT CCCCATGTC 3000
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AAAGTCTTAC GTCAAGCTAG CTTTGCAGTG GCAGTACCGT AGCCAATGAG ATTTATCCGA 3180
GACGCGATTA TTGCTAATTG GAAATTTTCC CAATACCCCA CCGTATGATC TTGAAATATA 3240
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Seq ID NO: C205 DNA Sequence

Nucleic Acid Accession #: NM\_002250.1

Coding sequence: 397..1680

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GCTGACGACC TGCAAGCCAC AGTGGCTGCC CTGTGCGTGC TGCGAGGTGG GGGACCCCTG 360
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Seq ID NO: C206 DNA Sequence

Nucleic Acid Accession #: NM\_025257.1

Coding sequence: 1..2139

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 CCCACGACAG CAGCCACTCT TGGATATGTG CTCTGGGCAT CCAACATCAG CTCCCCTGGC 1200  
 TGTGAGAAAG TGGCAATAAA TACATCATGC AACCCACCG CCCACTTGT GAACTCCTCG 1260  
 TGCCAGGGC TGATGTGCGT CTTCAGGGC TACTCATCCA AAGGCTTAAT CCAACGTTCT 1320  
 GTCTTCAATC TGCAAACTTA TGGGGTCTTG GGGCTCTTCT GGACCTTAA CTGGGTACTG 1380  
 GCGCTGGGCC AATGGTCTCT CGCTGGAGCC TTGCTCTCT TCTACTGGGC CTTCACAG 1440  
 CCCACGACAG TCCCTACCTT CCCCTTAATC TCTGCTTCA TCGCACACT CCGTTACCAC 1500  
 ACTGGTCTAT TGGCATTTGG AGCCTCATC CTGACCCCTG TGCAGATAGC CCGGTCTATC 1560  
 TTGGAGTATA TTGACACAAA GCTCAGAGGA GTGCAGAAC CTGTAGCCCG CTGCATCATG 1620  
 TGCTGTTCAC AGTGTGCTCT CTGGTGTCTG GAAAAATTTA TCAAGTCTCT AAACCGCAAT 1680  
 GCATACATCA TGATCGCCAT CTACGGGAAG AATTTCTGTG TCTCAGCCAA AAATGCGTTC 1740  
 ATGCTACTCA TGGCAAAACAT TGTCAAGGTG GTGCTCTGG ACAAGTCTAC AGACCTGCTG 1800  
 CTGTTCTTTG GGAAGCTGCT GGTGTGCGGA GCGGTGGGGT TCGTCTCTT CTTTTTTTTC 1860  
 TCGGCTGCA TCCCGGGGCT GGGTAAAGAC TTTAAGAGCC CCGACCTCAA CTATTACTGG 1920  
 CTGCCCATCA TGACCTCCAT CCTGGGGGCC TATGTCTATG CCAGCGGCTT CTTCAGGCTT 1980  
 TTGCGCATGT GTGTGGACAC GCTCTTCTCT TGCTTCTCTG AAGACCTGGA GCGGAACAA 2040  
 GGCTCCTCTG ACCGCGCCTA CTACATGTCC AAGAGCCTTC TAAAGATTCT GGGCAAGAA 2100  
 AACGAGCGC CCGCGGACAA CAAGAAGAGG AAGAAGTAC AGCTCCGGCC CTGATCCAGG 2160  
 ACTGCACCCC ACCCCACCG TCCAGCCATC CAACCTCACT TCGCCTTACA GGTCTCCATT 2220  
 TTGTGGTAAA AAAAGGTTT AGGCCAGGCG CCGTGGCTCA CGCTCTGTAAT CCAACACTTT 2280  
 GAGAGGCTGA GCGGGGCGGA TCACTGAGT CAGGAGTTG AGACCAAGCT GGCACACATG 2340  
 GTGAAAC 2347

Seq ID NO: C207 DNA Sequence  
 Nucleic Acid Accession #: NM\_016180.1  
 Coding sequence: 26..1618

1 11 21 31 41 51  
 45  
 50  
 55  
 60  
 65  
 70

CAGGAAGGTT CTCTCCAG TGGCCATGGG TAGCAACAGT GGGCAGGCTG GCGGCCACAT 60  
 CTATAAATCC CTAGCTGATG ATGGCCCTTT TGAATCTGTG GAGCGCGCTA AAAGACCCAC 120  
 CAGCAGACTC ATCATGCACA GCATGGCCAT GTTCGGAAGA GAGTCTGTCT ACGCGGTGGA 180  
 GGCAGGATAT GTGACCCAG TCCTGCTCAG CGTAGGTCTG CCCAGCAGCC TGTACAGCAT 240  
 TGTGTGGTTC CTGACCCCA TCCTGGGATT CTGTCTGTCG CCGGTGGTCT GATCGGCCAG 300  
 CGACACTGTC CCGTCCAGGT GGGGCGCGCG GAGACCTTAC ATCCTCACCC TGGGAGTCT 360  
 GATGCTGTGT GGCATGGCTC TGTAACTCAA TGGGGTACT GTTGTAGCAG CTTTGTATGC 420  
 TAACCAAGG AGGAAGCTGG TTTGGGCCAT AAGTGTCACT ATGATAGGTG TGTCTCTCT 480  
 TGAATTTGCT GCGACCTCA TTGATGGGCC CATCAAAGCC TACTTATTGT ATGTCTGCTC 540  
 CCATCAGGAC AAGGAGAAGG GCCTCCACTA CCATGCGCTT TCCACAGGTT TTGAGGTGTC 600  
 CCGGGTATC CTGTTGGGTG CTATAGACTG GGGCCATCTG GAGCTGGGAA GACTGTGGG 660  
 TACAGAAATC CAGGTCAATG TCTTCTCTCT TGCAATGGTG CTCACTTTGT GTTTTACTGT 720  
 TCATCTGTGC AGTATCTCTG AAGCCCACTT TACAGAGGTT GCAAGGGCA TTCCCCACA 780  
 GCAACCCCTC CAGGACCCCTC CATTTGATC AGATGGAATG TACGAGTATG GTTCTATCGA 840  
 GAAAGTTAAA AATGGTTACG TAAATCCAGA GCTGGCAATG CAGGGAGCAA AAAACAAAA 900  
 TCATGCTGAA CAGACTCGCA GGGCAATGAC ATTAAGTCA CTGCTGAGAG CACTGGTGAA 960  
 CATGCTCTCT CACTACCGCT ACCTTTGCAT CAGCCACCTC ATTGGATGGA CGGCTCTCT 1020  
 GTCCACATG CTGTTCTTCA CAGATTTCAT GGGCCAGATT GTGTACCGCG GGGATCCCTA 1080  
 TAGTGCACAC AACTCCACAG AGTTTCTCAT CTACGAAAGA GGAGTCGAGG TTGGATGTTG 1140  
 GGGCTTCTGC ATCAACTCCG TGTCTTCTCT ACCTTATTCT TACTTTTCTA AAGTTTGGT 1200  
 ATCCTCATTT GATTTAAAGG GTCTTACTT CAGGGATAT TTGCTGTTG GCCTGGGGAC 1260  
 GGGATTATT GGGCTCTTCC GGAATGTCTA CTCCACCTG GTCTGTGCA GCCTGTTTGG 1320  
 TGTAAATGTC AGCACCTGT ACCTGTGCTC CTTTAACTCT ATTACTGAGT ACCACCGCGA 1380  
 GGAAGAAAAG GAGAGGCAGC AGGCCCCAGG AGGGGACCCA GACAACAGCG TGAGAGGGAA 1440  
 GGGCATGGAC TGGGCCACCC TCACATGCAT GGTGAGCTG GCTCAGATCC TGGTCCGAGG 1500  
 TGGCTTGGC TTCTTGGTCA ACACAGCGG GACGCTTGTG GTCTGTGTA TCACAGGCTC 1560  
 TGGCTTGGCA CTGATAGGCT GTTGTCTTGT CGCTCTCTTT GTTAGATATG TGGATTAGGT 1620  
 CAATAAAGAG ACAATGACCC TAAAAAATA 1650

Seq ID NO: C208 DNA Sequence  
 Nucleic Acid Accession #: NM\_003273.1  
 Coding sequence: 255..2024

1 11 21 31 41 51  
 80  
 85  
 90

CGCGCGGGG CCGGATCCTC CGCGCGGGG AGTCCATCTC CTGGGAATG GGGCGGACAG 60  
 TGTTCCTTGT ACTGACTATT GTGAGCGCCC TCTCTCTCG GCGGAGCGGA GACCATGGCC 120  
 CCCACTCAGG CCGCGGGGCC CGCTGGAAT TGGAGGGGCC CTGGGTAAT GGGGAGAGAA 180  
 GATGGGACCT GGGGCAAGG CTAAGCGAAG GAGAGCTGGA GCGGGTGAAC TAAAGCGGG 240  
 GCGAGATCT GAGGATGAA GGCCTTGGGG GTGTGGAGG CAGAGGGACC CCGGGTGTG 300

5 CAGCGAAGGG TGTCTGGAGA GGGAGAGCTG AGGAGGGGGC GGTTCCTGGG GCTGCAGAAC 360  
 GGGGATTTAT GGTGTGCTACT GGGAGCAGGA GGAGGGGTCTT GGAGGGGGCT GGGGGCGGGG 420  
 GACTAAGATG GACGCTCTGG AAGGGAACCTG GGAGGCAGCG GGGTGCTCTG GGGCCGAGGG 480  
 CTGAGGACGG GGTGCGGAGG CGCACTCTGG GAATGCCGAG AGGGTCCCGC AGAGACGTCA 540  
 GGGCGCGGTG CCGGCGCGCG GGGAGCTGGG GGGCTAGGGG CGGACGCGGA CGTGATGGCC 600  
 CTTCGCGCAG GCGCGCGGCT TCTGCTACTG CTGCTGCGCG CCACCATGTT CCACTGCTC 660  
 CTGGCGGGCC GTTGGGGCCC CGCGCGCTG CTGGGTCCAC CCGGTCTCCT GCCCGGGCTG 720  
 GAGGTGCTGT GGAGCCACAG GGGCTGCTG CTGTGGCTCG CTTGGCTCGG CTGCAGGCG 780  
 10 GCGCTCTACC TACTGCGGCG GCGCAAGGTG CGGGCCCGCG TCGCGGACGC TCGGGGGAGG 840  
 GAAGCGAATG GGTCTGGCGA GGGAAAGGAC GCCCGGGGCC TTATCAGAGC CCGCTTGGAC 900  
 CGCAGTGGC CGAGGGGCGA GAATTGAAG ACAAGAGTGG CCTGCGCTAT CCTATTAAAG 960  
 GCTTCCAGGC CCTGGTGTG ACAGCCCTGT TGGTGGGGCT GGGGATGTCA GCGGGGCTGC 1020  
 TCTTGGGGGC GCTCCCGGAA ATGCTCTCTG CCTTGGGGTT TGTCCGCAAC CTCACCGCTT 1080  
 15 TCATCTTCAG CCTCTTCTC TACATGAAG CGCAGGTAGC CCGAGTTTGG GCGCTGGCAC 1140  
 CTGGGGGAA CTCAGCAAT CCGATTACG ACTTTTCTT GGGAGGAGAG CTCACCCCTC 1200  
 GTATCTGTTT CTTCGACTTC AAATATTTCT GTGAATGCG ACCCGGCTC ATCGGCTGG 1260  
 TCCTCATCAA CCTGGGCCCTG TTGATGAAG AGGCAGAGCT TCGAGGCAGT CCGTCACTGG 1320  
 CCAATGTGGT GGTCAATGGC TTCCAGTTGC TCTACGTGGG TGATGCCCTC TGGCAGGAG 1380  
 20 AGGCGTCTCT CACCACTATG GATATCACAC ATGACGGGTT TGGCTTCATG CTGGGTTTGG 1440  
 GGGACATGGC CTGGGTGCCC TTCACCTACA GCTGCGAGGC CCAATTCTCT CTGCACCAAC 1500  
 CGCAGCCCTT GGGGTGCCCC ATGGCTCTGT TCATCTGCCT CATCAATGCT ACTGGTTACT 1560  
 ACATCTTCCG TGGGGCGAAT TCCAGAAAA ACATTTCCG AAAGAACTCT TCTGACCCCA 1620  
 GAGTGGCTGG GCTTGAGACC ATCTCTACAG CCACAGGGCG GAAACTGCTG GTGTCTGGGT 1680  
 25 GGTGGGTATG GCTCCGCCAT CCCAACTATC TTGGAGACCT CATCATGCTT CTGGCTTGGT 1740  
 CCTTGGCCCTG CCGGGTGTCA CACCTGCTGC CCTACTCTTA CCTCTCTAC TTCACCGGCG 1800  
 TGCTGTGTGA CCGTGAGGCC CGGGATGAGC GGAGTGCTCG CAGAAGTACG GCGTGGCTCG 1860  
 GCAGGAGTAC TGGCGGCGTG TGCCCTTACC CATCATGCCC TACATCTACT GAAGGGGCTC 1920  
 CACCACCCCA GGTGGGCGAT GTGCCCACTC ATCCACCAGC ACACCCAGGA CCAGGAGCCT 1980  
 30 CGACACACTT GGGACTCAAG GGTCTGACCC CCACCCAGCC CTGAGGATGA ACAACCTCAG 2040  
 AGAAGAGGTT GTTTAGAGCA AGGAAAAAAA TGAAACCACT GACCAAAAAA AAAAAAAA 2100

Seq ID NO: C209 DNA Sequence  
 Nucleic Acid Accession #: NM\_015720.1  
 Coding sequence: 21..1838

35 1 11 21 31 41 51  
 CCAGTTCGCG CACGAGGACC ATGGGCGGCG TGCTGCGGGC CGCCCGGCTG CCGCGCTGCG 60  
 40 TTTCGCGCGT GCTGCTTCTG CTGGTTGGGG GAGCGTTCCT GGGTGCTCTG GTGGCTGGGT 120  
 CTGATGAGCG TGGCCAGAGG GGCCTCACTT CCACCTCCCT GCTAGACCTC CTGCTGCCCA 180  
 CTGGCTTGGA GCCACTGGAC TCAGAGGAGC CTAGTGAGAC CATGGGCGTG GGAGCTGGGC 240  
 TGGGAGCCCT TGGCTCAGGC TTCCCGAGCG AAGAGAATGA AGAGTCTCGG ATTCTGCAGC 300  
 CACCACAGTA CTTCTGGGAA GAGGAGGAAG AGCTGAATGA CTCAGTCTG GACCTGGGAC 360  
 45 CCATCTGAGA TTATGTTTTT CCGTACTTAA CTGAGAAGGC AGGTTCCTAT GAAGACACTA 420  
 GCCAGGCTCA AGGCTGGCCA AACCTCCCTT CTCCCTTGCC CAAGATGAAT CTGGTTGAGC 480  
 CTCCTGGGCA TATGCTCCCG AGAGAGGAGG AAGAAGAGGA AGAGGAAGAG GAGGAGAGGG 540  
 AGAAGGAAGA GGTAGAGAAA CAAGAGGAGG AGGAAGAGGA GGAGCTGCTC CCGTGAATG 600  
 GATCCCAAGA AGAAGCCCAAG CCTCAGGTCC GTGACTTTTC TCTCACCAGC AGCAGCCAGA 660  
 50 CCCAGGGGCG CACCAAAAGC AGGCATGAAG ACTCCGGGGA CCAGGCGCTCA TCAGGTGTGG 720  
 AGGTGAGAGG CAGCATGGGG CCCAGCTTGC TGCTGCGCTC AGTCAACCCA ACTACAGTGA 780  
 CTCGCGGGGA CCAGGACTCC ACCAGCCAAG AGGCAAGGCG CACAGTGTCT CCACTGTCAG 840  
 GCGTTGGGGT AGAGTTCGAG GCTCCTCAGG AAGCAAGCGA GGAAGCCACT GCAGGAGCAG 900  
 CTGGTTTGTG TGGCCAGCAC GAGGAGGTGC CGGCTTGGCC TTCAATCCCT CAAACCAAG 960  
 55 CTCCTAGTGG GCGCGAGCAC CCAGATGAAG ATCCCTTGGG CTCTAGAACC TCAGCCTCTT 1020  
 CCCCACCTGC CCTCTGAGC ATGGAACCTG CACCTTCTCT TGCTACCTTG GGAACAAGAG 1080  
 ATCTCAACCA GCAGCTCTTA GAAGGGCAGG CAGCTGAAGC TCAATCCAGG ATACCTTGGG 1140  
 ATTCTAGCCA GGTGATCTGC AAGGACTGGA GCAATCTGGC TGGGAAAAAC TACATCATTC 1200  
 60 TGAACATGAC AGAGAACATA GACTGTGAGG TGTTCGGGCA GCACCGGGGG CCACAGCTCC 1260  
 TGGCCCTGGT GGAAGAGGTG CTGCCCCGCC ATGGCAGTGG CCACCATGGG GCGTGGCACA 1320  
 TCTCTCTGAG CAAGCCAGC GAGAAGGAGC AGCACTTCT CATGACACTG GTGGGGGAGC 1380  
 AGGGGGTGGT GCCCACTCAA GATGTCTTCT CCATGCTGGG TGACATCCGC AGGAGCCTGG 1440  
 AGGAGATTGG CATCCAGAAC TATTCACAAA CCAGCAGCTG CCAGGCGCGG GCCAGCCAGG 1500  
 TGCGCAGCGA CTACGGCAGG CTCTTGTGGG TGCTGGTGGT CATTTGGGGC ATCTGCATCA 1560  
 65 TCATCATTGC GCTTGGCCTG CTCTACAAT GCTGGCAGCG CCGGCTGCCC AAGCTCAAGC 1620  
 ACGTGTGCGA CGCGAGGAG CTGCGCTTGG TGGAGAACGG CTGCCACGAC AACCCCAAGC 1680  
 TGGAGCTGGC CAGCGACAGC CAGTCGGAGA TGCAGGAGAA GCACCCAGC CTGAACGGCG 1740  
 GCGGGGCGCT CAACGGCCCG GGGAGCTGGG GGGCGCTCAT GGGGGGCAAG CGGAGCCCGG 1800  
 AGGACTCGGA CGTGTTCGAG GAGGACACGC ACCTGTGAGC GCAGCGAGGC GCAGGCGGAG 1860  
 70 TGGGCGGCGA GGACCAAGCG AGGTGGAACC CGAAACGGAG GCGCGGAGC CCGCACCAGC 1920  
 CCGCGGCTTA CCGCGCGGCC CCGCGGCTG GCCCTCGGCG CGGCTCTCTT CCGCTTCCC 1980  
 CCGACTTCACT ACGGGGGCTT CGGACCAACT CCTCACTCC CGCCGAGGGG GCAGGCTCTCA 2040  
 AAGCCCGGCT TGGCCCGGCT TTCCCGCCCC TGAACCCCGG CCGCGGGGGC GCGGGGCGCG 2100  
 75 CTCTCTGCGC CCGGGGACTC AATTAAACCC GCGCGGAGAC CACGCGGGCC CAGCGAAAAA 2160  
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 2220  
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 2269

Seq ID NO: C210 DNA Sequence  
 Nucleic Acid Accession #: NM\_001197.3  
 Coding sequence: 61..543

80 1 11 21 31 41 51  
 GACACGAAGC CTCGCGGGTG GCTTACAGAC GCTGCCAGCA TCGCGCGCGC CAGAGGAGAA 60  
 ATGTCTGAAG TAAGACCCCT CTCAGAGAC ATCTTGATGG AGACCTCTCT GTATGAGCAG 120

5 CTCTGGAAC CCCGACCAT GGAGGTTCTT GGCATGACTG ACTCTGAAGA GGACCTGGAC 180  
 CCTATGGAGG ACTTCGATTTC TTGGAATGTC ATGGAGGGCA GTGACGCATT GGCCCTGCGG 240  
 CTGGCCCTGCA TCGGGGACGA GATGGACGTG AGCCTCAGGG CCCCGCGCCT GGCCACGCTC 300  
 TCGAGGTGG CCATGCACAG CCTGGGTCGT GCTTTTCATCT ACGACCAGAC TGAGGACATC 360  
 AGGGATGTTT TTAGAAGTTT CATGGACGGT TTCACACAC TTAAGGAGAA CATAATGAGG 420  
 TTCTGGAGAT CCCGAAACCC CGGGTCCTGG GTGTCTCGCG AACAGGTGCT GCTGGCGCTG 480  
 CTGCTGCTGC TGGGCTGCT GCTGCCGCTG CTCAGCGGGG GCGTGCACCT GCTGCTCAAG 540  
 TGAGGCCCGG GCGGCTCAGG GCGGGGCTGG CCCCACCCCG ATGACCACCTG CCTGGAGGT 600  
 10 GGCGGCTGCG TGCTGTTATC TTTTAACTG TTTTCTCATG ATGCGTTTTT ATATTTAAAC 660  
 CCGGAGATAG TGCTGGAACA CTGCTGAGGT TTTTACTCA GGTTTTTTGT TTTTTTTTAA 720  
 TTCCAGTTTT CGTTTTTTCT AAAAGATGAA TTCTATGGC TCTGCAATTG TCACCGGTTA 780  
 ACTGTGGCCT GTGCCAGGA AGAGCCATTG ACTCTGCCC CTGCCACAC GGCAGGTAGC 840  
 AGGGGGAGTG CTGCTCACAC CCTGTGTGA TATGTGATGC CCTCGGCAA GAATCTACTG 900  
 15 GAATAGATTG CGAGGACGAG GAGTGCTCAA TAAATGTTG GTTTCAGCA AAAAAAAAAA 960  
 AAA 963

Seq ID NO: C211 DNA Sequence

Nucleic Acid Accession #: AF272357

Coding sequence: 83..1060

20 1 11 21 31 41 51  
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 GCTGCTCCCG ACGCGGAGCC GCGAGCCCGC GCGAGCCCGC TGGCCTCGCG GTGCCATGCT 60  
 GCGCCGCGCG GCGGCTGAA GATGGGCGAC GCGCTGCGCT CGCCCTCCC CGCGGCACCT 120  
 25 GCGGCTGCTG CCGCTGCTGC TCTCCGCGCT CGTCTCGGCG GCGCCCTGCG GTGGAGCCGC 180  
 GCGCGCCAC CCGATGTAG CCGCTGTCC CCGGAGCCTG GACTGTGCC TGAAGAGGCG 240  
 GGCAGGTGT CCTCTGGTG CACATGCTCG TGGGCCCTGC CTTCAGCCCT TCCAGGAGGA 300  
 CCAGCAAGGG CTCTGTGTGC CCAGGATGCG CCGGCTCCA GCGCGGGGCC GCGCCACGCC 360  
 30 CAGACTGAAA GATGAGATTG ACTTCTGGC CCAGGAGCTT GCGCGAAGG AGTCTGGACA 420  
 ATCAACTCG CCCCTACCCA AGGACCGACA GCGGCTCCCG GAGCCTGCC CCTGGGCTT 480  
 CTCGGCACCG GCGCAGGGGC TGGAGCTGGG CCTCCCTCC ACTCCAGGAA CCGCCACGCC 540  
 CACGCGCCAC ACCTCCCTGG GCTCCCTGT GTCATCCGAC CCGGTGCACA TGTGCGCCCT 600  
 GGAGCCCGCG GGAGGGCAAG GCGACGCGCT CGCCCTGTG CTGATCCTGG CGTCTGTGT 660  
 GCGCGGTGCA GCGCGCTCT CCGTAGCCTC CTTCTGCTGG TGCAGGCTGC AGCGTGAGAT 720  
 35 CCGCCTGACT CAGAAGGCGG ACTACGCCAC TCGGAAGGCC CCTGGCTCAC CTGCAGCTCC 780  
 CCGGATCTCG CCTGGGGACC AGCGGCTGGC ACAGAGCGCG GAGATGTACC ACTACCAGCA 840  
 CCAACCGCAA CAGATGCTGT GCTTGGAGCG GCATAAAGAG CCACCAAGG AGCTGGACAC 900  
 GGCTCTCTCG GATGAGGAGA ATGAGGACGG AGACTTCAGG GTGTACAGAT GCGCGGCCCT 960  
 GCGCCCGACC GCGGAATGAG AGGTGCGCAA CCTCTGTTC GACCAAGCGG CACTGTCCGC 1020  
 40 GCGCCTGCGG GCGCCAGCT CACCGCCTGC ACTGCCATGA CCTGGAGGCA GACAGACGCC 1080  
 CACCTGTCTC CCGACCTCGA GCGCCCGGG GAGGGGCGAG GCGTGGAGCT TCCCACTAAA 1140  
 AACATGTTT GATGCTGTGT GCTTTTGGCT GGGCCTCGGG CTCACGGCCC TGGGACCCCT 1200  
 TGCCAGGGAG ACCCCGGAAC CTTTGTGCCA GGACACCTCC TGGTCCCTCG CACTCTCTCT 1260  
 45 GTTCGGTTTA GACCCCAAAA CTGGAGGGGG CATGGAGAAC CGTAGAGCGC AGGAACGGGT 1320  
 GGGTAATTCT AGAGACAAAA GCAATTAAA GTCCATTTC AAAAAAAAAA A 1371

Seq ID NO: C212 DNA Sequence

Nucleic Acid Accession #: NM\_004445.1

Coding sequence: 799..3819

50 1 11 21 31 41 51  
 | | | | |  
 CGGAGGGGGC GGGCCGGGCT GCGTTGCTC CAGCCGCGCG TCTACAGCAG CGGGCGGGCG 60  
 GACCCGGGAC CCAGCTTGGC GACGGGATTT CTGAGCGGG GCGCCACGGA TTCTCCGGCG 120  
 55 GCGCCACCTC TGGAGCAGCC CCGCGGCCA GCGTCAGGTC CACCCGGA TCCAGGGGAC 180  
 TCTCGGCGCC GAACGACCC GGGCGGTCG AACGGGTCC CCGGACTGGA GAAGAGCGCG 240  
 GTGGCACCGT GCGAGCTCCA GGAGCCCGG GTCCACTGCG AGGCTCGGG GGGCGCAGAC 300  
 CTGCAGAGAC TGGGCCAAC GGAAGAAAT AAAGGGATTA TAGTCCACCC AATTACAGCA 360  
 60 CTTCTGAGAC TCAGACAGA GGAGAGATAG AGAACCGCCA ATCTCTAGAT CAACAAGCAA 420  
 AGGAGGTGCC AAGCCTGTTT GTCTTCAATG TGACACTGGA GTCTAGATGC TGGGAAGTCC 480  
 AAGATCAGGG TGGCGCATG GTCAGTTCT GCGGAAGCCT CTCTCTAGG TTTCAAGCTG 540  
 CCCTCTTCTT TGTGTGTCC TCGAATGGCA GAAAAGGGG TGGCTGTTGG AGGAAGGGAG 600  
 GAGAGTAAAT GAAGAGAAAG AACTGGAATA ACCCTTGCA GAAAAAAAAA AAAAGGGAG 660  
 65 CTTAGCTGTA CACCTGAGT CTTGCAAAAG CTGCAGCCCC ACCCAGGAGC AGGGTGTGTG 720  
 CTGGGGCGAT GGTGGAAGCC CTGAAGATGT CCGATGGCTA CTGAAGGGGC TGCCAGTTA 780  
 GGGAAACAGAG TGGCGGGCAT GGTGTGTAGC CTATGGGTGC TGCTCCTGGT GTCTTCAGTT 840  
 CTGCTCTGCG AAGAGGTATT GCTGGACACC ACCGAGAGAG CATCTGAGAT TGGCTGGCTC 900  
 ACCTACCCAC CAGGGGGGTG GGACGAGGTG AGTGTCTCG AGACCCAGCG ACGCTGACT 960  
 70 CCGACCTTGG AGGCAATGTA TGTGGCAGGG GCGCCTCCAG GCACCGGGCA GGACAAATGG 1020  
 TTGCAGACAC ACTTTGTGGA GCGCGCGGG GCGCAGAGGG GCACATTGG ACTCCACTTC 1080  
 TCTGTGCGGG CATGCTCCAG CCTGGGTGTG AGCGCGCGCA CTGCGGGGA GACCTTCACC 1140  
 CTTTACTACC GTGAGGCTGA GGAGCCCGAC AGCCCTGACA GCGTTTCTCT CTGGCACCTC 1200  
 AAAAGCTGGA CCAAGGTGGA CACAATTGCA GCAGAAGAGA GCTTTCCCTC CTCTCTCTCC 1260  
 75 TCTCTCTCT CTCTCTCTCT TGCAGCGTGG GCTGTGGGAC CCCACGGGGC TGGGCGCGCG 1320  
 GCTGGAAGTC AACTGAAGT CAAAGAGCG AGCTTTGGGC CTCTCACCCA ACGCGGCTTC 1380  
 TAGGTGGCCT TCCAGGACAC GGGGGCCTGC CTGGCCCTGG TCGTGTCTAG GCTCTTCTCC 1440  
 TACACCTGCC CTGCGGTGCT CCGATCTCTT GCTTCTCTTC CAGAGACGCA GGCCAGTGGG 1500  
 GCTGGGGGGG CTTCTCTGTT GGCGAGCTGT GGCACCTGTG TGGCTCATGC AGAGCCAGAG 1560  
 80 GAGGATGAG TAGGGGCCA GGCAAGAGGC AGCCGCCCA GGTGCACTG CAAAGGGGAG 1620  
 GGCAAGTGA TGTAGCTGT CCGGGGCTGC CGCTGCCAGC CTGGATACCA ACCAGCACGA 1680  
 GGAGACAAGG CCTGCCAAGC CTGCCCAAGG GGGCTCTATA AGTCTTCTGC TGGGAATGCT 1740  
 CCTGTCTCAC CATGCCCTGC CCGCAGTCAC GCTCCCAACC CAGCAGCCCC CGTTTGGCCC 1800  
 TGCTGGAGGG GCTTCTACCG GGCCAGTTCC GACCCACAG AGGCCCCCTG CACTGGTCTC 1860  
 CCACTCGCTC CCCAGGAGCT TTGTTTGTAG GTGCAAGGCT CAGCACTCAT GCTACACTGG 1920

5	CGCCTGCTC	GGGAGCTGG	GGGTGAGGG	GACCTGCTCT	TCAATGTCGT	GTGCAAGGAG	1980
	TGTGAAGGCC	GCCAGGAACC	TGCCAGCGGT	GGTGGGGGCA	CTTGTCAACG	CTGCAGGGAT	2040
	GAGGTCCACT	TCGACCTTCG	CCAGAGAGGC	CTGACTGAGA	GCCGAGTGT	AGTGGGGGA	2100
	CTCCGGGCAC	ACGTACCTTA	CATCTTAGAG	GTGCAGGCTG	TTAATGGGGT	GTCTGAGCTC	2160
	AGCCCTGACC	CTCCTCAGGC	TGCAGCCATC	AATGTTCAGCA	CCAGCCATGA	AGTGCCTCT	2220
	GCTGTCCCTG	TGGTGACCA	GGTGAGCCGG	GCATCCAACA	GCATCACGGT	GTCCTGGCCG	2280
	CAGCCCGACC	AGACCAATGG	GAACATCCTG	GACTATCAGC	TCCGCTACTA	TGACCAGGCA	2340
	GAAGACGAAT	CCCACTCCTT	CACCTTGACC	AGCGAGACCA	ACACTGCCAC	CGTGACACAG	2400
10	CTGAGCCCTG	GCCACATCTA	TGGTTTCCAG	GTGCGGGCCC	GGACTGCTGC	CGGCCACGGC	2460
	CCCTACGGGG	GCAAGATCTA	TTTCCAGACA	CTTCTCAAG	GGGAGCTGTC	TTCCAGCTT	2520
	CCGGAAGGAC	TCTCCTTGGT	GATCGGCTCC	ATCCTGGGGG	CTTTGGCCTT	CCTCCTGCTG	2580
	GCAGCCATCA	CCGTGCTGGC	GGTCTGTCTC	CAGCGGAAGC	GGCGTGGGAC	TGGCTACACG	2640
	GAGCAGCTGC	AGCAATACAG	CAGCCACAGG	CTCGGGGTGA	AGTATTACAT	CGACCCCTCC	2700
15	ACCTACGAGG	ACCCCTGTCA	GGCCATCCGA	GAACCTGCCC	GGGAAGTCGA	TCCTGCTTAT	2760
	ATCAAGATTG	AGGAGTTCAT	TGGGACAGGC	TCTTTTGAG	AAGTGCGCCA	GGGCCGCTG	2820
	CAGCCACGGG	GACGAGGGA	GCAGACTGTG	GCCATCCAGG	CCCTGTGGGC	CGGGGGCGCC	2880
	GAAAGCCTGC	AGATGACCTT	CCTGGGCGGG	GCCGAGTGC	TGGGTCAAGT	CCAGCACCCC	2940
	AACATCTGTC	GGCTGAGGGG	CGTGGTCACC	AAGAGCCGAC	CCCTCATGTT	GCTGACGGAG	3000
20	TTCATGAGAT	TTGGCCCTCT	GGACAGCTTC	CTCAGGCAGC	GGGAGGGCCA	GTTGAGCAGC	3060
	CTGACGCTGG	TGGCATGCA	GCGGGGAGTG	GCTGCTGCCA	TGCAGTACCT	GTCCAGCTTT	3120
	GCCTTCGTCC	ATCGCTGCTG	GTCTGCCAC	AGCGTGTCTG	TGAATAGCCA	CTTGGTGTGC	3180
	AAGGTGGCCC	GTCTTGGCCA	CAGTCTCTAG	GGCCCAAGTT	GTTTGCTTCG	CTGGGAGGCC	3240
	CCAGAGGTCA	TTGCATGCG	AAGGCATACA	ACATCCAGTG	ATGTCTGGAG	CTTTGGGATA	3300
25	CTCATGTGGG	AACCTGATGAG	TTATGGAGAA	CGGCCTTACT	GGGACATGAG	TGAGCAGGAG	3360
	GTAATAATG	CAATAGAGCA	GGAGTTCGGG	CTGCCCCCGC	CTCCAGGCTG	TCCTCCTGGA	3420
	TTACATCTAC	TTATGTGGA	CACCTGGCAG	AAGGACCGTG	CCCGGCGGCC	TCATTTTGAC	3480
	CAGCTGGTGG	CTGCATTGGA	CAAGATGATC	CGCAAGCCAG	ATACCTTGCA	GGCTGGGGGG	3540
	GACCCAGGGG	AAGGGCCTTC	CCAGGCCCTT	CTGACCCCTG	TGGCCCTGGA	CTTTCCTTGT	3600
30	CTGGACTCAC	CCAGGCCCTG	GCTTTCAGCC	ATTGGACTGG	AGTGTACCCA	GGACCACTTC	3660
	TCCAAGTTTG	GCCTCTGTAC	CTTCAGTGAT	GTGGCTCAGC	TCAGCCTAGA	AGACCTGCCT	3720
	GCCTTGGGCA	TCACCTTGGC	TGGCCACAGG	AAGAAGCTGC	TGCACCAT	CCAGCTCCTT	3780
	CAGCAACAGT	TGAGGAGGCA	GGGCTCAGTG	GAGGTCTGAG	AATGACGATA	CCCGTGACTC	3840
	AGCCCTGGAC	ACTGTCGCGA	GAAGGGACAT	GTGGGACGTG	AGCCGGGCTC	CAACAGCCTC	3900
35	TGTGAGAGAT	GCCCCACACC	AAACCCAAACC	CTCCGATGG	CTGCATTCCC	TGGTCTCCG	3960
	CCTCTCCACC	AGCCCCCTCC	TCATTAAAGG	GAAAGAAGGG	AATTTCGAAA		4010

Seq ID NO: C213 DNA Sequence  
Nucleic Acid Accession #: XM\_043340.4  
Coding sequence: 195..1067

40	1	11	21	31	41	51	
	GGGCGGCGCC	CAATGGGCTG	CGCGGAGCGT	CACTTCCCGG	CAGCGGGAGG	CGAGTGGCGA	60
45	GTGGCGAGTG	GCGAGTGTCA	GGGGGGCGGC	CGGCGGGGGC	GGGGCGGCGG	GAGGAGGCGT	120
	TGGCAGCGGG	CTGGAGCCCA	CGCGGCGCGG	CGGCCCGCCT	GGCCTGCAGC	GCTCCACCCC	180
	CCGCGGGCGG	CACGATGCCC	TTTGACTTCA	GGAGGTTTGA	CATCTACAGG	AAGGTGCCCA	240
	AGGACCTTAC	GACGCCAAGC	TACACCGGGG	CCATTATCTC	CATCTGCTGC	TGCTCTTCA	300
	TCCTCTTCTT	CTTCTCTCTG	GAGCTCACCG	GATTTATAAC	GACAGAAGTT	GTGAACGAGC	360
50	TCTATGTCCA	TGACCCAGAC	AAGGACAGCG	GTGGCAAGAT	CGACGTCAGT	CTGAACATCA	420
	GTTTACCCTA	TCTGCCTCTG	GAGTTGGTTG	GGCTTGACAT	TCAGGATGAG	ATGGGCAGGC	480
	ACGAAGTGGG	CCACATCGAC	AACTCCATGA	AGATCCCGCT	GAACAATGGG	GCAGGCTGCC	540
	GCTTCGAGGG	GCAGTTCAGC	ATCAACAAGG	TCCCGGCAAA	CTTCCAAGTG	TCCACACACA	600
	GTGCCACAGC	CCAGCCACAG	AACCCAGACA	TGACGATGT	CATCCACAAG	CTCTCTTTTG	660
55	GGGACACGCT	ACAGGTCAG	AACTCCACG	GAGCTTTCAA	TGCTCTCGGG	GGAGCAGACA	720
	GACTCAGCTG	GCCTCCACG	ACTACATCCT	GAAGATTGTG	CCACCGTTT	CCACCGTTT	780
	ATGAGGACAA	GAGTGGCAAG	CAGCGGTACT	CCTACCAAGT	CACGGTGGCC	AACAGGAAT	840
	ACGTGCGCTA	CAGCCACACG	GGCCGATCA	TCCCTGCAAT	CTGGTTCCGC	TACGACCTCA	900
	GCCCCATCAC	GGTCAAGTAC	ACAGAGAGAC	GGCAGCCGCT	GTACAGATTG	ATCACCACGA	960
60	TCTGTGCCAT	CAITGGGGGG	ACCTTCAACG	TGCGCGGCAT	CCTGGACTCA	TGCATCTTCA	1020
	CAGCCTCTGA	GGCCTGGAAG	AAGATCCAGC	TGGGCAAGAT	GCATTGACGC	CACACCCAGC	1080
	CTAATGGCGG	AGGACCCCTG	GCATGCGCAG	CCTTGCTCC	AGTGCCCTGT	CTCCTTTGGC	1140
	CCTCAATCTG	GTCCCAATC	TGGCTGTGTC	CCAAAGGGTG	TGTGGGAAGT	GGGGGGAAG	1200
	TAGAGGATGG	CTGATGTGTT	TGCAGCTACC	TCTTTTCCCC	GTGTTTCTTT	TTAGACAAAT	1260
65	TACACTGCCT	GAAGTTGCAG	TTCCCTTTTC	CCTGGGGAGC	CCCAAGAAC	GAGTCAGGCA	1320
	AGGGGTGGGG	AGTCCAGGGG	AACATCCAG	AATGCATATC	GATCAGCTCT	CAGCCAGGCT	1380
	TGACCAATCT	CGCAGCCCCC	ACTAGGTGGA	CACATTAATG	ATTGGTTC	TCCCTGGGCG	1440
	AGCCAACTGT	CCCCAGAGGC	ACCAGACCTG	GGCTTTCAGC	TTTGGGACCA	GGCTGCCCAA	1500
	AGGTACTCCT	TTATACACCC	GGCACCTTCC	AOGAAAGATG	GTACTTCCCA	AGCAAGCCCC	1560
70	TATGATTGTT	CACATAGAT	GGAATGTGT	GGCATGCACA	TGAGTTGAAA	TTCTTTTATG	1620
	CATTTTCTTG	AAGAAAAAAA	AAAAAACAA	TCTGAGGACA	TAGGGGATGT	CAGTTTCTTA	1680
	TGGAAGAGAC	ACCTCTGACC	CGTTATTTCT	ATAATCAAAA	TCTGAAGGGA	AAAAAATGTT	1740
	TTAGTTCTTT	CCCCACTCGT	TGGTTTCAAC	TAGATTAAAA	GGCTGATTTT	CAG	1793

Seq ID NO: C214 DNA Sequence  
Nucleic Acid Accession #: NM\_002151.1  
Coding sequence: 246..1499

80	1	11	21	31	41	51	
	TGAGCCCGCC	TTTCCAGGGA	CCCTACCTGA	GGGCCACAG	GTGAGGCAGC	CTGGCTAGC	60
	AGGCCCCACG	CCACCGCTTC	TGCTTCCAGG	CGGCCGCTG	CTGGGGGGCC	ACCATGCTCC	120
	TGCCACGGCC	TGAGACTGGA	CCCGACCCCG	GCATACCTC	GAGGCTCCGC	CCCCACCTGC	180
	TGGACCCACG	GGTCCACCCC	TGGCCACAGG	GGTCAGCCAG	GGAATCATTA	ACAAGAGGCA	240
	GTGACATGGC	GCAGAAGGAG	GGTGGCCGGA	CTGTGCCATG	CTGCTCCAGA	CCCAAGGTGG	300

5	CAGCTCTCÁC	TGCGGGBACC	CTGCTACTTC	TGACAGCCAT	CGGGGCGGCA	TCCTGGGCCA	360
	TTGTGGCTGT	TCTCCTCAGG	AGTGACCAGG	AGCCGCTGTA	CCCACTGCAG	GTGAGCTCTG	420
	CGGACGCTCG	GCTCATGGTC	TTTGACAAGA	CGGAAGGGAC	GTGGGGGCTG	CTGTGCTCCT	480
	CGCGCTCCAA	CGCCAGGGTA	GCGGACTCA	GCTGCGAGGA	GATGGGCTTC	CTCAGGGCAC	540
	TGACCCACTC	CGAGCTGGAC	GTGCGAACC	CGGGGCGCAA	TGGCACGTCG	GGCTTCTTCT	600
	GTGTGGACGA	GGGAGGCTG	CCCCACACCC	AGAGGCTGCT	GGAGGTCACT	TCCGTGTGTG	660
	ATTGCCCCAG	AGGCGGTTTC	TTGGCCGCCA	TCTGCCAAGA	CTGTGGCCGC	AGGAAGCTGC	720
	CGGTGGACCG	CATCGTGGGA	GGCCGGGACA	CCAGCTTGGG	CGGTGGCCGC	TGGCAAGTCA	780
10	GCCTTCGCTA	TGATGGAGCA	CACCTCTGTG	GGGGATCCCT	GCTCTCCGGG	GACTGGGTGC	840
	TGACAGCCCG	CCACTGTCTC	COGGAGCGGA	AOCGGGTCTT	GTCCCGATGG	CGAGTGTTTG	900
	CGGTGTGCTG	CGCCAGGGCC	TCTCCCCACG	GTCTGCAGCT	GGGGGTGCAG	GCTGTGGTCT	960
	ACCAACGGGG	CTATCTTCCC	TTTGGGGACC	CCAACAGCGA	GGAGAACAGC	AACGATATTG	1020
	CCCTGGTCCA	CCTCTCCAGT	CCCTTGCCCC	TCACAGAATA	CATCCAGCCT	GTGTGCCCTC	1080
15	CAGCTGCCGG	CCAGGCCCTG	GTGGATGGCA	AGATCTGTAC	CGTGACGGGC	TGGGGCAACA	1140
	CGCAGTACTA	TGGCCAAACAG	GCGCGGTAC	TCCAGGAGGC	TGGAGTCCCC	ATAATCAGCA	1200
	ATGATGTCTG	CGGTGGGCTG	GACTTCTATG	GAACCCAGAT	CAAGCCCAAG	ATGTTCTGTG	1260
	CTGGGTACCC	CGAGGGTGGC	ATTGATGCCT	GCCAGGGCGA	CAGCGGTGGT	CCCTTGTGTG	1320
	GTGAGGACAG	CATCTCTCGG	ACGCCACGTT	GGCGGCTGTG	TGGCATTTGT	AGTTGGGGCA	1380
20	CTGGCTGTGC	CTTGGCCCCA	AAGCCAGGCG	TCTACACCAA	AGTCAGTGAC	TTCCGGGAGT	1440
	GGATCTTCCA	GGCCATAAAG	ACTCACTCCG	AAGCCAGCGG	CATGTGTACC	CAGCTCTGAC	1500
	CGGTGGCTTC	TGCTGTGGCA	GCTTCCAGGG	CCCGAGGTGA	TCCCGGTGGT	GGGATCCACG	1560
	CTGGGGCGAG	GATGGGAAGT	TTTCTCTCTT	GGGCCCGGTC	CACAGGTCCA	AGGACACCCT	1620
	CCCTCCAGGG	TCCTCTCTTC	CACAGTGGCG	GGCCCACTCA	GCCCGAGAGC	CACCCACCTT	1680
25	CACCTCTCTG	ACCCCATGTG	AAATATTGTT	CTGCTGTCTG	GGACTCCTGT	CTAGGTGGCC	1740
	CTGATGATGG	GATGCTCTTT	AAATAATAAA	GATGGTTTGG	ATT		1783

Seq ID No: C215 DNA Sequence  
Nucleic Acid Accession #: AB037745.1  
Coding sequence: 26..1744

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	GTACAAGGGC	ATGACAGGCT	GGGAGGTGGC	TGGTGATCAC	ATTACACAG	CTGCTGGAGC	120
35	CTCAGACAA	GACTTCATGA	TTCTCACTCT	GGTTGTGCCA	GGATTAGAC	CTCCGAGTCC	180
	GGTGATGGCA	GACACAGAGA	ATAAAGAGGT	GGCCAGAAATC	ACATTTGTCT	TTGAGACCTC	240
	CTGTTCTGTG	AACGTGTAGC	TCTACTTCAT	GGTGGGTGTG	AATTCTAGGA	CCAACTCTCC	300
	TGTGGAGAGC	TGGAAGAGTT	CCAAAGGCAA	ACAGTCCCTAT	ACCTACATCA	TTGAGGAGAA	360
	CACATACGAG	AGCTTCACTC	GGGCCTTCCA	GAGGACCACT	TTTCATGAGG	CAAGCAGGAA	420
40	GTACACCAAT	GAOGTTGCCA	AGATCTACTC	CATCAATGTC	ACCAATGTTA	TGAATGGCGT	480
	GGCCTCCCTAC	TGCCGTCCCT	GTGCCCTAGA	AGCCTCTGAT	GTGGGCTCCT	CCTGCACCTC	540
	TTGTCTGTCT	GGTTACTATA	TTGACCGAGA	TTACAGGAACC	TGCCACTCCT	GGCCCCCTAA	600
	CACAAATCTG	AAAGCCCAAC	AGCCTTATGG	TGTCCAGGCC	TGTGTGCCCT	GTGTTCCAGG	660
	GACCAAGAAG	AACAGATACC	ACTCTCTGTG	CTACAATGAT	TGCACTTCTC	CACGCAACAC	720
45	TCCAACCAAG	ACTTTCAACT	ACAACCTTCTC	CGCTTTGGCA	AACACCGTCA	CTCTTGCTGG	780
	AGGGCCCAAGC	TTCACTTCCA	AAGGGTTGAA	ATACTTCCAT	CACCTTACCC	TGAGTCTCTG	840
	TGGAAGACAG	GGTAGGAAAA	TGTCTGTGTG	CACCGACAAT	GTCACTGACC	TCCGGATTCC	900
	TGAGGGTGTG	TGAGGGTCTT	CCAAATCTAT	CACAGCCTAC	GTCTGCCAGG	CAGTCACTAT	960
50	CCGCCAGAG	GTGACAGGCT	ACAAGGCCGG	GGTTTCTCTA	CAGCCTGTCA	GCCTTGCTGA	1020
	TGCACTTATT	GGGGTGACAA	CAGATATGAC	TCTGGATGGA	ATCACCTCCC	CAGCTGAATC	1080
	TTTCCACCTG	GAGTCCCTGG	GAATACCGGA	CGTGATCTTC	TTTATAGGT	CCAATGATGT	1140
	GACCCAGTCT	TGCACTTCTG	GGAGATCAAC	CACCATCCGC	GTCAAGTGCA	GTCCACAGAA	1200
	AACGTCTCTC	GGAGGTTTGC	TGCTGCCAGG	AACGTGCTCA	GATGGGACCT	GTGATGGCTG	1260
	CAACTTCCAC	TTCTGTGTGG	AGAGGCGCGC	TGCTTGCCCG	CTCTGCTCAG	TGGCTGACTA	1320
55	CCATGCTATC	GTACAGAGCT	GTGTGGCTGG	GATCCAGAA	ACTACTTACG	TGTGGCGAGA	1380
	ACCCAAAGCTA	TGCTCTGGTG	GCAATTTCTC	GCCTGAGCAG	AGAGTCAACA	TCTGCAAAAC	1440
	CATAGATTTT	TGGCTGAAGA	TGGGCATCTC	TGCAGGCACC	TGTACTGCCA	TCTGTCTCAC	1500
	CGTCTTGACC	TGCTACTTTT	GGAAAAAGAA	TCAAAACTA	GAGTACAAAT	ACTCCAAGCT	1560
	GGTGATGAAT	GCTACTCTCA	AGGACTGTGA	CTTGCCAGCA	GCTGACAGCT	GCGCCATCAT	1620
60	GGAAGGGCAG	GATGTAGAGG	ACGACCTCAT	CTTTACAGC	AAGAAGTCA	TCTTTGGGAA	1680
	GATCAAAATCA	TTTACCTCCA	AGCAGCCAGC	TCTGTCTACC	ATCTCTCTTT	CAGAGGACTC	1740
	CTGATGGATT	TGACTCAGTG	CGCTGAAGA	CATCCTCAGG	AGGCCAGAC	ATGGACCTGT	1800
	GAGAGGCACT	GCCTGCCCTCA	CCTGCTCCT	CACCTTGCA	AGCACTTTG	CAAGCCTCGG	1860
	GCGATTTGGG	TGCCAGCATC	CTGCAACACC	CACCTGTGGA	AATCTCTTCA	TTGTGGCTTT	1920
65	ATCAGATGTT	TGAATTTTCA	ATCTTTTTTT	ATAGAGTACC	CAAACTCTCC	TTTCTGCTTG	1980
	CCTCAAACTT	GCCAAATATA	CCCACTTTT	GTTTGTAAAT	TATGCCCTTG	CTTGTATCTT	2040
	GTTTCCCAAA	ATGGCCCATC	CGCCAGAGCC	ATAGCTTGGT	CTGCTCATAA	TTCTTATAGC	2100
	TTTGGAAATGA	AAATATTTCT	ATCTTCTTAA	GTATAGAAAC	TATTTCTCTC	GTCTCTTAAC	2160
	TTAAGGGCAG	AAACAGCTGG	GAGTTTTCCT	CGCATGCCCT	CAGCTCATGA	TCTCTTTCAGG	2220
70	AGAGAGGCTG	GGTGAGGAGG	GTGTGGGGGT	TCCCTGGTGG	ATAATCTTCA	TAGCAGCCTG	2280
	GATCCATTTT	CCCTGGATAA	CCAGCTCAAA	GGGAGTGAAA	ATGGTAGTCT	GAGGGCAAGG	2340
	GGAGCAAGGC	CTGGGTGAAGA	AAAGCCTTGA	AAAGCATAAA	AAGAGGCGGG	GCGCGTGGC	2400
	TCACGCTGTG	AATCCCGACA	CTTTGGGAGG	CGAGGCGGGG	CAGATCATGA	GGTGGGAGAA	2460
	TTGAGACCAT	CCTGGCTAAC	ACGGTGAAGC	CCGCTCTCTA	CTGAAAATAC	AAAAAATTAG	2520
75	CGGGCGGTG	TGGCGGGTGC	CTGTGGTCCC	AGCTACTCGG	GAGGCTGAGG	CGGGAGAAAT	2580
	GCGTGGGCTT	GGAAGGCGGA	GCTTGCAGTG	AGCCGAGATC	GCGCCACTGC	ACTCCATCCA	2640
	GCTGGGTGA	CAGAGTGAGA	CTCTGCCTCA	AAAAAAGAAA	AAAAAAGAAA	AAGCACAAGG	2700
	AGAGGCAACA	AGGAATGTTT	TGTTTGTGA	GACAGGCTCT	CACCTGTGCA	CCTAGGCTGG	2760
	AGTGAGTGG	CGTAATCACT	GTTCAGTGCA	GCTCAAGCT	CTTGGGCTCA	GGCTATCCTC	2820
80	CCATCTCAGC	CTCTCAAGTA	GCTGGGACTA	CGAGTGTGCA	CCACCAGGCT	CACATATTTT	2880
	TGTGTTTTTT	GTAGACACGG	GGTTTCACCG	TGTTGCCAG	GCTGTCTCTC	AACTCCTGGG	2940
	CTCAAGTGT	CTGTCCGCTT	CGGCCTCCCA	AACTGTCTGG	ATTACAGGCA	TAAGCCACTG	3000
	CACCTCAGCT	TTTATTTGTT	TTTTAAACCA	CGTAGCTCAT	TGCTTCTCTC	TAAGTAAATG	3060
	ATAGATATTC	TCACTGAAGC	CAAAGGAATA	AGTTTCATCA	GAAAAAGGCC	AAAGCCCTGG	3120

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TGGATACATC CTCCTATCT TTTTTTAA CCTTCCACTA TCACCTATG AACTGAAAA 3180  
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GACATAGCAA ACCCTGTCAG TGAGGAAAAT TCCCATCCT TGAGTGCCCC CGTCTAGAA 3300  
GTTTGGGCCA TATTATGGAA CAGGGGTCTC TTATTGAAA AGAGCACAAG GAGGCCAAGA 3360  
TTTTAATGGG GCACCTTAGG GGATACAGCC CACAATGGCA TGGGCTGAG GTGGCCGTGA 3420  
TGTCGTCTTC TAAGCTTAAC GCATCTGCTC AGGCACAGAA TAAACGTCTA GGCTGGCCAA 3480  
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TGCTGCCCTG GCAATGGCTT TGTAAAGTC AATGAGAAT AGAGCCAGGC TGTGGTCCCT 4200  
GGCCATCAAC AGTGTGGTG ACGCCAGGA GTCCCTTGG TTTAATAAAT CCAGTTTTC 4260  
TTTGGGTATC CAAATTCCTC CTCTCTTGG TAGGAGTCAG GCTCTCAGAA CCTGTGTCCA 4320  
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CAAAGGCCAC AGACAGCCCT TAGACTATT CCGAAAACAGT AGGAAAAAT ACATATGTCT 4500  
TTGACTTCTT TATTCTGACT CCACCTGATT TAGCCATAAT ACTTTAAGGA GCTACTTTT 4560  
ACTACCCCTT ACCGTGCTGA CTTCTGAGG TCTGCCCTGT GACCTGTGAG GAACCTCTGA 4620  
GTTACGCTAC TGGGGTACC TGTGTCTCC CTAGCAAGT AGGCATGTCA TATATTTT 4680  
ACAGCTTAT TGAGATATAA TTCACATATT ATACAATTCA CCTTTAAAC ATACGATTCA 4740  
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CCTCCCACT AGCTGGGATT ACAGGCATGC GCCACCAAGC CTAGCTAATT TTTGTGTTT 4980  
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ATCCACCCAC CTCGCCCTCC CAAAGTGTG GATTTGACAG TGTGAGCCAC CGTGCTGGC 5100  
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ATACAATGA AGATTGTGT GTATTCAAGC AGTAGGGTTT TTGCTTTTGT TTTTGTTTA 5340  
GTGCCAACAA AACTTTTTT TGTCTGACTA CATTAAAGAT AAGACTGACT ATATTATAC 5400  
AACAGAAATC TTCTTATAGA TTTTTCAGC TTTGTGAAT CGAATTTTTT TTCATCAGG 5460  
CTGGTTGGAT TTCTTTTTA CCTGTAACT CAAGCGTAA TAGTTTGTGA GAAGATGGGT 5520  
TATTGCATGT CACTTTTTT TTTTGTAAA ATAAAAACAT ACCTTAC 5567

Seq ID NO: C216 DNA Sequence

Nucleic Acid Accession #: NM\_004864.1

Coding sequence: 26-952

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ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACG AGGCTGCGGG CCAACAGAG 240  
CTGGGAAGAT TGAACACCG ACCTGTCTCC GGCCCTGCA GTCCGGATAC TCACGCCAGA 300  
AGTGCGGCTG GGAATCCGCG GCACCTGCA CCTGCTATC TCTCGGGCGG CCTTCCCGA 360  
GGGGCTCCCC GAGGCTCCC GCCTTCACCG GCTCTGTTTC CGGCTGTCTCC GAGCGGGTC 420  
AAGGTGTGGG GAGCTGACAC GACCGCTGCG GGTCTGAGTC AGCCTTGCAA GACCCCAAGC 480  
GCCCGCGCTG CACCTGCGAG TGTGCGCGCC GCGGTGCGAG TCGGACCAAC TGCTGGCAGA 540  
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CCGCAAGCGG CGTGGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGG GTTGCTGCCG 660  
TCTGCACACG GTCGGCGGCT CGCTGGAAGA CCTGGGCTGG GCGGATTTGG TGCTGTGGCC 720  
ACGGGAGGTG CAGATGACCA TGTGATCGG CGGTGCCCC AGCCAGTTCC GGGCGGCAAA 780  
CATGCAAGCG CAGATCAAGA CGAGCTGCA CGGCTGAAG CCGACACGG AGCCAGCGCC 840  
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TTATTTATTA TTAATTTAT GGGGTGAAC TCTTGGGAC TCGGGGGCTG GTCTGATGGA 1140  
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AAAA 1204

Seq ID NO: C432 DNA Sequence

Nucleic Acid Accession #: NM\_052858.1

Coding sequence: 54..1259

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80

1 11 21 31 41 51  
GGCACGAGGT GTTGCCCTCA GGTGCTCTCC GGGGCGGAC ACGGAACCG GCCATGGAAG 60  
ATCCGTGCGG GGTCTGCGAG CCCCGGGCCC GGCGAGAGA GCGGAGCCG GACCGCGCC 120  
CCACCCAGAA CCAAGCGCGC ACCCAAGATC GACCGCGGGA CCGACCCGGG GACCCGCGCA 180  
GGAAGCGAAG CAGCGACGGG AACCGGCGAA GGGACGGGGA CCGGACCCG AAGAGAGACC 240  
AGGAGAGGGA CCGGAACCGG GACCGGAACC GGGACCGGGA GAGGAGAGGA GAGAGGGAAA 300  
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AACACGAGGT TTGGGAAAA CGCGGCAAA GCGGAGCGG GAGCGGAGCC CGGGGACTGA 420  
CCTGGGACGC AGCGCGCCT CCGGGGCGG CGCCTGGGA AGCCCGGAG CCGCGCAGC 480



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 CAGGGGGCTA CACGGGCATC ACCAGCTTGG GGGGCATTTA CTACTATCAG TTCGAGGGGG 780  
 CTTACAGTGG CTTTGATGGT GCTGACGGGG AGAAGGCCCA GCAACTGGAT GTCCAGTTCT 840  
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 AGGGCTACCG AAAAGTTAGG AAGCTAAAAG AGAAGCCAGC AGAAATGTTT GAATTTTAA 1260  
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 TAAATACAAA AAAAATTAGC CAGGCGTGGT GCGGGCGGCC TGTAAATCCA GCTACTTGGG 1680  
 AGGCTGAGCG AGGAGAATCG CTTGAATCTG GGAGGCGGAG ATTGCAGTGA GCCGAGATCC 1740  
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Seq ID NO: C434 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 261..2861

1 11 21 31 41 51  
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 CGGCGCGGGG AGCCAGCGGG GCTGAGCGCG GCCAGGCTCT GAACCCAGAT TTCACGACT 120  
 AGCTACCACT CGCTTGTGCC ACGCCCGGG AGCTCGCGGC GCCTGGCGGT CAGCGACCA 180  
 ACGTCCGGGG CGCTGCGCT CTTGGCCCGG GAGGCGGTAC ACTGTCTCGG CTACAGACCC 240  
 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGSCCA 300  
 35 TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCCTGG GGCACATACC ACAGTGGCTG 360  
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 ACCATGTGCA TATGGCCGAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT 480  
 CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT 540  
 40 TGCGAAACCG GCACATCTCG ATTGACAAAG GAGGAGAGCT GCATGCTGGG AGTGCCTCT 600  
 GCGCTTTCCA GGGCAATTTT ACCATCATTT TGTATGGAAG GGCTGATGAA GGTATTGAGC 660  
 CGGATCCCTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTTGAGTTGC 720  
 ATGGAGTGA AAGCTCTCTC TGGACATTTT TGAACAAGAC CCTTCACCCA GGTGGCATGG 780  
 CAGAAAGGAG CTATTTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA 840  
 45 TGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA 900  
 AAGAGAGTGA ACGTCTGGTC CAGTATTTGA ACGCGGTGCC CGATGGCAGG ATCCTTTCTG 960  
 TTGCACTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA 1020  
 AATTGGGAAG CAACACCTTC CTGCACTCTG GATTTAGACA CCCTTGGAGT TTTCTAAGT 1080  
 TGAAAGGAAA TCCATCATCT TCAGTGGGAG ACCATATTGA ATATCATGGA CATGAGGCT 1140  
 50 CTGCTGCTGC CCGGTATTTC AAATTGTTCC AGACAGAGCA TGGGGAATAT TTCAATGTTT 1200  
 CTTTGTCCAG TGAAGTGGTT CAAGACGTGG AGTGGAGCGA GTGGTTGAT CATGATAAAG 1260  
 TATCTCAGAC TAAAGGTGGG GAGAAAATT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA 1320  
 TATGCAATCG TCCCATGTAT ATACAGGCCA CTACAATGGA TGGAGTTAAT CTCAGCACCG 1380  
 AGGTTGTCTA CAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT 1440  
 55 GCGGAGCTA CCGGTAGCGG TTCTCTGTG GGAAGCCTGT GAGGCCCAAA CTCACAGTCA 1500  
 CCATTGACAC CAATGTGAAC AGCACCAATC TGAACCTGGA GGATAATGTA CAGTCATGGA 1560  
 AACCTGGAGA TACCCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCGA GCAGAAAGAT 1620  
 TCCAGGTGCT TCCCTGCAGA TCTGCGGCC CCAACCAAGT CAAAGTGGCA GGGAAACCAA 1680  
 TGTACTGCA CATCGGGGAG GAGATAGAG GCGTGGACAT GCGGGGCGAG GTTGGGCTTC 1740  
 60 TGAGCGGAAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800  
 ACATCTGCAA TTCTTTGAC TTGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT 1860  
 TTAAGGCAGC AACTTGGAG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGTTGGGTC 1920  
 AGTACCCGAT TCACCTCCAC CTGCGCGGTG ATGTAGACGA AAGGGAGGT TATGACCCAC 1980  
 CCACATACAT CAGGACCTC TCCATCCATC ATACATTCTC TGCTGCGTC ACAGTCCATG 2040  
 65 GCTCCAATGG CTTGTGATC AAGGACGTG TGGGCTATAA CTCTTGGGC CACTGCTTCT 2100  
 TCACGGAAGA TGGGCGGAG GAAAGCAACA CTTTGTACCA CTGCTTGGC CTCCTGTGTA 2160  
 AGTCTGGAAC CTTCTCCCTC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCAGAGAGG 2220  
 ACTCTTACCC AGGGTACATC CCCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT 2280  
 GGATGGCCAA TACCAACAC AACCTCATCA ACTGTGCGCG TGCAGGATCT GAGGAAACTG 2340  
 70 GATTTTGGTT TATTTTTCAC CACGTACCAA CCGGCCCCCT CGTGGGAATG TACTCCACAG 2400  
 GTTATTGAGA GCACATTCCA CTGGGAAAT TCTATAACAA CCGAGCACAT TCCAATACC 2460  
 GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCAACGA GGCTCTGCC AAGGACAGC 2520  
 GGGCGTTCT CTCAATCATC TCTGCCAGAT ACAGCCCTCA CCAGGAGGCC GACCCGCTGA 2580  
 AGCCCGGGA GCGGCGCATC ATCAGACACT TCATTGCTTA CAAGAACCAAG GACCAAGGCG 2640  
 75 CCGGCTGGG CCGGCGGGAT GTGTGGCTGG ACAGCTGCCA TTTCAGAGGG GAGGCTCAGG 2700  
 AAGGCTCTT GCTTACAGGA ATGAAGGCTG GGGGCATTTT GCTGGGGGA GATGAGGCG 2760  
 CCTCTGGAAT GGCTCAGGGA TTCAGCCCTC CTGCGGCTG CTGCTGAAG CTGGTACTA 2820  
 CCGGGTGGCC CTTTGTCTAC GTCTCTCTGG CCCACTCATG ATGGAGAAGT GTGGTCAGAG 2880  
 GGGAGCAATG GCGTTTGTCT CTTATGAGCA CAGAGGAATT CAGTCCCGAG GCAGCCCTGC 2940  
 80 CTCTGACTCC AAGAGGGTGA AGTCCACAGA AGTGAAGTCC TGCTTAGGG CCTCATTTGC 3000  
 TCTTCTCCA GGAAGCTGAG CACAGGGGCG CTCAGGAGA CCTAGATGT GCTGTACTC 3060  
 CCTGGGCTG GGAATTCAGA GCTGGAAATA TAGAAAATAT CTAGCCCAAA GCCTTCATTT 3120  
 TAAACAGATG GGAAGGTGAG CCCCCAAGAT GGAAGAAAGC CACACAGCTA AGGAGGGGCC 3180  
 TGGGGAGGCC CACCTAGCC CTTGCTGCCA CACCACTTG CCTCAACAC CCGCCACAGA 3240  
 GTGCCAGGC ACTCCTGAGG TAGCTTCTGG AAATGGGAGC AAGTCCCTC GRAGGAAAGG 3300



5 AAATGACTAG AGTAGAATGA CAGCTAGCAG ATCTCTTCCC TCCTGCTCCC AGCGCACACA 3360  
 AACCCGCCCT CCCCTTGGTG TTGGCGGTCC CTGTGGCCTT CACTTGTTC ACTACCTGTC 3420  
 AGCCCGCCTT GGGTGACACG TAGCTGCAAC TCCCATTTGG TGCTACCTGG CTCTCCTGTC 3480  
 TCTGCAGCTC TACAGGTGAG GCCCAGCAGA GGGAGTAGGG CTCGCCATGT TTCTGGTGAG 3540  
 CCAATTGGGC TGATCTTGGG TGCTCTGAACA GCTATTGGGT CCACCCCACT CCCTTTCAGC 3600  
 TGCTGCTTAA TGCCCTGCTC TCTCCCTGGC CCACCTTATA GAGAGCCCAA AGAGCTCCTG 3660  
 TAAGAGGGAG AACTCTATCT GTGGTTTATA ATCTTGCAAG AGGCACCAAG GTCTCCCTGG 3720  
 GTCTTTGTAT GAACTACATT TATCCCCCTT CTGCCCCCAA CCACAACTC TTCTCTTCAA 3780  
 10 AGAGGGCCTG CTTGGCTCCC TCCACCCAAC TGCACCCATG AGACTCGGTC CAAGAGTCCA 3840  
 TTCCCCAGGT GGGAGCCAAC TGTACGGGAG GTCTTTCCCA CCAACATCTT TTCAGCTGCT 3900  
 GGGAGGTGAC CCAAGGCTC TGCTTTTAAA GATATGGCTG CTTCAAAGGC CAGAGTCACA 3960  
 GGAAGGACTT CTTCCAGGGA GATTAGTGGT GATGGAGAGG AGAGTTAAAA TGACCTCATG 4020  
 TCCTTCTTGT CCAAGGTTT GTTGAGTTTT CACTCTTCTA ATGCAAGGCT CTCACACTGT 4080  
 15 GAACCACTTA GGATGTGATC ACTTTCAGGT GGCCAGGAAT GTTGAATGTC TTGGCTCAG 4140  
 TTCAATTAAA AAAGATATCT ATTTGAAAGT TCTCAGAGTT GTACATATGT TTCACAGTAC 4200  
 AGGATCTGTA CATAAAGTT TCTTCTCTAA ACCATTCAAC AAGAGCCAAT ATCTAGGCAT 4260  
 TTTCTTGSTA GCACAAATTT TCTTATTGCT TAGAAAAATG TCCTCTCTGT TATTCTGTGT 4320  
 TGTAAGACTT AAGTGAGTTA GGTCTTTAAG GAAAGCAACG CTCCTCTGAA ATGCTTGTCT 4380  
 20 TTTTCTGTGT GCGGAAATAG CTGGTCCTTT TTCCGGAGTT AGATGTATAG AGTGTGTGTA 4440  
 TGTAACACTT TCTTGTAGGC ATCACCATGA ACAGAGATAT ATTTCTTATT TATTATTATT 4500  
 ATGTGCACTT CAAGAAGTCA CTGTCAAGA AATAAAGAA TGTCTTAAAT GTCATGATTG 4560  
 GAGATGTCCT TTGCATTGCT TGGAAAGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620  
 TTGGAATAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680  
 25 AAAAAAATAA AAAAAAATAA AA 4702

Seq ID NO: C217 Protein Sequence  
Protein Accession #: NP\_005805.1

30 1 11 21 31 41 51  
 MVGKMPVLVH TLCAVRVTVD AISVETPDQV LRASQGKSVT LPCTYHTSTS SREGLIQWDK 60  
 LLLTHTSRVV IWPFSNKNYI HGELYKNRVS ISNNAEQSDA SITIDQLTMA DNGTYECSVS 120  
 LMSDLEGNK SRVRLLVLP PSKPECIGIE ETIIIGNNIQL TCQSKESGPT PQYSWKRYNI 180  
 35 LNQEOPLAQP ASGGQVSLKN ISTDTSGYII CTSSNEEGTQ FCNITVAVRV PSMNVALYVG 240  
 IAVGVVAALI IIGIIYCCG CRGKDDNTED KEDARPNREA YBEPPEQLRE LSREREEDDD 300  
 YRQEBQRSTG RESPDHLDQ 319

Seq ID NO: C218 Protein Sequence  
Protein Accession #: Eos sequence

40 1 11 21 31 41 51  
 MGSRTFESPL HAVQLRWGPR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60  
 GFSVEFYRPG TDGVSVLVGA PKANTSQPOV LQGGAVYLCP WNASPTQCTP IEFDSKGSRL 120  
 45 LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVTCYLSL 180  
 DNPTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFQ GQILSATQEQ 240  
 IAESYYPEYL INLVGQQLQT RQASSIYDSS YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY 300  
 GYVTLILNGD IRSLYNFSGE QMASYFYGAV AATDVNGDGL DDLVVGAPLL MDRTPDGRPQ 360  
 50 EVGRVYVYIQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420  
 QQGVVVFPPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGNG YPDLIVGSFG 480  
 VDKAVVYRGR PIVSASASLT IFFAMFNPEE RSCSLEGNFV ACINLSFCLN ASGKHVADSI 540  
 GFTVELQLDW QKQKGGVRRR LPLASRQATL TOTLLIQNGA REDCREMKIY LRNESEFRDX 600  
 55 LSPHIALINF SLDPQAPVDS HGLRPLAHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660  
 GEQNHVYLG D KVALNLTFEA QNVGEGGAYE AELRVTAPE AEYSGLVHRP GNFSSLSCDY 720  
 FAVNQSRLLV COLGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFDQILSK NLNNSQSDVV 780  
 SFRLSVEAQA QVTLNGVSKP EAVLFPVSDV HPRDQPKKEE DLGPAVHVY ELINQGPSSI 840  
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPGSLHH QOKREAPSR 900  
 60 SASSGQPIKL CPEACFRLR CELGPLHQOE SQSLQLHFRV WAKTFLOREH QPFSLQCEAV 960  
 YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020  
 YKLGFFKRSI PYGTAMEKAQ LKPPATSDA 1049

Seq ID NO: C219 Protein Sequence  
Protein Accession #: NP\_002412.1

65 1 11 21 31 41 51  
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGFV 60  
 VEKLQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120  
 70 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180  
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSGLSHST DIGALMYPST 240  
 TFSGDVQLAQ DDIDGIAIY GRSQNPVQPI GPQTPKACDS KLTPDAITTI RGEVMFPKDR 300  
 FYMRTNPFYF EVELNFIISV WPLPLNGLEA AYEPADEDEV RPFKGNKYWA VQGQNVLEHY 360  
 75 PKDIYSSGFG PRTVKHIDAA LSEENTGKTY FPFVANKYRWY DEYKRSMDPG YPKMIAHDFP 420  
 GIGHKVDVAF MKDGFYFPFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C220 Protein Sequence  
Protein Accession #: Eos sequence

80 1 11 21 31 41 51  
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGFV 60  
 VEKLQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120  
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180  
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSGLSHST DIGALMYPST 240

5 TFSGDVQLAQ DDIDIGIAIY GRQNFVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300  
 FVMRTNPFYP EVELNFISVF WPQLFNGLEA AYEFADRDEV RFFKGKNKYWA VQGGQNVLHG 360  
 PKDIYSSFGF PRTVRIHDA LSEENTGKTY FFFVANKYWRV DEYKRSMDRG YPKMIARDFF 420  
 GIGHKVDVAF MKDGGFFYFFH GTRQYKFDPK TKRILTQKA NSWFNCRKN 469

Seq ID NO: C221 Protein Sequence  
 Protein Accession #: NP\_055146.1

10 1 11 21 31 41 51  
 MVRKPVVSTI SKGGYLQGNV NGRLPSLGNK EPPGOEKVQL KRKVTLLRGV SIIIGTIIGA 60  
 GIFISPKGVL QNTGSVQMSL TIWTVCGVLS LFGALSYAEL GTTIKKSGGH YTYILEVFGP 120  
 LPAFVRVWVE LLIRPAATA VISLAFGRYI LEPPFIQCEI PELAIKLITA VGITVVMVLN 180  
 SMSVSWASARI QIFLTPCKLT AILIIIVPGV MQLIKGQTQN PKDAFSGRDS SITRLPLAFY 240  
 15 YGMAYAGWF YLNFVTEVEE NPEKTIPLAI CISMATIGV YVLTNVAYFT TINAEELLS 300  
 NAVAVTFSEF LQNFSLAVP IFVALSCPGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360  
 RKHTPLPAVI VLHPLTMIML FSGDLDSLNL FLSPARWLF GLAVAGLTYL RYKCPDMHRP 420  
 SEKPLFIPAL FSPFCLFMAV LSLYSDPPST GIGFVITLTG VPAYLFIW DKPKRWFPRM 480  
 20 SEKITRTLQI ILEVVEEDK L 501

Seq ID NO: C222 Protein Sequence  
 Protein Accession #: NP\_003237.1

25 1 11 21 31 41 51  
 MGLAWGLGVL FLAHVCGTNR IPESGGDNV FDIPELTGAA RKSGSRLRV GPDSPSPAPR 60  
 IEDANLIPPV PDKFQDLVD AVRAEKGFLL LASLRQMKKT RGTLLALERK DHSQGVFSV 120  
 SNGKAGTDL SLTVQKGQHV VSVEEALLAT GQWKSITLTV QEDRAQLYID CEKMEAEELD 180  
 VPIQSVFTRD LASLARLRIA KGGVNDNFQV VLQNVRFVFG TTPEDILRNK GCSSSTSVLL 240  
 30 TLNNVNVNGS SPAIRTNVIG HKTDLQAIC GISCELSM VLELRGLRTI VTTLQDSIRK 300  
 VTENKELAN ELRRPPLCYH NGVQYRNNEE WTVDSCTECH QNSVTICK VSCPIMPASN 360  
 ATPDGECCP RCWPSDSADD GWSFSEWTS CSTSCNGIQ QRGRSCDSL NRCEGSSVQT 420  
 RTCHIQECDK RFKQDGGWSH WSPSSSCSVT CGDGVITRIR LCNSPSPQMN GKPCGEARE 480  
 TRACKDACP INGGWGPWSP WDCSVTCGG GVQKRSRLCN NPAPQFGKD CVGDVTENQI 540  
 35 CNKQDCPIDG CLSNPCFAGV KCTSYPDGSW KCGACPPGYS GNGIQCTDVD ECKEVPDADF 600  
 NNHGEHRCEN TDPGYNCLPC PPRFTGSQPF GQGVHEHATAN KQVCKPRNPC TDGTHDCNKN 660  
 AKCNYLGHYS DPMYRCECKP GYAGNGIICG EDTDLGWPEN ENLVCVANAT YHCKKNCNPN 720  
 LPNSGGEDYD KQDGDACDD DDDNDKIPDD RDNCPFHYNP AQDYDVRDDV GDRCDNCFYN 780  
 40 HNPDAQDTN NGEGDACAD LDGDGILNER DNCQYVYVND QRDTRMDGVG DQCDNCPLEH 840  
 NPQQLSDSDS RIDGTCNNQ DIDEHGHQNN LDNCPYVFNQ NQADHDKDGK GDACDHDDN 900  
 DGIPDDKNC RLVPNDQKD SDGDDGRDAC KDDPDHDSVP DIDDICPEN DISETDPRR 960  
 QMIFLDFKGT SQNDPNWVVR HQGKELVQTV NCDPGLAVGY DEFNAVDFSG TPFINTERDD 1020  
 DYAGFVFGYQ SSSRFVVMVM KQVTSQYWDY NPTRAQGYSG LSVKVVNSTT GPGEHLRNAL 1080  
 45 WHTGNTPGQV RTLWHDPRHI GWKDFYAYRW RLSHRPKTGP IRVVMYEGKK IMADSGPIYD 1140  
 KTYAGRLGL VVPSQEMVFF SDLYEEDRP 1170

Seq ID NO: C223 Protein Sequence  
 Protein Accession #: NP\_002183.1

50 1 11 21 31 41 51  
 MPLLWLRGFL LASCWIIVR SPTPGSEHGS AAPDCPSAL AALPKDVNS QPEMVEAVKK 60  
 HILNMLLKK RPDVTQPVPK AALLNAIRKL HVGKVGNGY VEIEDIGRR AEMNELMEQT 120  
 SEIITPAESG TARKTLHFEI SKEGSDLSV ERAEVWFLK VPKANRTRK VTIRLPQQK 180  
 55 HPQSLDTGE EAEVGLKGE RSELLLSEKV VDARKSTWV FVSSSIQRL LDQKSSLDV 240  
 RIACEQCQES GASLVLLGKK KKKKEEGEGK KKGGEGBGAG ADEEKEQSHR PFLMLQARQS 300  
 EDHPHRRRR GLECDGKVIN CCKKQFFVSF KDIGWMDWII APSGYBANYC EGECPSHIAG 360  
 TSGSSLSFHS TVINHYMRG HSPFANLKSC CVPTKLRPMS MLYYDDGQNI IKKDIQNMIV 420  
 60 EECGCS 426

Seq ID NO: C224 Protein Sequence  
 Protein Accession #: NP\_000086.1

65 1 11 21 31 41 51  
 MVPDTACVLL LTALALGASG QGQSPILGSDL GPQMLRELQR TNAALQDVND WLRQQVREIT 60  
 FLKNTVMBCD ACGMQSVRT GLPSVRPLH CAPGPCFPGV ACIQTESGGR CGPCPAGFTG 120  
 NGSHCTDVNE CNAHPCPPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180  
 70 INECETQGN CVFNSVCINT RGSFPQCGPQ PGFVGDAQSG CQGAQRFCP DGSPESECH 240  
 ADCVLERDGS RSCVCRVWGA GNGILOGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSSQ 300  
 EDVDRDGIGD ACDPDADGSD VFNKDNCPFL VRNPDQRNTD EDKWDACDN CRSQNRNDQK 360  
 DTDQDGRGDA CDDIDGDRRI RNQADNCPRV FNSDQKDSGD DGIGDADNDC PQKSNPDQAD 420  
 VDHDVFGDAC DSDQDQDGDG HQDSRDNCPV VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480  
 75 RDNCRFLVNP GQEDADRQGV GDVCQDDFDA DKVVDKIDVC PENAETLTD FRAFQTVVLD 540  
 PEGDAQIDFN WVVLQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDYAGFI 600  
 FGYQDSSSFY VVMWKQMEQT YWQANPFRV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660  
 ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRY EGPELVADSN VVLDITMRGG 720  
 80 RLGVFCFSQE NIINANLRYR CNDTIPEDYE THQLRQA 757

Seq ID NO: C225 Protein Sequence  
 Protein Accession #: NP\_612464

1 11 21 31 41 51

MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKKGKQA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSFG ANGIPTGTFGI PGRDGFKGK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120  
 GKIAECTFTTK MRSNSALRLVL FSGSLRLKCR NACCQRNYFT FNGAECSGPL PIEAIILYDL 180  
 GSPENNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240  
 LPK 243

Seq ID NO: C226 Protein Sequence  
 Protein Accession #: NP\_003216.1

1 11 21 31 41 51  
 MATMENKVIC ALVLVSMMLAL GTLABAQTTET CTVAPRERQNG CGFPFGVTPSQ CANKGCCFDD 60  
 TVRGVPWCFY PNTIDVPPEE ECEF 84

Seq ID NO: C227 Protein Sequence  
 Protein Accession #: NP\_056234.1

1 11 21 31 41 51  
 MPKRAHWGAL SUVLLILLNGH PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI 60  
 NLGFNSIQAL SETSPAGLTK LELLMHNGNE IPSIPDGALR DLSSLQVFKF SYNKLRLVITG 120  
 QTLQGLSNLM RLHIDHNKIE FIHPQAFNGL TSLRLHLLEG NLLHQLHPST PSTFTFLDYF 180  
 RLSTIRHLYL AENMVRLTLP SMLRNMPLLE NLYLQGNPWT CDCEMRWFLE WDAKSRGILK 240  
 CKDKAYEGG QLCAMCFSPK KLYKHEIHKL KDMTCLKPSI ESPLRQNRER SIEEEQEQEE 300  
 DGGSQLELEK FQLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHNLQT DPPDIDINAT 360  
 VALDFECPMT RENYEKLWKL IAYYSEVPVK LHRELMLSKD PRVSQYQRQD ADEEALYYTG 420  
 VRAQLIAEPE WVMQPSIDIQ LNRRQSTAKK VLLSYTYQYS QTISTKDTRO ARGRSWVME 480  
 PSGAVQRDQT VLEGQFCQLS CNVKASESPS IFWVLPDGS I LKAPMDPDFS KFSILSSGWL 540  
 RIKSMEPSDS GLYQCIQAVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPQN 600  
 ALAIPAEHLS WILPNRRIIN DLANTSHVYM LPNGTLSIPK VQVSDSGYYR CVAVNQGGAD 660  
 HFTVGITVTK KSGSGLPSKRG RRPKAKALSR VREDIVEDEG GSGMGDEBNT SRLLHHPKDQ 720  
 EVFLKTKDDA INQDKKAKKG RRLKILWKHS EKEPETNVAE GRRVPFESRRR INMANKQINP 780  
 ERWADILAKV RGINLPGKTE VPPLIKTTSP PSLSLEVTTP FPAVSPSPAS PVQTVTSAGE 840  
 SSADVPLLGE EEHVLTGISS ASMGLEHNNH GVILVEPEVT STPLEEVVDD LSEKTEBTS 900  
 TEGDLKGTAA PTLISEPYEP SPTLHTLDTV YEKPTHEETA TEGNSAADVG SSPEPTSSEY 960  
 EPPLDAVSLA ESEPMQYFDP DLETKSQPDE DKMKEDTFAH LTPTPTIWN DSSTSQLFED 1020  
 STIGEPGVPG QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLQGG NMLEGDPHSS 1080  
 RSSESEGGES KSITLDPSTL GIMSSMSPVK KPAETTVGTL LDKDTTIVTT TPRQKVAPSS 1140  
 TMSTHPSRRR PNRRRLRFPN KFRHRHKQTP PTTAPSETP STQPTQAPDI KISSQVESSL 1200  
 VPTANVDNTV NTPKQLEMEK NAEPTSKGTP RRGHGRPNK HRYTPSTVSS RASGSKPSPS 1260  
 PENKRNIVT PSSETILLPR TVSLKTEGYP DSLDYMTTTR KIYSSYPKVQ ETLFVYTKPT 1320  
 SDGKEIKDDV ATNVDKHKSD ILVTGESITN AIPTSRSLVS TMGEFKEESS PVGFGPTPTW 1380  
 NPSRTAQPCR LQYDIPVTTG GENLTDPLL KELEDVDFTS EFLSSLTVST PFHQEAGSS 1440  
 TTLSSIKVEV ASSQABTTTL DQDHELTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500  
 MSLGQTTTK PALPSPRISQ ASRDSKENVF LNYVGNPTE ATPVNNBGTQ HMSGFNLST 1560  
 PSSDDADAFNL STKLELEKQV FGSRSLEPRG DSQRQDGRVH ASEQLTRVPA KPILPTATVR 1620  
 LPEMSQAS RYFVTQSPPR HWINKPEITT YPSGALPENK QFTTPLRLST TIPLEPLHMSK 1680  
 PSIPSKFTDR RTDQFNGYSK VFGMNNIPEA RNPVGKPPSP RIPHYSNGRL PFFTNKTLSE 1740  
 PQLGVTRRRQ IPTSPAPVMR ERKVINGSYN RIHSHSTFHL DFGPPAPPLL HTPQTGSPS 1800  
 TNLQNLPMVS STQSSISFIT SSVQSSGSPH QSSSKFPAGG PPASKFWSLG EKPQLITKSP 1860  
 QTVSVTAETD TVPFCBATGK PKPFVTTKV STGALMTENT RIQRFELVN GTLVIRKQVQ 1920  
 QDRGQMCCTA SNLHGLDRMV VLLSVTVQQP QILASEYQDV TVYLGDTIAM ECLAKGPAP 1980  
 QISWIPFDRR VWQTVSPVES RITLHENRTL SIKEASPSDR GUYKCVASNA AGADSLAIRL 2040  
 HVAALPPVH QKLENIISLP PGLSIHICT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100  
 VFPNGTYLIR NLAPOKSGRY ECVANLVGS ARRTVQLANQ RAAANARITG TSPRRTDVRY 2160  
 GGTLKLDGSA SGPDPWPRILW RLPSKRMIDA LFSFDSRIKV FANGTLVKS VTDKADAGYL 2220  
 CVARNKVGDS YVVLKVDVVM KPAKIEHKEE NDHKVFGGD LKVDCAVTLG PNEISWSLP 2280  
 DGSVLNPFMQ SDDSGGRTRK YVVFNNGTLY FNEVGMREEG DYTCAENQV GKDEMRVRVK 2340  
 VVTAPATIRN KTYLAVQVPY GDVVTVACEA KGEPMPKVTV LSPTINKVPT SSEKYQIYQD 2400  
 GTLLIQKAQR SDSGNYTCLV RNSAGEDRKT VWIHNVPQPP KINGNPNPIT TVREIAAGSS 2460  
 RKLDIDCAEG IPTPRVLWAF PEGVVLPAFY YGNRITVHGN GSILDIRSLRK SDSVLQVCMA 2520  
 RNEGGEARLI VQLTVLEPME KPIPHDPIS KITAMAGHTI SLNCSAAGTP TPLVWVLPN 2580  
 GTDLQSGQQL QRFYHKADGM LHSGLSSVD AGAYRCVARN AAGHTERLVS LKVGKLPKAN 2640  
 KQYHNLSII NGETLKLCT PPGAGQGRFS WTLFNGMHLE GPQTLGRVSL LDNGTLTVRE 2700  
 ASVEDRGTYV CRMETEYGPS VTSIFVIVIA YPRITSEPT FVIYTRPGNT VKLNCMANGI 2760  
 PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820  
 KTTYIHFV 2828

Seq ID NO: C228 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MPGKTLIRTG APADYRVILK TSQDELDVPP DDISVRVMSS QSVLVSVDVP VLEKQKKVVA 60  
 SRQYTVRYRE KGELARNDYK QIANRRVLIE NLIFDVTVEF AVRSQGERD GKWSTSVQPR 120  
 TPESAPTTAP ENLNVWVNG KPTVVAASWD ALPETEGKVK VCLLDGTGLFS VSSFQPSAKS 180  
 PQNTFFHTPR LSNHLEQSPS PILETLALLP WMVCSLGNAI FSKSGPQTGE ANDLTPKPSL 240  
 SLCCQECSCST QKDFCLAYL IDIQTKQVKN DPQLEGSVFG PCFLFYFLTF MLDIGGFSPI 300  
 MCYEDFPVSS LTGNSLSKVA ASKADVQONT EDNGKPEKPE PSSSPSPAPA SSQHPSPVAS 360  
 PQGRNAKDLL LDLLKNILAN GGAPRKPQLR AKKAEELDLQ STBITGEEEL GSREDSFMS 420  
 SDTQDQKRTL RPPSRHGHV VAPGRTAURA RMPALPRREG VDKPGFSLAT QPRGAPPSA 480  
 SASPAHAST QGTSRPSLP ASLNDNDLVD SDEDERAVGS LHPKGAFAPQ RPALSPSRQS 540  
 PSSLVLRDSS VHPGAKPAS ARRTPHSGAA EEDSSASAPP SRLSPPHGGS SLLLTQPHL 600  
 SSPLSKGGKD GSDAPATNSN APSRSTMSSS VSHSLSSRTQ VSEGAASDG BSHGDGDRD 660

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GGRQAEATAQ TLRARPASGH PHLLRHKPPA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR 720  
 AHPRVPSHSD SHPKLSSGIH GDEEDEKPLP ATVVNDHVPS SSRQPISRGW EDLRRSPQRG 780  
 ASLHKESPIP ENPKSTGADT HPQGYSSLA SKAQDVQOST DADTEGHSPK AQPGSTDRHA 840  
 SPARPPAARS QQHPSPVPRM TPGRAPQEQP PPPVATSQHH PGQSRDAGR SPQSPRLSLT 900  
 AQGRFRPTSQ GRSHSSSDPY TASSRGMLEP ALQNDQDEAQ GSYDDSDTEV EAQDVRAPAH 960  
 AARAKEAAS LPKHQQVESP TGAGAGGDHR SQRGHAASPA RPSRPGGPQS RARVPSRAAP 1020  
 GKSEPPSKRP LSSKSQSVS AEDEEEEDAG FFKGGKEDLL SSSVPKWPSS STPRGGKDAD 1080  
 GSLAKEEREP AIALAPRGS LAPVKRPLPP PPGSSPRASH VPSRPPPSA ATVSPVAGTH 1140  
 PWPRYTTRAP PGHFTTTPML SLRQRMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVLV 1200  
 GSNKGPNQOR IINGPQGTGW VVDLDRGLVL NABGRYLQDS HGNPLRIKLG GDGRTIVDLV 1260  
 GTFVVSVDGL PLFGQGRHGT PLANAQDKPI LSLGGKPLVG LEVIKKTTHP PTTIMQPTTT 1320  
 TTPLPTTTTP RPTTATIMQP TTTTTPLPPT TPRPTTATTR RTTTRRPTTT VRTTTRTTT 1380  
 TTPKPTTPIP TCPPTGLERH DDDGNLIMSS NGIPECYAEE DEFSGLETDT AVPTTEAYVI 1440  
 YDEDEYFETS RPTTTEPST TATTPRVPE EGAISSFPPE EFDLAGRKRFP VAPYVTVLTK 1500  
 DPSAPCSLTD ALDHQVDSL DEIIPNDLKK SDLPQGHAPR NITVVAVEGC HSFVIVDWDK 1560  
 ATPGLVLTGY LVYSASYEDF IRNKFSTQAS SVTHLPIENL KPNTRYFFKV QAQNPHGYGP 1620  
 ISPSVSFVTE SDNPLLVVRP PGDELGGSHS LSNMIPATRT AMDGNM 1666

20 Seq ID NO: C229 Protein Sequence  
 Protein Accession #: NP\_003005.1

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30

1 11 21 31 41 51  
 MFLSILVALC LMLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60  
 YEELVDVNCV AVLRFFFCAM YAPICTLEPL HDPIKPKCKSV CQRARDDCEP LMKMYNHSWP 120  
 ESLACDELFP YDRGVCISPE AIUTDLPELV KWIDITFEDM VQERPLDVDC KRLSPDRCKC 180  
 KKKVPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTVVDV KBIFKSSSPI PRTPQVPLTN 240  
 SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300  
 KKKTAGRTSR SNPKPKGKGP PAKPASPKK NIKTRSAQKR TNPKRV 346

35 Seq ID NO: C230 Protein Sequence  
 Protein Accession #: NP\_005931.1

40  
45

1 11 21 31 41 51  
 MAPAAWLRSA AARALLPPML LLLLPFPPLL ARALFPDVHH LHAERRGQP WHAALPSSPA 60  
 PAPATQEAEP PASSLRPPRC GVPDPDSGLS ARNRQKRFVL SGRWEKTDL TYRIIRFPWQ 120  
 LVQEQVRQTM AEALKVWSDV TPLTFTVEHE GRADIMIDFA RYWHGDDLPF DGPGLLAHA 180  
 FFPKLTREGD VHPDYDETWT IGDDQGTDL QVAAREFGHV LGLQHTTAAK ALMSAFYTFR 240  
 YPLSLSPDDC RGQHLGYGP WPTVTSRTPA LGPQAGIDTN ETAPLEPDAP PDACEASFDA 300  
 VSTIRGELEF FKAGFVWRLR GGQLQPGYPA LASREWQGLP SPVDAAFEDA QGHINFFQGA 360  
 QYVWYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YPFRGRDYWR FHPSTRRVDS 420  
 VPPRRATDRL GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC 480  
 AEPANTFL 488

50 Seq ID NO: C231 Protein Sequence  
 Protein Accession #: NP\_076927

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1 11 21 31 41 51  
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFPF IIVIGIILI 60  
 LALAIGLGIH PDCSGKYRCR SSPKCIELIA RCDGVSDCKD GEDEYRCRV GGQNAVQLVF 120  
 TAASWKTMCV DDWKGHYANV ACAQLGFPSY VSSDNLVSS LEGQPREEFV SIDHLLPDDK 180  
 VTALHHSVVV REGCASHGHR TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240  
 LCGGSVITPL WIITAAHCYV DLYLPSWTI QVGLVSLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QVCLPNSEE NPPDGKVCWT SGWGATEDGG DASPVLNHAA 360  
 VPLISNKN CNRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVQERR LKWLVGATSF 420  
 GIGCAEVNKF GVTYRVSFL DWIHEQMERD LKT 453

65 Seq ID NO: C232 Protein Sequence  
 Protein Accession #: NP\_003211

70  
75

1 11 21 31 41 51  
 MLWKLTDNIK YEDCEDRHG TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP 60  
 PYQPIYPQSQ DPYSHVNDPY SLNPLHAQPO PQHPGWPGQR QSQESGLLHT HRGLPHQLSG 120  
 LDPRRDYRRH EDLLHGPHAL SSGLDLSTH SLFHAIEBVP HVEDPGINIP DQTVIKKGPV 180  
 SLSKSNSNAV SAIPINKNL FGVVNPNEV FCSVPGRLSL LSSTSKYKVT VAEVQRRLSP 240  
 PECLNASLLG GVLRRAKSKN GGRSLREKLD KIGLNLFAGR RKAANVTLLT SLVEGEAVHL 300  
 ARDFGYCET EPPAKAVAEF LNRQHSDFNE QVTRKNMLLA TKQICKEPTD LLAQDRSPLG 360  
 NSRPNPILFP GIQSCLTFFN LISHGFGSPA VCAAVTALQN YLTEALKAMD KMYLSNNPNS 420  
 HTDNNAKSSD KEEKHRK 437

80 Seq ID NO: C233 Protein Sequence  
 Protein Accession #: NP\_002979.1

1 11 21 31 41 51  
 MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKPIVDYSET SPQCPKPGVI 60  
 LLTKRGRQIC ADFNKKWQK YISDLKANA 89

Seq ID NO: C234 Protein Sequence  
 Protein Accession #: NP\_004054.1

	1	11	21	31	41	51	
5	MILQAHLSL	CLMLYLATG	YGQEGKFSGP	LKPMTFSIYE	GQEPSQIIFQ	FKANPPAVTF	60
	ELTGETDNIF	VIERBGLLYY	NRALDRETRS	THNLQVAALD	ANGIIVEGPPV	PITIEVKDIN	120
	DNRPTFLQSK	YEGSVRQNSR	PGKPFLLVNA	TDLDDPATPN	GQLVYQIVIQ	LEMINNVMYF	180
	QINNKTGAIS	LTREGSQELN	PAKNPSYNLV	ISVDMGGQS	ENSFSDTTSV	DIIVTENINK	240
	APKPVEMVEN	STDPHPKIT	QVRWNDPGAQ	YSLVDKEKLP	RFPFSIDQEG	DIYVTQPLDR	300
10	EKKDAYVPYA	VAKDYGKPL	SYPLEIHVKV	KDINDNPFTC	PSPVTVFVQV	ENERLQNSIG	360
	TLTAHDRDEE	NTANSFLNVR	IVEQTPKLEP	DGLFLIQTYA	GMLQLAKQSL	KKQDTPOYNL	420
	TIEVSDKDFK	TLCFVQINVI	DINDQIPIFE	KSDYGNLTLA	EDTNIGSTIL	TIQATDADEP	480
	FTGSSKILYH	IIKGDSEGR	GVDTPHTNT	GYVIIKKPLD	FETAAVSNIV	FKAENPEPLV	540
	FGVKYNASSF	AKFTLIVTDV	NEAPQSQHV	FQAKVSEDA	IGTKVGNVTA	KDPEGLDISY	600
15	SLRGDTRGWL	KIDHVTGEIF	SVAPLDREAG	SPYRVQVAT	EVGSSSLSSV	SEPHLILMDV	660
	NDNPPRLAKD	YTGLPFCHPL	SAPGSLIFEA	TDDDQHLFRG	PHFTFSLGSG	SLQNDWEVSK	720
	INGTHARLST	RHTFEEREY	VVLIRINDGG	RPPLEGIVSL	PVTFPCSCVEG	SCFRPAGHQT	780
	GIFTVGMVAG	ILLTLLVIG	IILAVVFIRI	KKDKGKDNVE	SAQASEVKPL	RS	832

Seq ID NO: C235 Protein Sequence  
Protein Accession #: NP\_004434.1

	1	11	21	31	41	51	
25	MARARPPPPP	SPPPGLLP	PPLLLP	LPAGCRALER	TLMDTKWVTS	ELAWTSHPES	60
	GWEEVSGYDE	AMNPRTYQV	CNVRESSQNN	WLRGTGFIWR	DVQRVYVELK	FTVRDCNSIP	120
	NIPGSCKETP	NLFYVADSD	VASASSPFWM	ENPYVKVDTI	AFDESFSRLD	AGRVTNKRVS	180
	FGPLSKAGFY	LAFQDQGACM	SLISVRAFYK	KCASTTAGFA	LFPETLTGAR	PTSLVIAPGT	240
	CIPNAVEVSV	PLKLYCNGDG	EMWVPVGACT	CATGHEPAAK	ESQCRPCPPG	SYKAKQGEGP	300
30	CLPCFPNSRT	TSPAASICTC	HNNFYRADSD	SADSACTTVP	SPPRGVISNV	NETSLILEMS	360
	EPRLDGRDD	LLYNVICKKC	HGAGGASACS	RCDNVEFVP	RQLGLTERRV	HISHLAHR	420
	YTPEVQAVNG	VSGKSPLP	YAAVNITNQ	AAPSEVPTLR	LHSSGSSSLT	LSWAPPERPN	480
	GVILDYEMKY	FEKSEGIAT	VTSQMSVQL	DGLRPDARYV	VQVRARTVAG	YQGYSRPAEF	540
	ETTSESGSGA	QQLQEQPLI	VGSATAGLVE	VVAVVIAIV	CLRKQRHSGD	SEYTEKLQYQ	600
35	IAPGMKVYID	PFTYEDPNEA	VREPAKEIDV	SCVKIEEVIG	AGEFGEVCRG	RLKQPGRRV	660
	FVAIKTLKVG	YTERQRDPL	SEASIMQPD	HPNIIIRLEGV	VTKSRPVMIL	TEFMENCALD	720
	SFLRLNDGGF	TVIQLVGLMR	GIAAGMKYLS	EMNVVHRDLA	ARNILVNSNL	VCKVSDPGLS	780
	RFLEDPSDP	TYTSSLGGKI	PIRNTAPEAI	AYRKFTSASD	VMSYGIWMVE	VMSYGERPYW	840
40	DMSNQDVINA	VEQDYRLPPP	MDCPTALHQL	MILDCHVRDRN	LRPKPSQIVN	TLDKLIIRNAA	900
	SLKVIASAGS	GMSQPLDRT	VPDYTTFTTV	GMWLDAIKMG	RYKESFVSAG	FASFDLVAQM	960
	TAEDLLRIGV	TLAQHQKIL	SSIQDMRLQM	NQTLFVQV			998

Seq ID NO: C236 Protein Sequence  
Protein Accession #: NP\_001795.1

	1	11	21	31	41	51	
45	MYVGVYLDKD	SPVYPGPARP	ASLGLGPANY	GPPAPPPAPP	QYPDFSSSYH	VEPAPAPPTA	60
	WGAPFPAPKD	DWAAAYGPGP	AAPAAASPASL	APGPPPDFSP	VPAPPGPGPG	LLAQPLGGPG	120
50	TPSSPGAQRP	TPYEMRRSV	AAGGGGSGK	TRTKDKYRVV	YTDHQRLELE	KEPHYSTRYT	180
	IRKSELAAN	LGLTERQVKI	WFQNRRAKER	KVNKKKQQQQ	QPPQPPMAHD	ITATPAGPSL	240
	GGLCPSNTSL	LATSSPMFVK	EEFLP				265

Seq ID NO: C237 Protein Sequence  
Protein Accession #: NP\_068813.1

	1	11	21	31	41	51	
60	MGSDRARKGG	GGPKDFGAGL	KYNSRHEKVN	GLEEGVEFLP	VNNVKKVEKH	GPGRWVVLAA	60
	VILGILLVLL	GIGFLVWHQ	YRDVRVQKVF	NGYMRITNEN	FVDAYENSNS	TEFVSLASKV	120
	KDALKLLYS	VPFLGPHYKE	SAVTAFSBGS	VIAYVSEFS	IPQHLVEEAE	RVMAEERVVM	180
	LPPRARSLKS	FVVTSVVAFP	TDSKTVQRTQ	DNSSCSFGLHA	RGVELMRFTT	PGFPDSPYPA	240
	HARQWALRG	DADSVLSLTP	RSPDLASCODE	RGSDLVTVYN	TLSPMEPHAL	VQLCGTYPSP	300
	YNLTFFSSQN	VLLITLITNT	ERRHPGFEBT	FFQLPRMSSC	GGRLRKAQQT	FNSFYYPGHY	360
65	PNIDICTWNI	EVPMNQHVKV	RKFPPYLLFP	GVPACTCPKD	YVEINGEKYC	GERSQFVVT	420
	NSNKITVRFH	SDQSYTDGTF	LAEYLSYDSS	DPCPGQFTCR	TGRCIRKELR	CDGWADCTDH	480
	SDELNCSODA	GHQFTCKNKF	CKPLFWVCD	VNDGDNDSDE	QGCSCPAQTF	RCSNGKCLSK	540
	SQQCNGKDDC	GDGSDASCP	KVNVTCTKH	TYRCLNGLCL	SKGNPECDGK	EDCSGDSDEK	600
	DCDCGLRSFT	RQARVVGTD	ADEGEWFWQV	SLHALGQCHI	OGASLISPWN	LVSAAHCYID	660
70	DRGFRYSDF	QWTAFLGLHD	QSQRSAFVQ	ERRLKRIISH	PPNDPTFDY	DIALLELEKP	720
	AEYSSMVRPI	CLPDASHVFP	AGKAIWVTGW	GHTQYGGTGA	LILQKGEIRV	INQTTCEML	780
	PQITPRMNC	VGFLSGGVDS	CQGDSCGGLS	SVEADGRIFQ	AGVVSWDGDC	AQRNKGVTY	840
	RLPLFRDNWK	ENTGV					855

Seq ID NO: C238 Protein Sequence  
Protein Accession #: Bos sequence

	1	11	21	31	41	51	
80	MPPFLLEAV	CVPLFSRVFP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMPLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQSSSTPH	LEFPLDSPST	QOEVKARIKR	120
	MVFKGGRTET	BLALKYLLHR	GLPGGRNASV	PQILIVTDG	KSQGDVALPS	QQLKERGVTV	180
	FAVGVRFRPM	BEIHALASEP	RGQHVLLABQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCZERTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCFFYSWK	RVFLTHPATC	YRTTCCPGPCD	300
	SQPCQNGGTC	VFEGLDGYQC	LCPLAFGGEA	NCAKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360

5 RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVFDLVWSL DGIPFRGGPT 420  
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480  
 EAVRAELEEI TGSFKHVMVY SDPDLFNQI PELQGLCSR QRPGRCTQAL DLVFMLD TSA 540  
 SVGPENFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVLT GGRGAEDAAV PAQKLNNNGI 660  
 SVLVVGVGVPV LSEGLRLLAG PRDSLHVAA YADLRYHQDV LIEWLCEGAK RPNVLCCKPSP 720  
 CMNEGSCVLQ NGSYRCKCRD GWGPHCENR FLRRP 755

10 Seq ID NO: C239 Protein Sequence  
 Protein Accession #: Eos sequence

15 1 11 21 31 41 51  
 | | | | |  
 MPFFLLLEAV CVFLPSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60  
 SVGKGSFERS KHAITVCDG LDISPERVRV GAFQFSSTPH LEFFLDSPST QQEVKARIKR 120  
 MVFKGRTET ELALIKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180  
 FAVGVRFPRW EELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPGPCD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDS SAGTTLDGFL 360  
 20 RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVFDLVWSL DGIPFRGGPT 420  
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480  
 EAVRAELEEI TGSFKHVMVY SDPDLFNQI PELQGLCSR QRPGRCTQAL DLVFMLD TSA 540  
 SVGPENFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 25 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVLT GGRGAEDAAV PAQKLNNNGI 660  
 SVLVVGVGVPV LSEGLRLLAG PRDSLHVAA YADLRYHQDV LIEWLCEGAK RPNVLCCKPSP 720  
 CMNEGSCVLQ NGSYRCKCRD GWGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780  
 RTPPSNYREG LGTEMVPTFM NVCAAPG 807

30 Seq ID NO: C240 Protein Sequence  
 Protein Accession #: XP\_097386.1

35 1 11 21 31 41 51  
 | | | | |  
 MPKSEPLGCL SPASRAPGSA AATGAWLPAA SGGPGPLGPP CTCPPRSLGR GRAGSRAGSS 60  
 PSGCVCVSGI LRVVSVGDPA SRRWVDLSN SEDLSLLTF MIVGTGGVGG GWARGWVPAQ 120  
 EKEVAEGSGH AGRGNRRRLQ RVYGARSWIL GRKPCQLRLL PASGGPVQPP PCPSPATACR 180  
 WGFKFGVAFW GAAQHPPLCR LGGGRVPSA TRTLDGF 217

40 Seq ID NO: C241 Protein Sequence  
 Protein Accession #: CAC03433

45 1 11 21 31 41 51  
 | | | | |  
 MLSSTDTFTA SWELVVRVDH PNEEQQKDV LRVSGDLHVG GVMLKLVEQI NISQDWSDEA 60  
 LWWEQKHCWL LKHTWTLDKY GVQADAKLLF TPQHKMLRLR LPNLKMWRLR VSPSAVVFKA 120  
 VSDICKILNI RRSEELSLK PSQDYFKKK KDKNNKEPI IEDILNLESS PTASGSSVSP 180  
 GLYSKIMTPI YDPINGTPAS STMTWFSDSF LTEQNCSTLA PSQPPQSPEA LADMYQPRSL 240  
 VDKAKINAGW LDSSRSLMEQ GQDEDEQLLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI 300  
 50 LLEBIDCTEB EMLIPALQY HISKLSLSAE TQDPAGESEV DEIBAALSNL EVTLEGGKAD 360  
 SLLEDITDIP KLDADNLKLF PKLLPKAFK QYWIFIKDTS IAYFNKLELE QGEPLKLNIL 420  
 RGCEVVPDYN VAGRKFGIKL LIPVADGME MYLRCDHENQ YAQWMAACML ASKGTMAADS 480  
 SYQPEVLNLL SFLEMKNRNS ASQVASSLEN MDMNPECFVS PRCAKHKHSK QLAARILEAH 540  
 QNVAQNPVLE AKLRFIQAMQ SLPEFGLTY LVRPKGSKKD DILGVSYNRL IKIDAATGIP 600  
 55 VTTWRFTNIK QMNVNWRQ VVIEFDQNVF TAFTCLSDAC KIVHEYIGGY IFLSTRSKDQ 660  
 NETLDEDLFH KLTGGQD 677

60 Seq ID NO: C242 DNA Sequence  
 Nucleic Acid Accession #: NM\_005170  
 Coding sequence: 337..918

65 1 11 21 31 41 51  
 | | | | |  
 GGGCGTGAGA AAGGOGACGG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TTA AAAACCA 60  
 GCGGCTCTGC CCGGCGCTGC GGAGACCTGG GAGAGTCGG CCGCACGCGC GGGACACGAG 120  
 CGTCCACAGC TCCCTGGCGC GTACGGCGCT CCACCACTAG GCTCTCTATC CCGGGCTCTC 180  
 AGACGACCTA GGAGCGCTGC CTTGGGGAGT TGCTTGGCGG CGCGGTGCCA GAAGCCCCCT 240  
 TGGGGCGCCA CAGTTTTCCT CGTCGCTCTC GGTTCCTCTG CTGCACTCTT CTGCGGCGCG 300  
 GCGGGGAACT GGAGCGGGCG GGTGGATGCA GCGCGATGG ACGGCGCAC ACTGCCAGG 360  
 70 TCCGCGCCCC CTGCGCCCCC GTCCCTGCTC GGCTGCGCTG CCGGCGGAG ACCCGCTCTC 420  
 CCGGAACCTG TGCGCTGCG CCGGCGGCG CGACCGGCCA CCGCAGAGAC CGGAGGCGGC 480  
 GCAGCGGCGG TAGCGCGCG CAATGAGCGC GAGCGCAACC GCGTGAAGCT GGTGAACCTG 540  
 GGCTTCAGG CGCTGCGGCA GCACTGCGG CACGCGGCG CAGCAAGAA GCTGAGCAAG 600  
 GTGAGAGCGG TGCGCTCAGC CGTGAGATAC ATCGCGCGCG TGCGAGCGCT GCTGGCGGAG 660  
 75 CACGAGCGCG TGCGCAAGCG GCTGGCGGGA GGGCTGAGGC CGCAGGCGGT GCGGCGGTCT 720  
 GCGCGCGCGG GCGCGCGAGG GACCACCGCG GTGCGCGCT CGCCCTCCCG CGCTTCTCTG 780  
 TCCCGGGGCC GCGGGGGCAG CTCGGAGGCC GGCTCCCGCG GTTCCGCTCA CTGCTGGAGC 840  
 GACAGCGGCT GCGAAGGCG GCTGAGTCT GCGGAGCGCG AGCTACTCGA CTCTCCAGC 900  
 80 TGGTTAGGGG GCTACTGAGC GCCCTCGACC TA 932

Seq ID NO: C243 Protein Sequence  
 Protein Accession #: NP\_060233.1

1 11 21 31 41 51

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MSGGHQLQLA	ALWFWLLMAT	LQAGFGRTGL	VLAADVESER	SAEQKAVIRV	IPLKMDPTGK	60
LMLTLEGVFA	GVAEITPAEG	KLMQSHPLYL	CNASDDNLE	PGFISIVKLE	SPRRAPRPL	120
SLASKARMAG	ERGAVALFED	ITEDRAAAEQ	LQQLGLTWP	VVLIWGNDAE	KLMEFYVKNQ	180
KAHVRIELKE	PPAWPDYDVW	ILMTVVGTIF	VIIILASVLRI	RCRPRHSRDP	PLQQTAWAI	240
SQLATRRYQA	SCROARGSWP	DSGSSCSSAP	VCAICLEEPS	EGQELRVISC	LHEFHRCVD	300
PWLHQHRTCP	LCVFNITBGD	SFSQSLGPSR	SYQEPGRRLH	LIRQHPGHAH	YHLPAAYLLG	360
PSRSAVARPP	RPGFPLPSQE	PGMGPRHHRF	PRAAHPRAPG	EQQLLAGAQH	PYAQGWGMSH	420
LQSTSQHPAA	CPVPLRRARP	PDSSGSGESY	CTERSGYLAD	GPASDSSSGP	CHGSSSDSVV	480
NCTDISLQGV	HGSSSTFCSS	LSSDFPLVY	CSPKGDPRV	DMQPSVTSRP	RSLSVSVVTG	540
ETQVSSHVHY	HRHRHHYKK	RFQWHGRKPG	PETGVQSRP	PIPRTPQPOE	PPSPDQQVTG	600
SNSAAPSRL	SNPQCPRALP	EPAPGPDAS	SICPSTSSLF	NLQKSSLSAR	HPQRKRRGGP	660
SEPTPGSRPQ	DATVHPACQI	FPHYTPSVAY	PWSPEAHPLI	CGPPGLDKRL	LPETPGPCYS	720
NSQPFVWLCLT	PRQPLEPHFP	GEGPSEWSSD	TAEGRPCYP	HCQVLSAQPG	SEEELEELCE	780
QAV						783

Seq ID NO: C244 DNA Sequence  
 Nucleic Acid Accession #: NM\_004289  
 Coding sequence: 493..1695

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1	11	21	31	41	51	
GCGCGCGCT	CGTCCACCGG	AGGAGCGGCG	GCCAGCGTGG	ACGGCGGCAG	CCAGGCTGTG	60
CAGGGGGGCG	GCGGGGACCC	CGAGCGGCT	CGGAGTGGCC	CCTTGGACGC	CGGGGAAGAG	120
GAGAAGGCAC	COGCGGAACC	GACGCTCAG	GTGCGGACG	CTGGCGGATG	TGCGAGCGAG	180
GAGATGGGG	TACTAAGAGA	AAAGCAGGAA	GCTGTGGATC	ATAGTTCCCA	GCATGAGGAA	240
AATGAAGAAA	GGGTGTCAGC	CCAGAAGGAG	AACTCACTTC	AGCAGAATGA	TGATGATGAA	300
AACAAAATAG	CAGAGAAACC	TGACTGGGAG	GCAGAAAAGA	CCACTGAATC	TAGAAATGAG	360
AGACATCTGA	ATGGGACAGA	TACTTCTTTC	TCTCTGGAAG	ACTTATTCCA	GTTGCTTTCA	420
TCACAGCCTG	AAAATTCACT	GGAGGGCAGC	TCATTGGGAG	ATATTCTCTT	TCCAGGCAGT	480
ATCAGTGATG	GCATGAATTC	TTCAGCACAT	TATCATGTAA	ACCTTCAGCCA	GGCTATAAGT	540
CAGGATGTGA	ATCTCTCATGA	GGCCATCTTG	CTTTGTCCCA	ACAATACATT	TAGAAGAGAT	600
CCACAGCAG	GGACTTCACA	GTCACAAGAA	CCATTTCTGC	AGTTAAATTC	TCATACCAAC	660
AATCCTGAGC	AAACCTCTCC	TGGAACCTAAT	TTGACAGGAT	TTCTTTCAAC	GGTTGACAAT	720
CATATGAGGA	ATCTAACCAAG	CCAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTGTAT	780
GAGATAAACT	TAATGTCACT	GGCCACAGAA	GACAACTTTG	ATCCAATCGA	TGTTTCTCAG	840
CTTTTGTATG	AACAGAGATC	TGATTCTGGC	CTTTCTTTAG	ATTCAAGTCA	CAATAATACC	900
TCTGTATCA	AGTCTAATTC	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
ACTGACCATG	AATCTAGTTC	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
GAACCCAGTA	AGCTTTGTCA	CTTGGATCAA	AGTGATTCTG	ATTTCCATGG	AGATCTTACA	1080
TTTCAACAGC	TATTTATATA	CCCACTTAC	CACCTACAGC	CAACTGCACC	AGAATCTACT	1140
TCTGATGTGA	TTCGTGGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CTTGAAGAC	1200
ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTTGCATAT	CCCTTTTCT	1260
GTAGATGAAA	TTGTCGGCAT	GCCTGTTGAT	TCTTTCAATA	GCATGTTAAG	TAGATAATTAT	1320
CTGACAGAGC	TACAAGTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
GCTGGCAGCA	ACTGTGTGTA	ACGCAAAATG	GACATAATTT	TGAATTTAGA	AGATGATGTA	1440
TGTAACCTTC	AAGCAAGAAA	GGAAACTCTT	AAGAGAGAGC	AAGCACAATG	TACAAAGCT	1500
ATTAACATAA	TGAACAGGAA	ACTGCATGAC	CTTTATCATG	ATATTTTATG	TAGATTAGAA	1560
GATGACCAAG	GTAGGCCAGT	CAATCCCAAC	CACATATGCTC	TCCAGTGTAC	CCATGATGGA	1620
AGTATCTTGA	TAGTACCCAA	AGAACTGGTG	GCCTCAGGCC	ACAAAAGGAA	AACCCAAAG	1680
GGAAAGAGAA	AGTGAGAGAA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTTCA	1740
GAAACTGATT	ATTTGGATCA	GAAACCATTG	AAACTGCTTC	AAGAATTGTA	TCITTAAGTA	1800
CTGCTACTTG	AATAACTCAG	TTAAAGCTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
CTTCAAGATG	ACACTTGTGG	GCAATCTGGG	GGAGCCACAA	CTTTTCATGA	AGTGCATTGT	1920
ATACAAAAAT	CATAGTTATG	TCCAAAGAAT	AGGTTAAACAT	GAAAAACCCAG	TAAAGACTTTC	1980
CATCTGGGCA	GCCATCTCTT	TTAAGAGTAA	GTTGGTTACT	TCAAAAAGAG	CAAACTCTGG	2040
GGATCAAAAT	ATTTTAAGAG	GTATTTCACT	TTTAAATGCA	AAATAGCCTT	ATTTTCATTT	2100
AGTTTGTATG	CACATATAGT	AGCTTTTCAA	ACACTATTTT	AATCTTTATA	TTTAACCTAT	2160
AAATTTTGCT	TTCT					2174

Seq ID NO: C245 Protein Sequence  
 Protein Accession #: NP\_004433

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1	11	21	31	41	51	
MALRRIGAAL	LLPLLAAVE	ETLMDSTTAT	AELGWMVHPF	SGWEEVSGYD	ENMNTIRTYQ	60
VGNVFESSQN	NWLRTKPIRR	RGAHRIHVEM	KFSVRDCSSI	PSVPGSCKET	FNLYYYEADP	120
DSATKTFPNW	MENPVVKVDT	IAADESPSQV	DLGGRVMKIN	TEVRSFPGVS	RSGLYLAQD	180
YGGCMSLLAV	RVFYRKCPRI	IQNGAIFQET	LSGAESTSLV	AARGSCIANA	EEVDVPIKLY	240
CNGDGEMLVP	IGRCMKAGF	EAVENGTVCR	GCPSTGTFKAN	QGDEACTHCP	INSRTTSEGA	300
TNCVCRNGYD	RADLDPLDMP	CTTIPSAPQA	VISSVNETSL	MLEWTPPRDS	GGREDLVYNI	360
ICKSGSGSRG	ACTRGGDNVQ	YAPRQLGLTE	PRYIYIDLLA	HTQYTFEIQ	VNGVTDSQSP	420
SPQFASVNI	TNQAPSAVS	IMHQVSRVTD	SITLSWSQPD	QPNQVILDYE	LQYKERELSE	480
YNATAIKSPT	NTVTYQGLKA	GAIVVFQVRA	RTVAGYGRYS	GKMYFQMTSE	AEYQTSIQEK	540
LPLIIGSSAA	GLVFLIADV	IAIVCNRRRG	FERADSEYTD	KLQHYTSGHM	TPGMKIYIDP	600
PTYEDPNEAV	REFAKEIDIS	CVKIEQVIGA	GEFGEVCSGH	LKLPKREIF	VAIKTLKSGY	660
TEKQRDRFLS	EASIMGQPDH	PNVIHLEGVV	TKSTPVMIIT	BPMENGSLDS	PLRQNDGQPT	720
VIQLVGMMLRG	IAAGMKYLDL	MNYVHRDLAA	RNILVNSNLV	CKVSDFGLSR	FLEDDTSDPT	780
YTSALGKXIP	IRWTAPEAIQ	YRKFTSASDV	WSYGIVMWVW	MSYGERPYWD	MTNQDVINAI	840
EQDYRLPPFM	DCPSALHQLM	LDCWQKDRNE	RPKPGQIVNT	LDMIRNPNFS	LKAMAPLSSG	900
INPLLDRTI	PDYTSFNTVD	EWLEAIKMGQ	YKESPANAGF	TSFDDVVSQMM	MEDILRVGLT	960
LAGHQKILIN	SIQVMRAQMN	QIQSVFV				987

Seq ID NO: C246 Protein Sequence

Protein Accession #: NP\_114148.1

5 1 11 21 31 41 51  
 MDARRVPQKD LRVKKNLKFF RYVKLISMET SSSDDSDSDS PASDNFANTR LQSVREGCRT 60  
 RSQCRHSGLP RVAMKFPARS TRGATMKKAE SRQPSSENSVT DSNDSDEDES GMPLEKRAL 120  
 NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180  
 TRSRSRILGS LDALPMESEE EEDKYMLVRK RKTVDGYMNE DDLPRSSRRS SSVTLPHIIR 240  
 PVEEITEGGV GERLQQPSKR RYITVHWALL VINAVRLLI PKQTAETQTA GAPEASSVAP 300  
 10 AFETVMVKRS GMLCWIRTGI ARLVEESATA VSAGSEMDGV RLGLSLCI 347

Seq ID NO: C247 Protein Sequence  
Protein Accession #: NP\_036577.1

15 1 11 21 31 41 51  
 MENPSPAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60  
 PLFRPPAQWS SLIGAASDSD YSMWRKNQYV SNGLRDPFAER GEAWALMKEI EAAGEALQSV 120  
 HAVFSAPAVP SGTGQTSAEL EVQRHSLVS FVVRIVPSPD WFGVDSLDL CDGDRWREQA 180  
 20 ALDLYPYDAG TDSGTFPSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT 240  
 LVRLRQSPRA FIPFAPVLPF RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GRCGRIGTKS 300  
 RTRYVRVQPA NNGSPCELE EEAECVPDNC V 331

Seq ID NO: C248 Protein Sequence  
Protein Accession #: NP\_063947.1

25 1 11 21 31 41 51  
 MLQDPDSQPF LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60  
 YFLOGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPFEPG AVAVRLSKOR STLQVLD SAT 120  
 GWNFSACPDN FTALAEATAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180  
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWFWQV SIQYDKQHC GGSILDPHW 240  
 LTAACFRKH TDVFNKVKRA GSKLGSFPS LAVAKIIIE FNPMPKND IALMKLQFPL 300  
 TFSQTVRPIK LPFFDEELTP ATPLIIGWG PTKQNGGKMS DILLQASVQV IDSTRNADD 360  
 35 AYQGEVTEKM MCAGIPEGGV DTCQDSDGGP LMYQSDQHW VGVSWGYGC GGPSTPGVYT 420  
 KVSAYLNWLY NVWKAL 437

Seq ID NO: C249 Protein Sequence  
Protein Accession #: NP\_003036.1

40 1 11 21 31 41 51  
 MGCKVLINIG QQLRRKVVVD CSRETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60  
 NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGNLILS 120  
 45 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIAVI IILILTGLLT 180  
 LGVKESAMVN KIFTCINLV LGFIMVSGVF KGSVKNQLT EEDFGNTSGR LCLNNDTKEG 240  
 KPGVGGFMPF GFSGLVSGAA TCFYAFVGF D CIATTGEEVK NPQKAI PVGI VASLLICFIA 300  
 YFGVSAALITL MPMFYCLDNN SPLPDAFKHV GWGAKYAVA VGSLCALSAS LLGSMFMPMR 360  
 50 VIYAAEDGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLDV LMSIGTLAY 420  
 SLVAACVLVL RYQPEQNLV YQMASTSDLE DPADQNELAS TNDSQLGLFLP EAEMFSLKTI 480  
 LSPKNMEPSK ISGLIVNIST SLIAVLIIIT CIVTVLGRE A LTKGALWAVF LLAGSALLCA 540  
 VVTGVIWRQP ESKTKLSFKV PFLPVLPILS IFNVVYLMMQ LDQGTWVRFA VWMLIGFIY 600  
 FGYGLWHEE ASLDADQART PDGNLDQCK 629

Seq ID NO: C250 Protein Sequence  
Protein Accession #: NP\_002767.1

60 1 11 21 31 41 51  
 MRAPHLHLISA ASGARALAKL LPLLMAQLWA AEAALLPOND TRLDPEAYGA PCARGSQPWQ 60  
 VSLFNGLSEH CAGVLVDQSW VLTAAHCGNK PLWARVGDH LLLLQGEQLR RTRRSVVHFK 120  
 YHQSGSPILP RRTDEHDLML LKLARPVVPG PRVRALQLPY RCAQPGDQCQ VAGWGTTAAR 180  
 RVKYNKGLTC SSITILSPKE CEVFPYGVVT NNMICAGLDR GQDPQCSDSG GPLVCDDELQ 240  
 65 GILSWGVYPC GSAQHPAVYT QICKYMSWIN KVIKRN 276

Seq ID NO: C251 Protein Sequence  
Protein Accession #: XP\_095088.3

70 1 11 21 31 41 51  
 MTRAATAEPG RVSPASPARS TAGLPRAFLO SLRTLLDILD DWQRGCVHLR EIQLSNVEAR 60  
 ELPSGVLEGL SQRRGPQPGA AVSRRRGGAV PRGARAVPER CAGTETRRGR RCGSLQRLGG 120  
 75 GFRGCPADPC ARSGEHRHTI TSGVDCGLLK QMKELEQKE VLLQGLEMA QGRDWYQQQL 180  
 QQVQERQRL GQSRASADFG AVGSPRPLGR LLPKVQEVAR WLGLLAEAC AGRALPTSSS 240  
 GPPECALTST SSPGWQQII LMLKEQNRL TQEVTEKSER ITQLEQKSAL IKQLFEARAL 300  
 SQQDGLSLPA GPHIEPLTRF RLPVLTWAGA LLSPHSPQLL LPLSADSGGP LHLEPDTWFF 360  
 AVLLAVPSPG KRTAHARLHF HQRPAEGAWQ LGCGAEAAPE TCGTLPHFES HKTTCBPDSL 420  
 GGPCPQEGDR SWSHLGAADF VAPAVAKVTF NREDAAGSRH GDICPLCPKG LLTFRDIAIE 480  
 80 FSLAEWQCLD HAQONLYRDV MLENYRNLF S LGMTVSKPDL IACLEQNKEP QNKRNEWMA 540  
 KHPVTCSEFN QDLQPEQSIK DSLQKVIPT YGKCGHENLQ LKCKCKRVDE CEVHKGGYND 600  
 LNQCISNTQN KIFQTHKCVK VFSKPSNSNR HNARYTGKHK LKCKKYGKSF CMPSHLNQHQ 660  
 IIHTKEKSYK CEECGKSNH SSGTTHKRI LTGKCPYRCE EOGKAPRWP NLTRHKRIHT 720  
 GEKPYACEC GQAFRRSSTL TNHRIHTGE RPYKCECGK AFSVSSALIY HKRIHTGEKP 780  
 YTCECGKAP NCSSTLTKTH IIHTGEKPYT CEEGRTFNC SSTVKAHKRI HTGEKPYKCE 840



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ECDAKAFKWS SLAKHKIHT GEKPYKCSDS KALAKSSEVQ KVSXGDEGNG IRVHKKKETO 900  
 GWLVRNKNEN RTGLFQIRAA VRPNRDPDSWQ QOEGSLTDPI QRKEEPDLQN HYDHQNALED 960  
 QNRTGVGGLL TFRDVIIEFS LEEMQCLDHA QNLYRDVML ENYRNLVSLG IAVSKPDLIT 1020  
 CLEQNKEPWN IKRNMVTKH PDLPPELGIK DSLQKVIPRR YKSGHDNLQ VKTCKSMGEC 1080  
 EVQKGGCNEV NQCLSTTQNK IFQTHKCVKV FGKFSNSNRH KTRHTGKKHF KCKYKGSFC 1140  
 MVSQHLQHQI IHTRENSYQC EBCGKPFNCB STLSKHKRIH TGEKPYRCEE CGKAPTWSST 1200  
 LTKHRRHTG EKPYTCEECG QAFSRSSSTA NHKRIHTGEK PYTCEECGKA PSLSSSLTYH 1260  
 KRIHTGEKPY TCEECGKAFN CSSTLKKHKI IHTGEKPYKC KECGKAFAPS STLNTHKRIH 1320  
 TGEFPYKCEE CDKAFKWSSS LANHKSMTGT EKPYKCE 1357

Seq ID NO: C252 Protein Sequence  
 Protein Accession #: NP\_114433.1

1 11 21 31 41 51  
 MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWPHYKSN CYGYFRKLRLN WSDAELECOQS 60  
 YNGAHLASI LSLKEASTIA BYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSG 120  
 KSMGDNKICA EMSSNNFLT WSSNECNKRQ HFLCKYRP 158

Seq ID NO: C253 Protein Sequence  
 Protein Accession #: XP\_051860.2

1 11 21 31 41 51  
 MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK PVRPKLITVI DTNNVSTILN 60  
 LEDNVQSWKP GDTLVIASTD YSMYQAEFQ VLPSCRSCAPN QVKVAGKPMY LHIGSEIDGV 120  
 DMRAEVLGLS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIFPAGLGP AHLEGTELK 180  
 HMQQQLVGQY PIHFHLAGDV DERGGYDPPY YIRDLSTHHT FSRCTVHGS NGLLIKDVG 240  
 YNSLGHCFPT EDGPERNTF DHCIGLLVKS GTLLPSDRDS KMKCMITGDS YPGYIPKPRQ 300  
 DCNAVSTFW ANFNMLINC AAGSEETGF WPIFHHVPTG PSVGMYSFGY SEHIPGLGKY 360  
 NNRAHNSYRA GMIDNGVKT TEASAKDKRP FLSTISARYS PHQDADPLKP REPAIRHFI 420  
 AYKNDQHGAW LRGGDWLDS CRFADNGIGL TLASGGTFPY DDGSKQBIKN SLFVGESGNV 480  
 GTEMMDNRIW GPQGLDHSGR TLPICQNPFI RGIQLYDGPI NIQCTFRKP VALEGRHTSA 540  
 LAFRLNNAWQ SCPHNVGTI AFEDVPITSR VFFGEPGFWP NQLDMDGDKT SVFHDVDSV 600  
 SEYPGSYLTN NDNLVVRHPD CINVPDWRGA ICSGCYQAMY IQAYKTSNLR MKIINKDFPS 660  
 HPLYLBSALT RSTHYQQYQP VVTLLQGYTI HWDQTAPAEI AIWLINFNKG DWIRVGLCYP 720  
 RGTTFBILSD VHNRLKQTS KTGVPVRTLQ MDKVEQSYPG RSHYYWDEDS GLLFLKLAQ 780  
 NEREKPAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLPQSOLK 840  
 TKDHFLEVM ESKQHFFHL WNDPAYIEVD GKYPSSSEDG IQVVVDIGNQ GRVVSHTSFR 900  
 NSILQGIWQ LFNYVATIPD NSIVLMASKG RYVSRGPWTR VLEKLADRG LKLKEQMAFV 960  
 GFKGSFRPIW VTLDTEHKA KIFQVVPFV VKKKKL 996

Seq ID NO: C254 Protein Sequence  
 Protein Accession #: NP\_055188.1

1 11 21 31 41 51  
 MTALSSENC S FQYQLRQTQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT CQNFMEYFCI 60  
 SLAPVDLLLL VNISILLYFR DVLISIRPT KYHICLPTQI ISPTYGFLHY PVFLTACIDY 120  
 CLNFSKTKL SFKQKLFYP FTVILWISV LAYVLGDPAL YQSLKAQNAV SRHCPFYVSI 180  
 QSYWLSFWM MILKVAITC WEEVTLVQA IRTSYMNET ILYFPFSSHS SYTVRSKKIF 240  
 LSKLIVCFLS TWLPFVLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300  
 LKDIGLELDP FVNNKCFPI LTIPNLEQIE KPISIMIC 338

Seq ID NO: C255 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MALVLGSLLL LGLGNSFSG QPSSSTDAPK AWNYELPATN YETQDSHKAG PIGILFELVH 60  
 IFLYVVOQRD FPEDTLRKPL QKAYESKIDY DKIVYYEAGI ILCCVLGLLF IILAPLVGYF 120  
 FCMCRCCNKC GGEMHQKQKE NGPFLRKCPA ISLLVICIII SIGIFYGFVA NHQVRTRIQR 180  
 SRKLADSNFK DLRTLLNETP EKIYILAQY NTKDKAPTQ LNSINSVLGG GILDRLRPNI 240  
 IPVLDEIKSM ATAIKETKEA LENMNSTLKS LHQQSTQLSS SLTSVKTSLR SSLNDPLCLV 300  
 HPSSETCNSI RLISLSQLNSN PELRQLPPVD AELDNVNNVL RTDLGLVQQ GYQSLNDIPD 360  
 RVQRQTTTVV AGIKRVLNSI GSDIDNVTRQ LPIQDILSAF SVYVNNTEYS IHRNLPTLEE 420  
 YDSYWLGLL VICSLTLTIV IFYLLGLLGG VCGYDRHATP TTRGCVSNTG GVPLMVGVGL 480  
 SFLFCWILMI IIVLTFVFGA NVEKLICEPY TSKELFRLVD TPYLLNEDWE YYLSGKLPNK 540  
 SKMKLTPEQY YSDCKKNRGT YGTLHLQNSP NISEHLNINE HTGSISSLE SLKVNLIIFL 600  
 LGAAGRKNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLIS PAYDLEAKN SLPPGNLRNS 660  
 LKRDQTTKT IHQQRVLPIE QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFQANFITN 720  
 NTSSVIEET KYGRTIIGY FEHYLQWIEF SISEKVASC PVATALDTAV DVFLCSYIID 780  
 PLNLFWFGIG KATVFLPAL IFAVKLAKY RRMDSQDVVD DVETIPMKMN ENGNNGYHKO 840  
 HVGIGHNPVM TSPSQH 856

Seq ID NO: C256 Protein Sequence  
 Protein Accession #: NP\_149038.1

1 11 21 31 41 51  
 MKAIHLTLT ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT 60  
 PSFPTATSPA PPIIETHSSS TIPTAPPII STHSSSTIPI PTAADSESTI NVNLSATSDI 120  
 ITASSPDQL ITMVPSETQS NNEMSPTEED NQSSGPPTGT ALLETSTLNS TGPSNCPQDD 180  
 PCADNSLCVK LHNTSFLCL EGYVNSSTC KKGKVPFGKI SVTVSETFDP EEKHSMAVQD 240

5 LHSEITSLPK DVFGTSVYQ TVILTVSTSL SPRSEMRADD KFNVTIVTI LAETTSNEK 300  
 TVTEKINKAI RSSSSNPLNY DLTLRCDYVG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360  
 VASSLKCPDA CNAQHKQCLI KKSOGAPECA CVPGYQEDAN GNCQKCAFY SGLDCKDKFQ 420  
 LILITIVGTIA GIVILSMIIA LIVTARSNNK TKHIEENLI DEDFQNLKLR STGFTNLGAE 480  
 GSVFPKVRIT ASRDSQMNP YSRHSSMRP DY 512

Seq ID NO: C257 Protein Sequence  
 Protein Accession #: NP\_001423.1

10 1 11 21 31 41 51  
 | | | | |  
 MTAGRRMEL CAGRVPALLL CLGPHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60  
 AQVSITKCSS DMNGYCLRGQ CIYLVMSQN YCRCEVGYTG VRCEHFLIV HQPLSKEYVA 120  
 15 LTVILITLFL ITVVGSTYYP CRWYRNKRSK EPKKEYERTV SGDPFLPQV 169

Seq ID NO: C258 Protein Sequence  
 Protein Accession #: AAC63902.1

20 1 11 21 31 41 51  
 | | | | |  
 MDRSKENCIS GPVKATAPVG GPKRVLVTTQ IPCQNPLPVN SGOAQRVLCF SNSSQVRVPLQ 60  
 AQKLVSSEHK VQNKQKQQLQ ATSVPHVPSR PLNNTQKSKQ PLPSAPENNP EELASKQKN 120  
 ESKRKQNAL EDFEIGRPLG KKGFGNVILA REKQSKFILA LKVLFKAQLE KAGVEHQLRR 180  
 25 EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQRLSKFDE QRTATYITEL 240  
 ANALSYCHSK RVIHREDIKPE NLLLSGAGEL KIADFGWSVH APSRRRTTLC GTLDYLPPEM 300  
 IEGRMHDEKV DLWSLGLVLCY EPLVGKPPFE ANTYQETYKR ISRVEFTFD FVTEGARDLI 360  
 SRLLRHNPQS RPLMLREVLEH PWITANSKPK SNOQNKESAS KQS 403

30 Seq ID NO: C259 Protein Sequence  
 Protein Accession #: NP\_037504.1

35 1 11 21 31 41 51  
 | | | | |  
 MSRTAYTVGA LLLLGLTLLP AAEKKKKSQ GAIPPPDKAQ HNDSEQTQSP QPGSRNRGR 60  
 GQCRGTAMPG EEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120  
 QCNSEFYIPRH IRKEBGSFQS CSFCKPKKFT TMMVTINLCE LQPPTKKRV TRVKQCRCIS 180  
 IDLD 184

40 Seq ID NO: C260 Protein Sequence  
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51  
 | | | | |  
 MKVGVWLWIS FFTFDGHHG FLGKNDGIKT KKEILVNKKK HLGPFVEEYQL LLQVTYRDSK 60  
 EKRDLRNFLK LLKPPLLNWH GLIRIIRAKA TTDCLNGLV LQCTCEDSYT WFPSPCLDPQ 120  
 NCYLHTAGAL PSCECHLNL SQSVNFCERT KIWGTFKINE RPTNDLLNS SAIYSKYANG 180  
 IEIQLKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK 240  
 LPFLEDGSFR VFGKAQNDI VFGPGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300  
 50 LSLLEELNKN FPMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNISLSL 360  
 ASHFVRSNST MEDVISIADN ILSASVTNW TVLLREEKVA SSRLLSTLEN ISTLVPPPTAL 420  
 PLNPSERKPID WKGIPVNSQ LKRGYSYQIK MCPQNTSIP RGRVLIGSDQ FQRLPETII 480  
 SMASLTIGNI LPSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDPS 540  
 HLQWNDAGCH LVNETQDIPT CQCTHLTSFS ILMSPFVPST IFPVVKNTY VGLGISIGSL 600  
 55 ILCLIEALF WKQIKKSQTS HTRRIQMVNI ALSLLIADVN FTVGATVDTT VNPSSVCCTAA 660  
 VFFTHFYLS LFFWMLMGI LLAYRIILVF HHMAQHLMA VGFCLGYGCP LIISVITIAV 720  
 TQPSNTYKRR DVCWLNWSNG SKPLAFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR 780  
 DDKATIIIRVG KSLLLITPL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL 840  
 LDSKLRLQLF NKLSALSSWK QTEKQSSDL SAKPKFSKFP NPLQNKGHYA PSHTGDSSDN 900  
 60 IMLTQFVSN 910

Seq ID NO: C261 Protein Sequence  
 Protein Accession #: NP\_000575.1

65 1 11 21 31 41 51  
 | | | | |  
 MTSKLAVALL AAFILISAALC EGAVLFRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH 60  
 CANTEIIVKL SDGRELCIDP KENWVQRVVE KFLKRAENS 99

70 Seq ID NO: C262 Protein Sequence  
 Protein Accession #: NP\_005594.1

75 1 11 21 31 41 51  
 | | | | |  
 MSTERDSETT FDEDSQPNDE VVPYSDDETE DELDDQGS AV EPQNRVNRE AEENREPFRK 60  
 ECTWQVKAND RKYHEQPHFM NTKFLCIKES KYANNAIKTY KYNAPTIFPM NLFEQPKRAA 120  
 NLYPLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAKDL VDDVARHKMD KEINNRCEV 180  
 IKDGRFKVAK WKEIQGVQVI RLKKNDFVFA DILLSSSEP NSLCYVETAE LDGETNLKPK 240  
 MSLEITDQYL QREDTILATFD GFIECEPNM RLDKFTGTLF WRNTSPFLDA DKILLRGCVI 300  
 80 RNTDFCHGLV IFAGADTKIM KNSGKTRFKR TKIDYLMNYM VYTIFFVVLIL LSAGLAIGHA 360  
 YNEAQVGNSS WLYYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420  
 WDLQMYAEK DTPAKARTTT LNEQLGQIHY IPSDKTGLT QNIMTFKKCC INQIYGDHR 480  
 DASQHNHMK EQVDFSWNTY ADGKLAFVDH YLIEQIQSGK EPEVRQFFFL LAVCHTVMD 540  
 RTDQQLNYQA ASPDEGALVN AARNFGFAFL ARTQNTITIS ELGERTYV LAILDFNSDR 600  
 KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQSTQ DALDIPANET LRTLCLCYKE 660

5  
10  
15  
20  
25  
30

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IEEKFTMN KKFMAASVAS TNRDEALDKV YEEIEKDLIL LGATAIEDKL QDGPVETISK 720
LAKADIKIWI LTGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780
KFAPVQESP FPPGKNRALI ITGSMWLEIL LEKKTNRKI LKLFPRTEE ERRMRTQSKR 840
RLEAKKEQRQ KNFVLDACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVRM 900
IKTAHIGVGI SQEGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRYFFYKNPA 960
FTLVHFWYSF FNGYSAQTAY EDWFITLYNV LYTSLPVLLM GLLDQDVSDK LSLRFPGLYI 1020
VGQRDLLENY KRFFVSLHGH VLTSMILPFI PLGAYLQTVG QDGEAPSDVQ SFAVTIASAL 1080
VITVNFQIGL DTSYWTFFNA FSIFGSIALY FGIMFDFHSA GIHVLFPSPF QFTGTASNAL 1140
RQPYIWLIII LTVAVCLLPV VAIRPLSMTI WPSEDKIQK HRKRLKAEEQ WQRQVQVFR 1200
GVSTRRSAYA FSHQRGYADL ISSGRSIRK RSLDAIVAD GTAERYRTGD S 1251

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Seq ID NO: C263 Protein Sequence  
Protein Accession #: XM\_044533

15  
20  
25  
30

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1 11 21 31 41 51
| | | | |
MLRTAMGLRS WLAAPWALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
RFEAEHISNY TALLSRDGR TLYVGAREAL FALSSNLSPL PGGEYQELLW GADAEKKQQC 120
SPKGDQPRD CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED 180
GKGRCPFPFN FSKTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240
VASAIPESL GSIQQDDDKI YFFPSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
TSFLKAQLLC SRPDGFPFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
FTMKDVQVVF SGLYKEVNR TQMYTIVTTP VTPRPGACI TNSARERKIN SSLQLPDRVL 420
NFKLDHFLMD GQVRSRMLLL QPQARYQVVA VHRVPGLEHT YDVLFLGTGD GRLHKAVSVG 480
PRVHIIIEELQ IFSSGQPVQN LLLDTHRGLL YAAHSGVVQ VPMANCSLYR SCGDCLLARD 540
PYCAWSSSC KHVSLYQPOL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQVQ 600
FQNTVNTLA CPILSNLATR LMLRNGAPVN ASASCHVLT GDLLVLGTQD LGFQPCWSLE 660
EGFQQLVASY CPVVEDGVA DQTDGGSVF VTIISTSRVSA PAGGKASWA DRSYWKFLV 720
MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHKPT CFVVLPPETR PLNGLGPPST 780
PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS BIRDSVV 837

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Seq ID NO: C264 Protein Sequence  
Protein Accession #: NP\_008950.1

35  
40

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1 11 21 31 41 51
| | | | |
MASQNRDPAI TSVAARKGA EPSGGAARGP VGKRLQQLM TLMMSGDKGI SAFFESDNLF 60
KWVGTIHGAA GTVYEDLRYK LSLEFPFGYP YNAPTVMKLT PCYHFNVDQ GNICLDILKE 120
KWSALYDVRT ILLSIQSLLG EPNIDSPLNT HAAELWKNPT AFKKYLQETY SKQVTSQEP 179

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Seq ID NO: C265 Protein Sequence  
Protein Accession #: NP\_055399.1

45  
50  
55

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1 11 21 31 41 51
| | | | |
MGRGWGFLFG LLGAVVLLSS GHGEEQPPET AAQRCFCQVS GYLLDDCTCDV ETIDRFNNYR 60
LFPRLQKLE SDYFRYKYVN LKRPCPFWMD ISQCGRRDCA VKPCQSDVFP DGIKSASYKY 120
SEENANLIEE CEQAEIRLGA DESLSEBTQK AVLQNTKEDD SSDNFCEADD IQSPBAEYVD 180
LLNLPERYTG YKGPDAWKI NVIYEENCFK PQTIKRPLNP LASGQGTSEE NTFFYSWLEGL 240
CVERAFYRL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITEPQQRFDG ILTEGEGPRR 300
LNLYFLYLI ELRALSKVLP FFERPFDQLF TGNKIQDEEN KMLLEILHE IKSFPPLHFE 360
NSFFAGDKKE AHKLKEDFRL HFRNISRIMD CVGCFKRLW GKLTQGLGT ALKILFSEKL 420
IANMPESGPS YEFILTRQEI VSLPNAFGRI STSVKELENF RNLLQNIH 468

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Seq ID NO: C266 Protein Sequence  
Protein Accession #: NP\_002879.1

60  
65

```

1 11 21 31 41 51
| | | | |
MQPRRQLPA FWSGPRGPRP TAPLLALLL LAPVAAPAGS GGPDDFGQPQ DAGVPRRLQ 60
QKARAALHFF NFRSGSPSAL RVLAEVQSGR AWINPKEGCK VHVVFSTERY NPESLLQEGE 120
GRLGKCSARV FPKNQKPRPT INVTCTRLIE KKKRQQEDYL LYKQMKQLKN PLBITVSPDN 180
HGHIDPRLRL IWDLAFLGSS YVMWEMTTQV SHYYLAQLTS VRQWVRKT 228

```

Seq ID NO: C267 Protein Sequence  
Protein Accession #: NP\_005400.1

70

```

1 11 21 31 41 51
| | | | |
MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF 94

```

Seq ID NO: C268 Protein Sequence  
Protein Accession #: FGENESH predicted

75  
80

```

1 11 21 31 41 51
| | | | |
MLRQVLRRLG QSFCHRLGLC VSRHPVFFLT VPAVLITITFG LSALNRFQPE GDLERLVAPS 60
HSLAKIERSL ASSLPFLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA 120
VLEMKVNHKG YNYTFSHLCV LRNQDKKCVL DDIISVLEDL RQAASVNKTT ARVQVRYFNT 180
KLKVCSCFCL LPIKEAALHP LP 202

```

Seq ID NO: C269 Protein Sequence  
Protein Accession #: NP\_002429.1

	1	11	21	31	41	51	
5	MRLPLLVLFA	SVIPGAVLLL	DTRQFLIYNE	DHKRCVDAVS	PSAVQTAACN	QDAESQKFRW	60
	VSESQIMSV	FKLCLGVPSK	TDWVAITLYA	CDSKSEFQKW	ECKNDTLLGI	KGEDLFFNYG	120
	NRQEKINIMLY	KSGGLWSRWK	IYGTDDNLCS	RGYEAMYTLL	GNANGATCAF	PFKFENKMYA	180
	DCTSAGRSDG	WLNCGTTTDY	DTDRLFGYCP	LKFEGSESLSW	NKDPLTSVSV	QINSKSALTW	240
	HQARKSCQQQ	NAELLSITEI	HEQTYLTGLT	SSLTSGLWIG	LNSLSFNSGW	QWSDRSPFRY	300
10	LWNLPGSPSA	EPGKSCVSLN	PGKNKRWENL	ECVQRLGYIC	KKGNTTLNSF	VIPSESDVPT	360
	HCPSQWMPYA	GHCYKIHRE	KKIQRDALTT	CRKEGGDLTS	IHTIEELDFI	ISQLGYEPND	420
	ELWIGLANDIK	IQMYFWSMDG	TPVTFTKWL	GEPSHENNRQ	EDCVVMKGKD	GYWADRGCEW	480
	PLGYICKMKS	RSQGPETIVE	EKGCRCGWKK	HHFYCYMIGH	TLSTFAEANQ	TCNNENAYLT	540
	TIEDRYEQAF	LTSFVGLRPE	KYFWTGLSDI	QTKGTFQWTI	EDEVFRTWNN	SDMPGRKPGC	600
	VAMRTGIAGG	LWDVLKCEK	AKFVCKHWAE	GVTHPPKPTT	TEPEKCPEDW	GASSRTSLCF	660
15	KLVAKGKHEK	KTFWESRDFC	RALGGDLASI	NNKBEQQTIN	RLITASGSYH	KLFWLGLTYG	720
	SPSEGFTWSD	GSPVSYENWA	YGEFNYYQNV	EYCGELKGGP	TMSWMDINCE	HLNNWICQIQ	780
	KGQTPKPEPT	PAPQDNPPVT	EDGWVIYKDY	QYFYSKEKET	MDNARAFCKR	NFGDLVSIQS	840
	ESEKFLWKY	VNRNDQASAY	FIGLLISLDK	KFAMMDGSKV	DYVSWATGEP	NFANEDENCV	900
20	TMYSNSGFWN	DINGGYPNAF	ICQRENSGIN	ATTVMPTMPS	VPSGCKEGWN	FYSNCKCFKIF	960
	GFMEBERKMW	QEARAKACIGF	CGNLVSIQNE	KEQAFITYHM	KDSTFSAWVG	LNDVNSEHTF	1020
	LWTDGRGVHY	TNWGKGYPGG	RRSSLSYEDA	DCVVIIGGAS	NEAGKWMDDT	CDSKRGYICQ	1080
	TRSDPSLTNP	PATIQDGFV	KYKSSSYSLM	RQKQWHEAE	TYCKLHNSLI	ASILDOPYSNA	1140
	FAWLQMETSN	ERVWIALNSN	LTDNQYTWTD	KWRVRYTNWA	ADEPKLSAC	VYLDLDGYWK	1200
	TAHCNESFFV	LCKRSDIPA	TEPPQLPGR	PRSDHTANIP	FHGCYVIES	SYTRNMGQAS	1260
25	LECLRMGSSL	VSIESAAESS	FLSYRVEFLK	SKTNEWIGLP	RNVEGTWLWI	NNSPVSPVNW	1320
	NTGDPSEGERN	DCVALHASSG	FWSNIHCSSY	KGYICKRPKI	IDAKPHELL	TTKADTRKMD	1380
	PSKPSSNVAG	VVIIVILLIL	TGAGLAAYFF	YKKRRVHLQP	EGAFENTLYP	NSQSSPGTSD	1440
	MDLVGNIEQ	NEHSVI					1456

Seq ID NO: C270 Protein Sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	MVLLHWCLLW	LLFPLSSRTQ	KLPTRDEELF	QMQIRDKAPP	HDSSVIPDGA	EISSYLFRDT	60
	PKRYFPVVEE	DNTPLSVTVT	PCDAPLEWKL	SLQELPEDRS	GBGSGDLEPL	EQKQOIINE	120
	EGTELFSYKG	NDVEYFISSS	SPSGLYQLDL	LSTEKDTDFK	VYATTPESD	QYPPELPYDP	180
	RVDVTSLGRT	TVTLAWKPS	TASLLKQPIQ	YCVVINKEHN	FKSLCAVEAK	LSADDAFMA	240
	KPKGLDFSPF	DFAHFGPPSD	NSGKERSPQA	KPSPKLGHRV	YSRPKVDIQK	ICIGNKNIFT	300
40	VSDLKPDQY	YFDVFFVNIN	SNMSTAYVGT	FARTKEERAK	KTVELKDGKI	TDVFKRKA	360
	KFLRPAFVSS	HQKVTFPIHS	CLDAVQIQVR	RDGKLLLSQN	VEGIQQFQLR	GKPKAKYLVR	420
	LKGNKKGASM	LKILATTRPT	KQSPFSLPED	TRIKAFDKLR	TCSSATVAWL	GTQERNKFCI	480
	YKKEVDNWN	EDQKKREQNG	CLGPDIRKKS	EKVLCKYFHS	QNLQKAVTTE	TIKGLQPGKS	540
45	YLLDVVYIGH	GGHSVKYQSK	VVKTRKFC				568

Seq ID NO: C271 Protein Sequence  
Protein Accession #: AAH34229.1

	1	11	21	31	41	51	
50	MEKVQLEFEN	QEMKKLQEF	RSTRNKEKED	RESSEYWKKS	GKVGKLVNQS	YMSQNKGNV	60
	VKPSAGVKVL	KLLKEQIQEP	VKPTVNYIQA	NSSECEKPKI	NGKVCQCEN	KAALLVLEC	120
	GEDYCSGCPA	NVHQKALKL	HRTTLQARS	QILFNVLDA	HQPIKDVNPD	EPKEENNSTK	180
	ETSKIQHKKP	SVLLQSSSE	VEITTMKRAQ	RTKPRKSLLC	EGSFDEEASA	QSPQEVLSQW	240
55	RTGNHDDNKK	QNLHAAVKDS	LEECEVQTNL	KIWRBFLNIE	LKEDILSYME	KLWLKIGHRT	300
	PQEQQLFCYQ	IRSHIEMKPL	VMSVLRMKT	MKIVMVRPK	YNTQLFYCQ		349

Seq ID NO: C272 Protein Sequence  
Protein Accession #: NP\_078963.1

	1	11	21	31	41	51	
60	MEKMLWKHHR	RTPQEQLFKM	LSDTFPHPE	TTGDAQCSQN	ENDESDGEE	TKVQHTALLL	60
	PVETLNIERP	EPSLKIVELD	DTYEEFEPA	ENIVPYKVKL	ADADSQRSCA	FHDQCKNSFP	120
65	YENGHQHVF	FDKGRDFLN	LCLRNSSTY	KDNSKGETSN	TDFDNIVDPD	VYSSDIEKIE	180
	ESTSEFNLIK	EKNIGLESNQ	KSDSDCVSLE	SKOTLLGRDL	EKAPIEEKLS	QDIKESLELS	240
	NLYKRPSFEE	SKTTKSSLLL	QBIACRSKPI	TKQYQGLERF	PIFDTNERLN	LLPSHRLECN	300
	NSSTRITLAE	DREWIPDHS	SEYADNAIVL	GVLQGAQSPS	SSRKQQRMGQ	KSRPSTANF	360
	PLNSVKESS	SCLSSSHPRS	RSAAAQSSSR	AASEISEIEY	IDITDQNELS	LDQTTDQHTL	420
70	DNLEKELQVL	RSLADTSEKL	YSLTSEEFDP	FSSQSLNISQ	ISTDFLKTSH	VRGPGVEEL	480
	SCSGRDTKIQ	SLLSLSESST	DEEEDFLNK	QHVITLFWSK	ST		522

Seq ID NO: C273 Protein Sequence  
Protein Accession #: NP\_005399.1

	1	11	21	31	41	51	
75	MKVSALLLCL	LIMTAAPNPQ	GLAQPDALNV	PSTCCFTFSS	KKISLQRLKS	YVITTSRCPC	60
80	KAVIFRTKLG	KICADPKEK	WVQNYMKHLG	RKARTLKT			98

Seq ID NO: C274 Protein Sequence  
Protein Accession #: BAC05158.1

	1	11	21	31	41	51
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1348

GSYEYFVAEK AELSCWEEGN GRIALQGTLL NTYVCSILIR TIMEVGFIVG QYFIYGIFLT 180  
 TLHVCRSPC PHPVNCVSR PTEKNVFIVF MLAVAALLSL LSLAELYHLG WKKIRQRFVK 240  
 PRQHMAKCQL SGPSVGVQVS CTPPPDFNQC LENGPGGKFF NPFSNNMASQ QNTDNLVTEQ 300  
 VRGQEQTPGE GFQIQRVYGGK PEVPNGVSPG HRLPHGYHSD KRRLSKASSK ARSDDLVS 358

Seq ID NO: C281 Protein Sequence  
 Protein Accession #: NP\_055274.2

1 11 21 31 41 51  
 | | | | |  
 10 MYLSICCCFL LWAPALTKN LNYSPVEEQG AGTVIGNIGR DARLQPLP AERGGGGRSK 60  
 SSGSYRVLENS APHLLDVAD SGLLYTKQRI DRESLCRHA KCQLSLEVPA NDKBICMIKV 120  
 EIQDINDNAP SFSSDQIEMD ISENAAPGTR FPLTSAHDFD AGENGLRXYL LTRDDHGLFG 180  
 15 LDVKSRRDGT KFPELVQKA LDREQNHHT LVLTAIDGGE PPRSATVQIN VKVIDSNDNS 240  
 PVFEAPSYLV ELFENAPLGT VVIDLNATDA DEGPNGEVLY SFSSYVPRV RELFSIDPKT 300  
 GLIRVKGNDL YEENGMLDID VQARDLGPNP IPAHCKVTVK LIDRNDNAPS IGFVSVRQGA 360  
 LSEAAPPPTV IALVRVTDRD SGKNGQLQCR VLGGGGTGGG GGLGGPGGSV PFKLEENYDN 420  
 FYTVVTRPL DRETQDEYNV TIVARDGGSP PLNSTKSPAI KILDENDNPP RPTKGLYVLQ 480  
 20 VHENNIPGEY LGSVLAQDFD LGQNGTVSYS ILPSHIGDVS IYTVSVNPT NGAIYALRSF 540  
 NFEQTKAFEF KVLAKDSGAP AHLESNATVR VTVLDVNDNA PVIVLPTLQN DTAEIVPRN 600  
 AGSLGLVSTV RALDSDFGES GRITYEIVDG NDDHLFEIDP SSGEIRTLHP FWEDVTPVVE 660  
 LVVKVTDHGK PTLSAVAKLI IRSVSGSLPE GVPRVNGEQH HWDMSLELIV TLSTISIILL 720  
 AAMITIAVKC KRENKEIRTY NCRIAEYSHP QLGGGKGGKK KINKNDIMLV QSEVEERNAM 780  
 25 NVMNVSSPS LATSPMYDY QTRLPLSSPR SEVMYLPAS NMLTVPQGH GCHTSFTGQG 840  
 TNASETPATR MSIIQTDNFP AEPNMGSRQ QFVQSISVAP RLRTQKEPA 889

Seq ID NO: C282 Protein Sequence  
 Protein Accession #: NP\_005592.1

1 11 21 31 41 51  
 | | | | |  
 30 MELCRSLALL GSSLGLMFCL IALSTDFWFE AVGPTHSAHS GLWPTGHGDI ISGYIHVTQT 60  
 FSIMAVLWAL VSVSFTVLSC PPSLFPPGHG PLVSTTAFAA AAISMVYAMA VYTSERWDQP 120  
 35 PHPQIQTFPS WSPYLGWVSA ILLCTGALS LGAHCGGPRP GYETL 165

Seq ID NO: C283 Protein Sequence  
 Protein Accession #: NP\_006424.2

1 11 21 31 41 51  
 | | | | |  
 40 MATWALLLLA AMLLGNPGLV FSRLSPEYVD LARAHLRDEE KSCPCLAQEG PQGDLLTKTQ 60  
 ELGRDYRTCL TIVQKLKMW DKPTORSVSN AATRVCRTRG SRWRDVCRNF MRRYQSRVTQ 120  
 GLVAGETAQQ ICEDLRLCIP STGPL 145

Seq ID NO: C284 Protein Sequence  
 Protein Accession #: NP\_005594.1

1 11 21 31 41 51  
 | | | | |  
 50 MKVSAALAV ILIATLCAPI ASASPYSSDT TPCCPAYIAR PLPRAHKEY FYTSGKCSNP 60  
 AVFVTRKRNR QVCANPEKKW VREYINSLEM S 91

Seq ID NO: C285 Protein Sequence  
 Protein Accession #: NP\_071437.1

1 11 21 31 41 51  
 | | | | |  
 60 MAPGRAVAGL LLLAAAGLGG VAEGPGLAFS EDVLSVFGAN LSLSAAQLQH LLEQMGAASR 60  
 VGVPEPGQLH FNOCLTAESI FSLHGFSNAT QITSSKFSVI CPAVLQQLNF HPCEDRPHK 120  
 TRPSSHSEVWG YGFLSVTIIN LASLLGLILT FLIKKSYFFK ILTFPVGLAI GTLFSNAIFQ 180  
 LIPEAFGPDV KVDYSVEKAV AVFGGFYLLP FFERMLKMLL KTYGQNGHHT FGNDNFGPQE 240  
 KTHQPKALPA INGVTCYANP AVTEANGHIH FDNVSVVSLQ DGKEPSSCT CLKGPKLSEI 300  
 65 GTIAWMITLC DALHNFIDGL AIGASCTLSL LQGLSTSLAI LCEEPFHELQ DPFVILLNAGM 360  
 STRQALLFNF LSACSCYVGL AFGILVGNMF APNIIPALAG GMFLYISLAD MPPEMNDMLR 420  
 EKVTVGRKTD TFFMIQNAGM LTGPTAILLI TLYAGEIELE 460

Seq ID NO: C286 Protein Sequence  
 Protein Accession #: NP\_004175.1

1 11 21 31 41 51  
 | | | | |  
 75 MPNSEPASLL ELFNISATQG ELVRSKAGN ASKDEIDSAV KMLVSLKMSY KAAAGEDYKA 60  
 DCPGPNPAPT SNHGPDTEA EEDFVDPTV QTSSAKGIDY DKLIVRFGSS KIDKELINRI 120  
 ERATGQRFPH FLRRGIFFSH RDMNQVLDAY ENKKPFYLYT GRGPSSEAMH VGHILPFIPT 180  
 KWLQDVFNVP LVLIQMTDEK YLWKDLTLQD AYGDVENAK DIIACGPDIN KTFIPSDLDY 240  
 MGMTSSGPKY VVKIQKHVTF NQVKGIPGFT DSDCIGKISF PAIQAAFPSS NSFPQIFRDR 300  
 80 TDIQCLIPCA IDQDPYFRMT RDVAPRIGYP KPALLHSTFF PALQGAQTKM SASDPNSSIF 360  
 LTDATKQIKT KVNKHAFFSG RDTIEHRQF GGNCDVDVSF MYLTFPLEDD DKLEQIRKDY 420  
 TSGAMLTGEL KKALIEVLQP LIAEHQARRK EVTDEIVKEF MTPRKLSPDF Q 471

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP\_004929.1

	1	11	21	31	41	51	
5	MTVFRQENV	DYYDTGEEIG	SGQFAVVKKC	REKSTGLQYA	AKFIKKRRTK	SSRRGVSR	60
	IEREVSILKE	IQHPNVITLH	EVYENKTDVI	LILELVAGGE	LFDFLAEKES	LTTEEATEFL	120
	KQILNGVYVL	HSLQIAHFDL	KPENIMLLDR	NVPKPRIKII	DFGLAHRKIDF	GNEFKNIFGT	180
	PEFVAPEIVN	YEPLGLEADM	WSIGVITYIL	LSCASPFPLGD	TQKETLANVS	AVNYEFEDFY	240
10	PSNTSALAKD	FIRRLLVKDP	KKRMTIQDSL	QHPWIKPKDT	QQALSRKASA	VNMEKPKKFA	300
	ARKKWKQSVR	LISLCQRLSR	SFLSRSNMSV	ARSDDTLDEE	DSFVMAKIIH	AINDDNVPLG	360
	QHLLGSLSMY	DVNGPKNHGT	PPLLIAAGCG	NIQILQLLIK	RGSRIDVQDK	GGSNVYVWAA	420
	RHGHVDTLKF	LSNENKCPDLV	KDKSGEMALH	VAARYGHADV	AQVTCASAAQ	IPISRTKEEE	480
	TPLHCAAMHG	YYSVAKALCE	AGCNVNIKNR	EGETPPLLTAS	ARGYHDIVEC	LAHAGADLNA	540
	CDKDGHIHAL	LAVRRQMEV	IKTLLSQGCF	VDYQDRHGNT	PLHVACKDGN	MPIVVALCEA	600
15	NCNLDISNKY	GRTPLHLAAN	NGILDVVRYL	CLMGASVEAL	TTDGKTAEDL	ARSEQHEHVA	660
	GLLARLRKDT	HRGLFIQQLR	PTQNLQPRIK	LKLFHSGSGS	KTTLVESLKC	GLRSFFRRR	720
	RPRLSSTNSS	RFPSPPLASK	PTVSVSINN	YPCENVSVR	SRSMMFPEGL	TKQMLEVFWA	780
	PTHHPHCSAD	DQSTKAIDIQ	NAYLNGVDF	SVNEFSGNFV	YFCQDYFAA	NDPTSIVHVV	840
20	FSLEEPYBQ	LNPVIFWLSF	LKSLVPVEEP	IAFGSKLQNP	LQVVLVATHA	DIMNVPRPAG	900
	GEFGYDKDTS	LLKEIRNRFG	NDLHISNKL	VLDAGASGSK	DMKVLNRHLQ	EIRSQIVSVC	960
	PPMTHLCEKI	ISTLPSWRKL	NGPNQLMSLQ	QFVYDVQDQL	NPLASEEDLR	RIAQQHLSTG	1020
	BEINIMQSETV	QDVLLLDPRW	LCTNVLGKLL	SVETPRALHH	YRGRTYVEDI	QRLVPDSDE	1080
	ELLQILDAMD	ICARDLSSGT	MVDVPAIKT	DNLHRSWADE	EDEVVMVGGV	RIVPVEHLTP	1140
	FPGGIFHKVQ	VNLCRWLHQF	STEGDADIRL	WVNGCKLANR	GAELLVLLVN	HGGQIEVQVR	1200
25	GLSTEKIKCC	LLLSVCSCTI	ENVMATLPG	LLTVKHVLS	QQLREHHEPV	MIYQPRDFPR	1260
	AQTLKETSLT	NIMGGYKESP	SSIMCFGCHD	VYSQASLGMD	IHASDLNLLT	RRKLSRLDDP	1320
	PDLGKDWCL	LAMNLGLPDL	VAKYNTNNGA	PKDFLPSPLH	ALLREWTTPY	ESTVGTLMSE	1380
	LRGLRRDAA	DLLLKASSVF	KINLDGNGQE	AYASSCNSGT	SYNSISSVVS	R	1431

Seq ID NO: C288 Protein Sequence  
Protein Accession #: NP\_002072.1

	1	11	21	31	41	51	
35	MELRARGWWL	LCAAAALVAC	ARGDPASKSR	SCGEVRQIYG	AKGFSLSDVP	QAEISGEHLR	60
	ICPGGYTCCT	SEMEENLANR	SHAELETALR	DSSRVLQAML	ATQLRSFDDH	FQHLNDSE	120
	TLQATFPFAG	GLYTYQNARA	FRDLYSELRL	YVRGANLHLE	ETLAEFWARL	LERLFQKLEP	180
	QLLLPDDYLD	CLGKQAEALR	PFGEAPREL	LRATRAFAVA	RSFVQGLGVA	SDVVRKVAQV	240
40	PLGPECSRAV	MKLVCARHL	GVPGARPCPD	YCRNVKGLCL	ANQADLDAEW	RNLLDSMVL	300
	TDKFWGTSRG	ESVIGSVHTW	LAEAINALQD	NRDTLTAKVI	QCGGNPKVNP	QGPPEEKRR	360
	RGLKAPRERP	PSGTLEKLVS	EAKAQLRDVQ	DFWISLPGTL	CSEKMAALST	SDRCRWNGMA	420
	RGRYLPVEMG	DGLANQINNP	EVEVDITKPD	MTIRQQIMQL	KIMTNRLRSA	YNGNDVDVFD	480
	ASDDGSGSGS						490

Seq ID NO: C289 Protein Sequence  
Protein Accession #: AAH30205.1

	1	11	21	31	41	51	
50	MIILYLFL	LWEDTQGWGF	KDGIFHNSIW	LERAAGVYHR	EARGSKYKLT	YAEAKAVCEP	60
	EGGHLATYKQ	LEAARKIGFH	VCAAGWMAKG	RVGYPIVKPG	PNCGFGKTGI	IDYGIRLNRS	120
	ERWDAYCNP	HAKCCGVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGPFVGRYC	GDDELDDIIS	TGNVMTLKFL	SDASVTAGGF	240
55	QIKYVAMDPV	SKSSQGRNTS	TTSTGKNFL	AGRPSEL			277

Seq ID NO: C290 Protein Sequence  
Protein Accession #: NP\_001973.1

	1	11	21	31	41	51	
60	MRANDALQVL	GLLFSLARGS	EVGNSQAVCP	GTLNGLSVTG	DAENQYQTL	KLIERCEVVM	60
	GNLEIVLTGH	NADLSFLQWI	REVTGYVLVA	MNEFSTLPLP	NLRVVRGTQV	YDGKFAIFVM	120
	LNYNNTSSHA	LRQLRLTQLT	BILSGGVYIE	KNDKLCHMDT	IDWRDIVDRD	DAEIVVKDNG	180
65	RSCPPCHEVC	KGRCWGPGE	DCQTLTKTIC	APQCNHCFPG	PNNQCCHDE	CAGGCSGPQD	240
	TDCFACRHFN	DSGACVPRCP	QPLVYNKLTIF	QLEPNPHTKY	QYGGVCVASC	PHNFVVDQTS	300
	CVRACPPDKM	EVDKNGLKMC	EPCGGLCPKA	CEGTGSGSRF	QTVDSNIDG	FVNCTKILGN	360
	LDPLITGLNG	DPWHKIPALD	PERKLVFRIT	REITGYLANQ	SWPPHMNF	VFSNLTTIGG	420
	RSLYNRGFSL	LIMQNLNVT	LGFRSLKEIS	AGRIYISANR	QLCYHSLN	TKVLRGPTEE	480
70	RDLIKHNRPR	RDCVAGKVC	DPLCSGGGCV	GGPGQCLSC	RNYSRGGVCV	THCNFLNGEP	540
	REFAEAEFCF	SCHEPCQPMG	GTATCNGSGS	DTCAQCAHFR	DGPHCVSSCP	HGVLAGKGP	600
	YKYPDVQNEC	RPCHENCCTG	CKGPELQDCL	GQTLVLIGKT	HLTMALTVIA	GLVVFMMLG	660
	GTFLYWRGRR	IQNKRAMRRY	LKRGESIEPL	DPSEKANKVL	ARIKTELEL	KLKVLGSGVF	720
	GTVHKGVNIP	EGESIKIPVC	IKVIEDKSGR	QSFAVTDHM	LAIGSLDHAH	IVRLGLGCPG	780
75	SSLQLVTOYL	PLGSLDLHVR	QHRGALGPQL	LLNWGVQIAK	GMYYLEEHGM	VERNLAAENV	840
	LLKSPSQVQV	ADFGVADLLP	PDDKQLLYSE	AKTPIKMMAL	ESIHFQKYTH	QSDVMSYGV	900
	VWELMTFGAE	PYAGLRLEAV	PDLLEKGERL	AQPQICTIDV	YVMVVKCMMI	DENIRPTPKE	960
	LANEPTRMAR	DPPRYLVIKR	ESGPGIAPGP	EPHGLTNKLL	EEVELEPELD	LDDLEAEED	1020
80	NLATTTLGSA	LSLFPVGTNR	PRGSGSLSP	SSGYMPHNGQ	NLGGSCQESA	VSGSSERCPR	1080
	PVSLHMPFRG	CLASESSEGH	VTGSEALQE	KVSMCRSRSR	SRSRPRGDS	AYHSQRHSL	1140
	TPVTPLSPPG	LESEEDVNGV	MPDTHLKGTP	SSREGLTSSV	QLSSVLGTZE	EDEDEYEYEM	1200
	NRNRHSPHPP	PPRPSLLEEL	GYEYMDVSGD	LSASLGSTQS	CPLHFPVIMP	TAGTTPDEDY	1260
	EYVNRQRDGG	GGPGDYAAMG	ACPAEQGYE	EMRAFQGGH	QAPHVHYARL	KTLSLEATD	1320
	SAFDNFDYWH	SRLFPKANQA	RT				1342

Seq ID NO: C291 Protein Sequence  
Protein Accession #: NP\_001207.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MAPLCPSFWL PLLIPAPAPG LTVQLLLSL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60
      GEEDLPSEED SPRREDDPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG 120
      DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
10     ELLGFGQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLEHLHWG AAGRPGSEHT 240
      VEGHRFPAPAI HVVHLSTAFAP RVDEALGRPG GLAVLAAPLE EGPEENSAYE QLLSRLEEIA 300
      EEGSETQVPG LDISALLPSD PSRYFYQYEGS LTTTPCAQGV IWTVFNQVTM LSAKQLHTLS 360
      DTLWPGDGR LQLNFRATQP LNRGVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
      GLLFAVTSVA FLVQMRQRHR RGTGKGVSYR PAEVAETGA 459

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15 Seq ID NO: C292 Protein Sequence  
Protein Accession #: NP\_004198.1

```

20     1      11      21      31      41      51
      |      |      |      |      |      |
      MGGAVVDEGP TGVKAPDGGW GMAVLPGCFV ITGFSYAPFK AVSVFFKELI QEFGIGYSOT 60
      AMISSILLAM LVGTGPLCSV CVNRFGCRPV MLVGGLPASL GMVAASFPRS IIQVYLTTGV 120
      ITGLGLALNF QPSLIMLNRY PSKRRPMANG LAAAGSPVFL CALSPLOQLL QDRYGRGGF 180
      LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLDL SVFDRGFVL YAVAASVMVL 240
      GLFVPPVFPV SVAKDLGVPD TKAAPLLTLT GFIDIFARPA AGFVAGLGKV RPYSVYLFSP 300
25     SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGMVGALQF EVLMAIVGTH KFSASIGLVL 360
      LMEAVAVLVG PPSGGKLLDA THVMYVPFIL AGAEVLTSSL ILLLGNFCCI RKKPKRPQPE 420
      VAAAESEELH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465

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30 Seq ID NO: C293 Protein Sequence  
Protein Accession #: NP\_000349.1

```

35     1      11      21      31      41      51
      |      |      |      |      |      |
      MALFVRLAL ALALALGPAA TLGAPAKSPY QLVLQHSRLR GRQHGPNVCA VQKVIGTNRK 60
      YFTNCKQYQY RKICCKSTVI SYECCPGYEK VPGKGCPCAA LPLSNLYETL GVGSTTTQL 120
      YTDRETKLRP EMEGPGSPFI FAPSNEAWAS LPAEVLDSLV SNVNIELNA LRYHMVGRV 180
      LTDELKRGMT LTMQNSNI QIRHYPNGIV TVNCARLLKA DHATNGVVH LIDKVISIT 240
      NNIQIIEIE DTFETLRAAV AASGLNMLE GNGQYTLAP TNEAFEKIPS ETLNRILGDP 300
      EALRDLNHN ILKSAMCAEA IVAGLSVETL EGTTLVGCSS GDMLTINGKA IISNKDILAT 360
40     NGVIHYDEL LIPDSAKTLF ELAAESDVST AIDLFRQAGL GNLSSGSERL TLLAPLNSVF 420
      KDGTPIIDAH TRNLLNHHI KDQLASKYLY HGQTLTLGG KKLRFVYVRN SLCIENS CIA 480
      AHDKRGVGT LFTMDRVLT PGTVMVDVLK GDNRFSLVA AIQSAGLTET LNRGVYTVF 540
      APTNEAFRAL PPRERSRLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
      LKNVSVSNK EPPAEFDIMA TNGVVHVTN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660
45     SRASQSVRL APVYQLLER MKH 683

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Seq ID NO: C294 Protein Sequence  
Protein Accession #: NP\_006527.1

```

50     1      11      21      31      41      51
      |      |      |      |      |      |
      MTQRSIAGPI CNLKFVTLIV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLSN 60
      IKEMITEASF YLFNATKRRV FFRNLIKILIP ATWKAMNSK IKQESYEKAN VIVTDWYGAH 120
      GDDPYTLQYR GCGKEGKYIH FTFNPLNDN LTAGYGSRRG VFWHEAHLR WGVFDEYNND 180
55     KPPYINGNQY IKVTRCSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQATASI 240
      MFMQSLSSVV EFCNASTHNQ EAPNLQNMCM SLRSAMDVIT DSADPHHSFP MNGTELPPPP 300
      TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAAPFLM QIVEIHTFVG IASFDKSGEI 360
      RAQLHGINN DDKRLVSVL PTTVSAKTDI SICSLKKGK EVVEKLANGKA YGSVMILVTS 420
      GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLSELSRLT GGLKFFVVDI SNSNSMIDAF 480
60     SRISSTGCDI PQHQIQLEST GENVKPHEQL KNTVTVDNTV GNDTMTFLVTW QASGPPEIIL 540
      FDPDGRKYIT NNFTITNLTFR TASLWIPGTA KPGHWYITLN NTHSLQALK VVTTSRASNS 600
      AVPPATVEAF VERDSLHFPF PVMYIANVKQ GFYPIINATV TATVEPETGD PVTLRLLDDG 660
      AGADVIKNDG IYSRYFPSPA ANGRYSKLVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720
      IQMNAPEKSV GRNEEERKMG PSRVSSGGSF SVLGVPAGPH PDVFPCKII DLEAVKVEEE 780
65     LTLSTAPGE DFDQGGQTSY EIRMSKSLQN IQDDFNAIL VNTSKRNQQ AGIREIFTFS 840
      PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFI PP NSDPVPARDY 900
      LILKGLVTAM GLIGIICLII VVTHETLSRK KRADKKENG T KLL 943

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70 Seq ID NO: C295 Protein Sequence  
Protein Accession #: Eos sequence

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75     1      11      21      31      41      51
      |      |      |      |      |      |
      MKFLILLILQ ATASGALPLN SSTSLKKNV LFGERYLEKF YGLEINKLEF TKMKYSGNLM 60
      KEKIQEMQHP LGLKVTGLD TSTLEMMHAP RCGVPDVHHP REMPGGFPVR KHYITRINN 120
      YTPDMNREDV DYAIRKAFQV WSNVTPKFS KINTGMADIL VVFARGAGD FHAFDGKGGI 180
      LAHAFPGPSG IGGDAHFDEP EFWTHTHSGT NLFALTAVHEI GHSILGLHSS DPEAVMFPPT 240
      KYVDINTFRL SADDIRGIQS LYGDQKENQ LNPFDNSEPA LCDPNLSFDA VTTVGKIFF 300
80     FKDRFFWLKV SERPKTSVNL ISSLMPTLPS GIEAAEIEA RNQVPLFKDD KYWLIENLRP 360
      BENYPSKIDS FGFPNFVKKI DAAVFNPRFY RYFPVDNQY WRDERRQNM DPGYPKLITK 420
      NEQIGPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNWFQGC 470

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Seq ID NO: C296 Protein Sequence  
Protein Accession #: Eos sequence



1 11 21 31 41 51  
 5 MKFLILLLLQ ATASGALPLN SSTLEKNNV LFGERYLEKF YGLEINKLPV TOMKYSGNLM 60  
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHHP REMPGGPVWR KHYITYRINN 120  
 YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHD FHAFDGKGGI 180  
 LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHAI GHSLGLGHSS DPKAVMFPTY 240  
 KYVDINTPRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300  
 FKDRPFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360  
 10 EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRVDERRQMM DPGYPKLITK 420  
 NFGQIGPKID AVFYISNKYKY YFFQGSNQFE YDFLLQRITK TLKSNWSWFGC 470

Seq ID NO: C297 Protein Sequence  
 Protein Accession #: NP\_008883.1

1 11 21 31 41 51  
 15 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYFLLEAT DNDDIYGAAW 60  
 IGIFVGLCLF CLSVLGIQVI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120  
 20 FLKQMLERYQ NNSPPNDDQ WKNNGVTKTW DRLMLQDNCC GVNQPSDNQK YTSAFRTENN 180  
 DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNGQCYE LISGPMNRHA WGVAVFGFAI 240  
 LCWTFWVLLG TMYWSRIEY 260

Seq ID NO: C298 Protein Sequence  
 Protein Accession #: NP\_001784.2

1 11 21 31 41 51  
 30 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60  
 QEPALPSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHGRDWV VAPISVPENG 120  
 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLEN KPLDREEIAK 180  
 YELGHAUSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAITYTN GUVAYSLSHQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 35 TDMXDGSTT TAVAVVEILD ANDNAPMFDQ QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360  
 AWRATYLING GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVP VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMDE DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540  
 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNEEGD 600  
 40 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFPLPVL 660  
 GAVLALLFL LVLALLVRKK RKIKEPLLLP EDDTRDNVFP YGEEGGGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTIIIP TMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEEDD 829

Seq ID NO: C299 Protein Sequence  
 Protein Accession #: NP\_005620.1

1 11 21 31 41 51  
 50 MAKSAENGI YVSGDEKKG FLIAPGPDGA PAKGDGPVGL GTPGRLAVP PRETWTRQMD 60  
 FIMSCVGFAY GLGNVWREFY LCYKNGGGVF LIPYVLIALV GGIPIFFLEI SLGQPMKAGS 120  
 INVWNICPLF KGLGYASMI VPYCNTYYIM VLAWGFYVLV KSFTTLTPWA TCGHTWNTPD 180  
 CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVL RSGGLEVPGA LNWVETLCLL 240  
 ACWVLVYFCV WKGVSSTGKI VYFTATFPYV VLVLVLRGV LPLGALDGI YLKPDPNSKL 300  
 55 GSPQVWIDAG TQIFFSYAIG LGALTALGSY NFNNNCYKD AILALINSQ TSFFAGFVVF 360  
 SILGMAAEQ GHVHSKVAES GPGLAPIAYP RAVTLMVPAP LWAALFFFM LLLGLDSQFV 420  
 GVEGFIITGL DLLPASYIFR FQREISVALC CALCFVIDLS MVTGGMYVVF QLFDYYSAGS 480  
 TLLWQAFWE CVVAVNYGA DRFMDDIACM IGYRCPNMK WCNSFFTPLV CMGFIIFNVV 540  
 YYPELVNNT YVYPWNGEAM GWAPALSSML CVPLHLGLCL LRAKGTMAER WQHLTQPIWG 600  
 60 LHHLEYRAQD ADVRLTTLT FVSESSKVVV VESVM 635

Seq ID NO: C300 Protein Sequence  
 Protein Accession #: NP\_006507.1

1 11 21 31 41 51  
 65 MEPSSKKLTG RLMLAVGGAV LGSLLQPGYNT GVINAPQKVI EEPYNQTVWH RYGESILPTT 60  
 LTLNLSLVA IPSVGGMIGS FSVGLFVNRF GRNNSMLMN LLAFAVSALM GFSKLGKSPF 120  
 MLILGRFIIG VYCGLTTFPV PMYVGEVSPT APRGALGTLH QLGIVVGILI AQVFLDSIM 180  
 70 GNKDLWPLLL SIIFIPALLQ CIVLPFCPS PRPLLNRNE ENRAKSVLKK LRGTADVTHD 240  
 LQEMKEESRQ MREKKVITIL ELFRSPAYRQ PILIAVVLQ SQQLSGINAV FYYSTSIFEK 300  
 AGVQQPVYAT IGSGLVNTAF TVVSLPVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360  
 LPWMSYLSIV AIFGVAFPE VGGPIPWFI VAEFLSQGPR PAATAVAGFS NWTNPNFVGM 420  
 CFQYVEQLCG PYVPIIFTVL LVLEFFITFY KVPETKGRTF DEIASGFRQG GASQSDKTPE 480  
 75 ELPHPLGADS QV 492

Seq ID NO: C301 Protein Sequence  
 Protein Accession #: XP\_035292.2

1 11 21 31 41 51  
 80 MAGAGPKRRA LAAPAAEKEE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLINGVAITV 60  
 GTIIGSGIFV TPTGVLKEAG SPGLALVWVA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120  
 LEVYGSLLAF LKYMIELLII RPSSQYIVAL VFATYLLKPL PPTCFVPPEA AKLVACLCLV 180  
 LLTAVNCYSV KAATRVQDAF AAAKLALAL IILLGFPVIG KGDVSNLDPN PSFECTKLDV 240

5  
 GNIVLALYSG LPAYGGWNYL NFWTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300  
 STEQMLSEEA VAVDFGNVHL GVMSNIIPVF VGLSCPGSVN GSLPTSSRLF FVGSREGHLP 360  
 SILSMIHQQL LTPVPVSLVFT CVMTLTYAPS KDIFSVINFP SFFNWLCLVAL AIIGMIWLRH 420  
 RKPELERPIK VNIALPVFFFI LACFLIYAVS FWKTPVECGI GFTIILSGLP VYPPGVWVWKN 480  
 KPKWLLQGIF STTVLCQKLM QVVPQET 507

Seq ID NO: C302 Protein Sequence  
 Protein Accession #: NP\_005259.1

10  
 1 11 21 31 41 51  
 | | | | |  
 MNWSIFEGLL SGVNYKSTAP GRIWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60  
 SNVCDFEFPF VSVVRLMALQ LILVTCPSLL VVMHVAYREV QEKRHREANG ENSGRLYLNP 120  
 GKRRGGLMWT YVCSLVFKAS VDIAPLYVPH SFYPKYLPP VVKCHADPCP NIVDCPISKP 180  
 15  
 SEKNIFTLEM VATAAICILL NLVELIYLV S KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240  
 DDLSSGDLIF LGSDSHPLL FDRPRDHVKK TIL 273

Seq ID NO: C303 Protein Sequence  
 Protein Accession #: NP\_005121.1

20  
 1 11 21 31 41 51  
 | | | | |  
 MKICSLTLLS FILLAAQVLL VEGKKKVKNG LHSKVSEQK DTLGNTQIKQ KSRPGNKGKF 60  
 VTKDQANCRW AATFQEGEGIS LKVECTQLDH EFSCVFAGNP TSCCLKDER VYWKQVARNL 120  
 25  
 RSQKIDICRY S KTAVKTRVCR KDFPESSLKL VSSTLFGNTK PRKEKTEMSP REHIKGETT 180  
 PSSLAVTQTM ATKAPECVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC 234

Seq ID NO: C304 Protein Sequence  
 Protein Accession #: AAH22542

30  
 1 11 21 31 41 51  
 | | | | |  
 MCSEIILRQE VLKDGFRDL LKVKFGESEI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60  
 RNITEAVMVS AATFIEAPNY LKSESEVLIY ARDSQCIDC FQAFLPVHCR YHRPHSEDCG 120  
 35  
 ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180  
 WNKMKKYSY KNVILQVVG LTVHTSLVCS VTLLITILCS KKKKK 225

Seq ID NO: C305 Protein Sequence  
 Protein Accession #: NP\_004985.1

40  
 1 11 21 31 41 51  
 | | | | |  
 MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEVLY RYGYTRVAEM 60  
 RGEKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDIGRFQTF EGDWKWHHN 120  
 45  
 ITYMIQYSE DLPRAVIDDA PARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180  
 FDGKDGLLAH AFPPGPIQG DAHFDDEDLW SLGKGVVVT RFGNADGAAC HFPFIFEGRS 240  
 YSACTTDRS DGLFWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGSYS 300  
 ACTTIDGRSDG YRNCATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360  
 CTSEGRGDGR LWCATTSNFD SDKKWGFCDP QGYSLFLVAA HEFGHALGLD HSSVPEALMY 420  
 50  
 PMYRFTGEP LKCDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSE 480  
 PTAGTGPFP AGFTGPFTAG PSTATTVPLS FVDDACVNI FDAIAEIGNQ LYLEKDGKYW 540  
 RFSEGRGSR QCFPLIADKV PALPRKLDV FEEPLSKLFP FFSGRQVWVY TGASVLGPRR 600  
 LDKLGLGADV AQTGALRSR RGMILLFSGR RLWRFDVKAQ MVDPRSAVEV DRMPFGVPLD 660  
 55  
 THDVFQYREK AYFQCDRFYV RVSSRSRLNQ VDQVGYVTYD ILQCPED 707

Seq ID NO: C306 Protein Sequence  
 Protein Accession #: NP\_000204

60  
 1 11 21 31 41 51  
 | | | | |  
 MAGPRPSEFA RLLLAALISV SLSGTLANRC KKAPVKSCTE CVRVDRDCAY CTDEMFRDRR 60  
 CNTQABELLA GQQRRESIVM ESSPQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL 120  
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SGLTSDYITG PGKFVDKVS 180  
 65  
 PQTDMRPEKL KEPWNSDPP SFSEKVISLT EDVDEFENKL QGERISGNLD APEGGFDAI 240  
 QTAVCTRDI WRPDSTHLLV FSTESAFHYE ADGANVLGI MSRNDERCHL DTTGTYYQYR 300  
 TDQYPSVPTL VRLAKHNII PIFAVTNYSY SYYEKLHYTF PVSSIGVLQE DSSNIVELLE 360  
 BAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGVGVYQV QLRALREV 420  
 THVQQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480  
 70  
 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN 540  
 PQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600  
 CHCHQQLSYT DTICEINYS A IHPGLCEDLR SCVQCQAWGT GEKKGRITCE CNFKVMVDE 660  
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDG APGFNSTVLV HKKDCPPGS FWMLIPLLL 720  
 LPLALLLLL LCKYCACCK ACLALLPCN RGHMVGFKEH HYMLRENLMA SDHLDTPMLR 780  
 75  
 SGNLKGDDV RNKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTR 840  
 AQLRQVEEN LNEVYRQISG VHKLQQTFR QQPNAKKQD HTIVDTVIMA PRSAKPA 900  
 LTKGVQERA FHDLVAPGY YTLTADQAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL 960  
 LVEADVDVAG TATLGRLLVN ITIIEKQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020  
 80  
 KSGVSYRTQD GTAQNRDYI FVEGELLFQF GEAWKELQVK LLELQEVDSL LRGROVRRFH 1080  
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPHGDLGAP QNPNAKAAGS 1140  
 RKIHFNWLPF SGKPMGYRVK YWIQGDESE AHLLDSKVP S VELTNLYPYC DYEMKVCAYG 1200  
 AQGEGPYSSL VSCRTHQEV SEPGRAPNV VSTVTQLSW AEPATNGEI TAYEVCYGLV 1260  
 NDDNRPPIGM KKVLDNPKN RMLLIENLRE SQPYRYTVKA RAGAGWPPER EAINLATQP 1320  
 KRPMISPIIP DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPVSVDSDTG CGWKPEPLL 1380  
 EELDRLRRVTW RLPELIPRL SASSGRSSDA BAPTAPRTTA ARAGRAAAVP RSATPGPPGE 1440

5  
 HLVNGRMDFA FPGSTNSLHR MTTTSAAYG THLSPHVPHR VLSTSTLTLR DYNLSLTRSEH 1500  
 SHSTTLPRDY STLTSSVSSH SRLTAGVPDT PTRLVFSALG PTLRLVSNQSE PRCEPFLQGY 1560  
 SVEYQLLNGG ELHRLNIPNP AQTSSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES 1620  
 QVHPQSPCLP LFGSAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCM 1680  
 AQGGGPATAF RVDGDSPESE LTVFGLSENV PYKFKVQART TEGFPGPEREG IITIESQDGG 1740  
 PFPQLGSRAG LFGHPLQSEY SSITTTHTSA TEPFLVDGLT LGAQHLEAGG SLTRHVTQEP 1800  
 VSRTLTSTGT LSTHMDQQFF QT 1822

10  
 Seq ID NO: C307 Protein Sequence  
 Protein Accession #: NP\_076404.1

15  
 1 11 21 31 41 51  
 MGFNLTAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILIN 60  
 GLAVWIFPHI RNKTSPIFYI KNIVVADLIM TLTPFPRIHV DAGFGPWYFK FILCRYTSVL 120  
 FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTPTKV LSVCVWVINA VLSLNPILIT 180  
 NGQPTEDNIH DCSKLKSPLG VKWHTAVTVV NSCLFVAVLV ILIGCVIAIS RYHKSSSRQF 240  
 ISQSSRRKRH NQSIKRVVAV PFTCFPLPYHL CRIPPTFSHL DRLLDESQAK ILYYCKEITL 300  
 FLSACNVCLD PIIYFFMCRS FSRRLPKKN IRTSRSESIRS LQSVRRSEVR IYDYTDV 358

20  
 Seq ID NO: C308 Protein Sequence  
 Protein Accession #: NP\_065840.1

25  
 1 11 21 31 41 51  
 MVWCLGLAVL SLVISQADG RGKPEVVSVV GRAESVVLG CDLLPPAGRP PLHVIEWLRF 60  
 GFLLPIPIQF GLYSFRIDPD YVGRVRLQKG ASLQIEGLRV EDQGWYECRV FFLDQHIPPED 120  
 DFANGSVVHL TVNSPPQFQE TPPAVLEVQE LEFVTLRCVA RGSPLPHVTW KLRGKDLQGG 180  
 QGQVQVNGT LRIRRVBRGS SGVYTCQASS TEGSATHATQ LLVLGPEVIV VPPKNSTVNA 240  
 SQDVSLACHA EAYPANLTVS WFQDNINVEH ISRLQPRVOI LVDGSLRLLA TQDDAGCYT 300  
 CVPNGLLHP PSASAYLTVL CMFPGVIRCFV RANPPLLVS WTKDGKALQL DKFPQWSQGT 360  
 EGSLLIALGN EDALGEYSCT PYNSLGTAGP SPVTRVLLKA PPAPIERPKE EYFQEVGREL 420  
 LIPCSAQGDP PFVVSWTQVG RGLQQAQVD SNSSLILRPL TKEAHGWEC SASNAVARVA 480  
 TSTNVVYVLT SHVVTNVSV VALPKGANVS WEPFGDGGYL QRFVWYTP L AKRFDMMHHD 540  
 WWSLAVPVGA AHLVPLGLP HTQYQFSVLA QNKLGSPPFS EIVLSAPEGL PTTAAPGLP 600  
 PTEIPPPLSP PRGLVAVRTP RGVLLHWDPP ELVPKRLDGY VLEGRQGSQG WEVLDPVAVG 660  
 TETELLVPGL IKDVLVEFRL VAPAGSFVSD PSNTANVSTS GLEVYPSRTQ LPGLLPQPV 720  
 AGVVGVCFL GVAVLVSILA GCLLNRRRAA RRRRKRLRQD PPLIFSPYTK SAAPSALGSG 780  
 SPDSVAKLKL QSPVPSLRQ SLLWGDPAQT PSFHPDPPSS RGLPLEPIC RGPDGRFVVG 840  
 PTVAAPQERS GREQAERTP AQRLARSFDC SSSSPSGAPQ PLCIEDISPV APPPAAPPSP 900  
 LFGPGPLQY LSLPPFREMN VOGDNWPLEE PSPAAPPDYM DTRRCPTSSF LRSPTETPVS 960  
 PRESLPGAVV GAGATAEPPY TALADWTLRE RLLPGLLPAA PRGSLTSQSS GRGSASFLEP 1020  
 PSTAPSAGGS YLSPAPGDT SWSAGFERWP RREHVVTYSK RRNTSDENY EWDSEFPQDM 1080  
 ELLETLLHGL ASSRLRPEAE TELGVKTPPE GCLLNTAEVT GPEARCAALR BEPLAFRRR 1140  
 DATRARLPAY RQPVFHPQA TLL 1163

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 Seq ID NO: C309 Protein Sequence  
 Protein Accession #:

55  
 1 11 21 31 41 51  
 MLTKPLQGP APPGTPTPPP GKKDREAFEA EYRLGPLLK GPGFTVFAGH RLTDRLQVAI 60  
 KVIPNRVLG WSPPLSDSVTC PLEVALLWKV GAGGGHPGVI RLIDWFETQE GFMLVLERPL 120  
 PAQDLFDYIT EKGPLGBGS RCFFGQVVA IQCHSRGVV HRDIKDNIL IDLRRCARL 180  
 IDFGSGALL DBPYTDFDGT RVYSPPFENIS RHQYHALPAT VWSLGLLYD MCGDIPFER 240  
 DQEILEAEH FFAHVSPPDC ALIRCLAPK PSSRPSLEE LLDPMQTPA EDVTPQPLQR 300  
 RCPFGVLVLA TISLAWPLA PNGKSHFMA MSQG 334

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 Seq ID NO: C310 Protein Sequence  
 Protein Accession #: NP\_002501.1

65  
 1 11 21 31 41 51  
 MECLYYFLGF LLLAARLPLD AAKRFHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP 60  
 VKRGDMRWK NSWKGGRVQA VLTSDSPALV GSNITFAVNL IFFRCQKEDA NGNIVYEKNC 120  
 RNEAGLSADP YVYNWTANSE DSDGNGTGQ SHNVFPDGG PFPHPGWRR WNPYVVFETL 180  
 GQYFQKLGRG SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPIAQVKDYY VVTDQIPV 240  
 TMFQKNDNS SDTEFLKDLF IMPDVLIHDP SHFLNYSTIN YKNSFGDNTG LRVSTNHTVN 300  
 HTYVINGTFS LNLTVKAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENCQIN 360  
 RYGHFQATIT IVEGILEVNI IQMTDVLMEV PWPESLIDF VVTCQGSIFT EVCTIISDPT 420  
 CEITQNTVCS FVDVDEMCLL TVRRTFNGSG TYCVNLTLGD DTSALATSTL ISVFDPRDPAS 480  
 PLRMANSAI SVGCIAIFVT VISLLVYKXH KEYNPIENSP GNVVRSKGLS VFLNRAKAVF 540  
 FPGNQEKDPL LRNQEPKGV 560

75  
 Seq ID NO: C311 Protein Sequence  
 Protein Accession #: Eos seq

80  
 1 11 21 31 41 51  
 MRILKFLAC IQLLCVCRLD WANGYYRQR KLVBEIGWSY TGA LNQRNG KKYPTCNPK 60  
 QSPINIDEDL TQVNVNLKQL KPQGWKTS L ENTFIENYTK TVBINLTNDY RVSGGVSEMV 120  
 FKASKITFHW GKCMSSDGS EHSLEGQKFP LEMQIYCPDA DRFSSPERAV KRGKRLALS 180  
 ILPEVGTGFE LDFKAIIDGV ESVSRFGKQA ALDPPILLNL LPNSTDKYI YNGSLTSPPC 240  
 TDTVDHIVFK DTVSISESQL AVFCBVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFPSSY 300

Seq ID NO: C312 Protein Sequence  
Protein Accession #: XP\_031379

Seq ID NO: C313 Protein Sequence  
Protein Accession #: NP\_002842

1355

5  
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PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPIISDDVGAI 840
PIKHPFKHVA DLHASSGFTE EFETLKEFYQ EVQSCITVDLG ITADSSNHPD NKHKMRYINI 900
VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960
VEVIVMITNL VEGRRKCDQ YPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
GSQGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
TGTYIVLDSM LQIQHEGTV NIFGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320
VLEVRHFQCP KWPNDSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380
MHQLEKENS VDYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
AALPDGNIAE SLESVL 1456

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Seq ID NO: C314 Protein Sequence  
Protein Accession #: Eos sequence

20  
25  
30  
35  
40  
45

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1 11 21 31 41 51
| | | | |
MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
MVFKASKITP HWKCKMSSD GSEHSLGQKP FPLEMQIYCF DADRFSSEFE AVKGGKRLRA 180
LSILFEVGTG ENLDFKAIID GVESVSRFGK QAALDPFILL NLLPNSTDKY YIYNGSLTSP 240
PCTDITDWIVF KDTVSISESQ LAVFCVLTQM QSGYVLMMD YLQNNFREQQ YKFSRQVPS 300
YTGKEEIEHA VCSSEPENVQ ADPENYTSLL VTWERPRVVY DTMIKFAVL YQQLDGEDQT 360
KHEFLTDGYQ DLGAILNNLL PNMSYVLQIV AICTNGLYGK YSDQLIVDMP TDNPELDLFP 420
ELIGTEEIIK EEEGKDIEE GAIVNPGRDS ATNQIRKKEP QISTTTHYNR IGTKYNEAKT 480
NRSPTRGSEF SGKGDVPNTS LNSTSQPVTK LATEKDISLT SQTVTELPFH TVEGTSASLN 540
DGSKTVLRSP HMLSGTAES LNTVSIYEY EESLLTSFKL DTGAEDSSGS SPATSAIPFI 600
SENISQGYIF SSENPETITY DVLPESARN ASEDSTSSGS EESLKDPME GNWFPSSST 660
ITAQPDVGSR RESFLQNTYT BIRVDESEK TKSPSAGPVM SQGPSVTDLE MPHYSTFAYF 720
PTEVTPHAPT PSSRQDLVST TVNVVYSQTT QVYNEASNS SHESRIGLAE GLESEKKAIV 780
PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPIISDDVGAI 840
PIKHPFKHVA DLHASSGFTE EFETLKEFYQ EVQSCITVDLG ITADSSNHPD NKHKMRYINI 900
VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960
VEVIVMITNL VEGRRKCDQ YPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
GSQGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
TGTYIVLDSM LQIQHEGTV NIFGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320
VLEVRHFQCP KWPNDSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380
MHQLEKENS VDYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
AALPDGNIAE SLESVL 1456

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Seq ID NO: C315 Protein Sequence  
Protein Accession #: Eos sequence

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55  
60  
65  
70  
75

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1 11 21 31 41 51
| | | | |
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QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFWH GKCKMSSDGS EHSLEGGQKP LEMQIYCFDA DRPSSFEAV KGGKGLRALS 180
ILFEVGTSEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
TDTVDWIVFK DTVSISESQL AVFCEVLTQM QSGYVLMMDY LQNNFREQQY KFSRQVPSY 300
TGKEEIEHAV CSSEPENVQ DPENYTSLLV TWERPRVVYD TMIEKFAVL YQLDGEDQTK 360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPDELDFPE 420
LIGTEEIIKE EEEGKDIEE AIVNPGRDSA TNQIRKKEPQ ISTTTHYNR GTKYNEAKTN 480
RSPTRGSEFS GKGDVPNTS NSTSQPVTKL ATEKDILSTS QTVTELPFHT VEGTSASLND 540
GSKTVLRSPH MNLSTAESL NTVSITYEY EESLLTSFKL DTGAEDSSGS PATSAIPFIS 600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE EESLKDRMEG NVWFPSSSTDI 660
TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSPSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
TEVTPHAPT SSRQDLVST VNVVYSQTTQ PVYNEASNS HESRIGLAE GLESEKKAIV 780
LVIVSALTFI CLVVLVGILI IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPIISDDVGAI 840
IKHPFKHVA DLHASSGFTE EFETLKEFYQ EVQSCITVDLG ITADSSNHPD NKHKMRYINI 900
AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAE DFWRMIWEHN 960
EVIVMITNL VEGRRKCDQ YPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
SQKGRPSGRV VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
GTIVLDSML LQIQHEGTV NIFGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
LDSDHIHAYV ALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
SRVAGTILLS QSNIQQSDYS AALKQCNREK NRTSSIIPVE RSRVGISSLS GEGTDYINAS 1260
YIMGYYSNE FIITQHPLLH TIKDFWRMIW DHNAQLVVM I PDGQNMAGE PVYWPNDKDEP 1320
INCESFKVTL MAEEHKCLSN EEEKLIQDPI LEATQDDYVL EVRHFQCPKW PNDSPISK 1380
FELISVIKEE AANRDGPMIV HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM 1440
RPGVFADIEQ YQFLYKVLIS LVGTRQEENP STSLDSNGAA LPDGNIAESL ESLV 1494

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Seq ID NO: C316 Protein Sequence  
Protein Accession #: Eos sequence

80

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1 11 21 31 41 51
| | | | |
MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFWH GKCKMSSDGS EHSLEGGQKP LEMQIYCFDA DRPSSFEAV KGGKGLRALS 180
ILFEVGTSEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240

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	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHFAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPEASNSH	420
5	ESRIGLAEGE	ESSEKKAIVPL	VIVSALTFIC	LVVLVGILY	WRKCFQTAHF	YLEDSTSPRV	480
	ISTPPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGFTFEE	ETLKEFYQEV	QSCVTDLGIT	540
	ADSSNHDPNK	HKNRYINIVA	YDHSRVKLAQ	LAEDKGKLT	YINANYVDGY	NRPKAYIAAQ	600
	GPKLSTAEDE	WRMIWEHNV	VIVMITNLVE	KGRKCDQYW	PADGSEBYGN	FLVTQKSVQV	660
	LAYYTVRNFT	LRNTKIKKGS	QKGRPSGRV	TQYHYTQWPD	MGVPEYSLPV	LTPVRKAAYA	720
10	KRHAVGPPVV	HCSAGVGRG	TYIVLDSMLQ	OIQHEGTVNI	FGPLKHRSQ	RNYLVQTEEQ	780
	YVFIHDTLVE	AILSKEETEVL	DSHIHAYVNA	LLIPGPAGKT	KLEKQFQLLS	QSNIIQSDYS	840
	AALKQCNREK	NRTSSIIIPVE	RSRVGISSLS	GEGTDYINAS	YIMGYQSN	FIITQHPLH	900
	TIKDFWRMIW	DHNAQLVVM	PDGQNMAGE	FVYWPNDKDEP	INCESFKVTL	MAEEHKCLSN	960
	EELKLIQDFI	LEATQDDYVL	EVRFQCPKW	PNDPSPIKST	FELISVIKEE	AANRDGPMIV	1020
15	HDEHGGVTAG	TFCALTLMH	QLEKENSVDV	YQVAKMINLM	RPGVPADIEQ	YQFLYKVILS	1080
	LVSTRQENP	STSLDSNGAA	LPGDNIAESL	ESL			1113

Seq ID NO: C317 Protein Sequence  
Protein Accession #: Eos sequence

20	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNKLKL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
25	FKASKITFW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPEEAV	KGKGLRALS	180
	ILFEVGTEN	LDPKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHFAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPE	420
30	LIGTEETIKE	EEBEGKIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTYKNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NWFFPSSTDI	660
	TAQPDVGSGR	ESPLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
35	TEVTPHAFIP	SSRQQLVST	VNVVYSQTQ	PVYNEASNS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTFEE	FETLKEFYQE	VQSCVTDLGI	TADSSNHDPN	KHKNRYINIV	900
	AHDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAE	FWRMIWEHNV	960
	EVIVMITNLV	EKGRKCDQY	WPADGSEBYG	NFLVTQKSVQ	VLAYYTVRNFT	TLRNTKIKKG	1020
40	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFFVRKAAY	AKRHAVGPPV	VHCSAGVGRG	1080
	GTIVLDSML	QIQIHEGTVN	IFGFLKHRS	QRNYLVQTEE	QYVFIHDTLV	EAILSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQGL	TLSPLRECRG	TISACHNLPL	PGLTDPPTAS	1200
	SRVARTILLS	QSNIIQSDYS	AALKQCNREK	NRTSSIIIPVE	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYQSN	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	PDGQNMAGE	FVYWPNDKDEP	1320
45	INCESFKVTL	MAEEHKCLSN	EELKLIQDFI	LEATQDDYVL	EVRFQCPKW	PNDPSPIKST	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTLMH	QLEKENSVDV	YQVAKMINLM	1440
	RPGVPADIEQ	YQFLYKVILS	LVSTRQENP	STSLDSNGAA	LPGDNIAESL	ESL	1493

Seq ID NO: C318 Protein Sequence  
Protein Accession #: Eos sequence

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	QSPINIDEDL	TQVNVNKLKL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
55	FKASKITFW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPEEAV	KGKGLRALS	180
	ILFEVGTEN	LDPKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHFAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPE	420
60	LIGTEETIKE	EEBEGKIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTYKNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NWFFPSSTDI	660
	TAQPDVGSGR	ESPLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
65	TEVTPHAFIP	SSRQQLVST	VNVVYSQTQ	PVYNEASNS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTFEE	FETLKEFYQE	VQSCVTDLGI	TADSSNHDPN	KHKNRYINIV	900
	AHDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAE	FWRMIWEHNV	960
70	EVIVMITNLV	EKGRKCDQY	WPADGSEBYG	NFLVTQKSVQ	VLAYYTVRNFT	TLRNTKIKKG	1020
	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFFVRKAAY	AKRHAVGPPV	VHCSAGVGRG	1080
	GTIVLDSML	QIQIHEGTVN	IFGFLKHRS	QRNYLVQTEE	QYVFIHDTLV	EAILSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQGL	QSNIIQSDY	SALKQCNRE	KNRTSSIIIPV	1200
	ERSRVGISSL	GEGTDYINA	SYIMGYQSN	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	1260
75	IPDGQNMAGE	FVYWPNDKDEP	PINCESFKVT	LMAEEHKCLS	NBEKLIQDF	ILEATQAWRS	1320
	DGRNFLCSN	PYAPTRKRKF	RGCLPGSQDD	QSDARSCLC			1359

Seq ID NO: C319 Protein Sequence  
Protein Accession #: XP\_002914.4

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	MKQIDIGKLR	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
	LDASMSQLR	ILDEBHPKGR	YHGLSALKP	IRTTSKHQHP	VDNAGLPSCM	TFSWLSLAR	120
	VAHKKGELS	EDVMSLSKHE	SSDVNCRRLR	RLNQEBLNEV	GPDAASLRV	WVIFCRTRLI	180

5	LSIVCLMITQ	LAFSGPAPM	VKHLLEYTQA	TESNLQYSLL	LVLGLLLTEI	VRWSLALTW	240
	ALNYRTGVR	RGAILTMAPK	KILKLNKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAGG	300
	PVVAILGMIY	NVILIGPTGF	LGSAPFIFY	PAMMFASRLT	AYFRKCVAA	TDERVQKNE	360
	VLTYIKFIKM	YAWKAPFSQS	VQKIREEERR	ILEKAGYFQS	ITVGAPIV	VIASVVTFSV	420
	HMTLGFDLTA	AQAFVTVTVF	NSMTFALKVT	PFSVKSLSEA	SVAVDRPKSL	FLMEEVHMIM	480
	NKPASPHIKI	EMQNATLAWD	SSHSSIQNSP	KLTPKMKDK	RASRGKKEKV	RQLQRTHEQA	540
	VLAEQKGHL	LDSDERPSPE	EEEGKHIHLG	HLRLQRTLHS	IDLEIQEGKL	VGICGSVSGG	600
	KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILPGKEYD	EERYNSVLNS	660
10	CCLRPDLAIL	PSSDLTEIGE	RGANLGGQR	QRISLARALY	SDRSIYLDD	PLSALDAHVG	720
	NHIFNSAIRK	HLKSKTVLTV	THQLQYLVD	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
	FNLLLGTEP	PVEINSKKE	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEGQL	VQLEEKQGS	840
	VPNSVYGVYI	QAAGGPLAF	VIMALFMLNV	GSTAFSTWWL	SYWIKQSGSN	TTVTRGNETS	900
	VSDSMKDNPH	MQYASIIYAL	SMAVMLILKA	IRGVVFPVGT	LRASSRLHDE	LFRRILRSPM	960
	KFFDTTPTGR	ILNRFPSKMD	EVDVRLPFQA	EMFIQNVILV	FFCVGMIAGV	FPWFLVAVGP	1020
15	LVILFSLVHT	VSRLVIRELK	RDNITQSPF	LSHITSSIQG	LATIHAYNKG	QEFLEHRYQEL	1080
	LDNDQAPFFL	FTCAMRWLAV	RDLISIALI	TTTGLMIVLM	HQIIPPAYAG	LAISYAVQLT	1140
	GLFQFTVRLA	SETEARFTSV	ERINHYIKTL	SLEAPARIKN	KAPSPDWQPE	GEVTFENAE	1200
	RYRENLPVL	KKVSPTIKPK	EKIGIVGRTO	SGKSSLGML	FRVLVSGGC	IKIDGVRISD	1260
	IGLADLRSLK	SIIPQEPVLF	SGTVRSNLD	FNQYTEDQIW	DALERTHME	CIAQLPLKLE	1320
20	SEVMENGDNF	SVGERQLLCI	ARALLRHCKI	LILDEATAAM	DTETDLIQE	TIREAFADCT	1380
	MLTIAHRLHT	VLGSDRIMVL	AQQQVVEFDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKG	1437

Seq ID NO: C320 Protein Sequence  
Protein Accession #: NP\_005679.1

25	1	11	21	31	41	51	
	MDIDIGKEY	IIFSPGYRSV	RERTSTSGTH	RDREDSKFRR	TRPLECQDAL	ETAARAEGLS	60
	LDAHMSQLR	ILDEEHPKKG	YHGLSALKP	IRTTSKHQHP	VDNAGLPSCM	TFSWLSLAR	120
30	VAHKKGELSM	EDVWSLSKHE	SSDVNCRRL	RLNQEBELNEV	GPDAASLRV	VWIFCRTRI	180
	LSIVCLMITQ	LAFSGPAPM	VKHLLEYTQA	TESNLQYSLL	LVLGLLLTEI	VRWSLALTW	240
	ALNYRTGVR	RGAILTMAPK	KILKLNKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAGG	300
	PVVAILGMIY	NVILIGPTGF	LGSAPFIFY	PAMMFASRLT	AYFRKCVAA	TDERVQKNE	360
	VLTYIKFIKM	YAWKAPFSQS	VQKIREEERR	ILEKAGYFQS	ITVGAPIV	VIASVVTFSV	420
35	HMTLGFDLTA	AQAFVTVTVF	NSMTFALKVT	PFSVKSLSEA	SVAVDRPKSL	FLMEEVHMIM	480
	NKPASPHIKI	EMQNATLAWD	SSHSSIQNSP	KLTPKMKDK	RASRGKKEKV	RQLQRTHEQA	540
	VLAEQKGHL	LDSDERPSPE	EEEGKHIHLG	HLRLQRTLHS	IDLEIQEGKL	VGICGSVSGG	600
	KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILPGKEYD	EERYNSVLNS	660
40	CCLRPDLAIL	PSSDLTEIGE	RGANLGGQR	QRISLARALY	SDRSIYLDD	PLSALDAHVG	720
	NHIFNSAIRK	HLKSKTVLTV	THQLQYLVD	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
	FNLLLGTEP	PVEINSKKE	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEGQL	VQLEEKQGS	840
	VPNSVYGVYI	QAAGGPLAF	VIMALFMLNV	GSTAFSTWWL	SYWIKQSGSN	TTVTRGNETS	900
	VSDSMKDNPH	MQYASIIYAL	SMAVMLILKA	IRGVVFPVGT	LRASSRLHDE	LFRRILRSPM	960
45	KFFDTTPTGR	ILNRFPSKMD	EVDVRLPFQA	EMFIQNVILV	FFCVGMIAGV	FPWFLVAVGP	1020
	LVILFSLVHT	VSRLVIRELK	RDNITQSPF	LSHITSSIQG	LATIHAYNKG	QEFLEHRYQEL	1080
	LDNDQAPFFL	FTCAMRWLAV	RDLISIALI	TTTGLMIVLM	HQIIPPAYAG	LAISYAVQLT	1140
	GLFQFTVRLA	SETEARFTSV	ERINHYIKTL	SLEAPARIKN	KAPSPDWQPE	GEVTFENAE	1200
	RYRENLPVL	KKVSPTIKPK	EKIGIVGRTO	SGKSSLGML	FRVLVSGGC	IKIDGVRISD	1260
	IGLADLRSLK	SIIPQEPVLF	SGTVRSNLD	FNQYTEDQIW	DALERTHME	CIAQLPLKLE	1320
50	SEVMENGDNF	SVGERQLLCI	ARALLRHCKI	LILDEATAAM	DTETDLIQE	TIREAFADCT	1380
	MLTIAHRLHT	VLGSDRIMVL	AQQQVVEFDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKG	1437

Seq ID NO: C321 Protein Sequence  
Protein Accession #: NP\_005553.1

55	1	11	21	31	41	51	
	MPALNLGCL	CPSLLLPAA	ATSRREVDC	NGKSRQCIFD	RELHRTQNG	FRCLNCNDNT	60
	DGILHCEKCN	GFYRHRERDR	CLPCNCSKG	SLSARCDNSG	RCSCPKGVGT	ARCDRLPGF	120
60	EMLTADAGCTQ	DQRLDLSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYINLDGNN	180
	PEGCTQCFYC	GHSASCRSSA	EYSVHKITST	FHQDQVDGKA	VQRNGSPAKL	QWSQRHQDV	240
	SSAQRDLDPVY	FVAPAKPLGN	QQVSYGQSLS	FDYRVDRGGR	HPSAHDVILE	GAGLRITAPL	300
	MPLGKTLPCG	LTKTYTFRNL	EHPNNWSPQ	LSYFEYRRL	RNLTLALRRA	TYGEYSTGYI	360
65	DNVTLISARP	VSGAPAPWVE	QICFPVGYKG	QPCQDCASGY	KRDSARLGPF	GTCIPNCQGG	420
	GGACDPDTGD	CYSGDENFDI	ECADCPIGFY	NDPFDPRSC	PCPCHNGFSC	SVMPEEEVV	480
	CNNCPPGVTC	ARCELADGY	FGDPFGERGP	VRPCQPCQCN	MNVDPASGN	CDRLTGRCLK	540
	CIHNTAGIYC	DQCKAGYFGD	PLAPNPADKC	RACNCPMGS	EPVGCERSGT	CVCKPGFGGP	600
	NCEHGAPSCP	ACYNQVKIQM	DQFMQQLQRM	EALISKAQGG	DGVVPDTELE	GRMQQAQAL	660
70	QDILRDAQIS	EGAERSLGLQ	LAKVRSQENS	YQSLDLDLKM	TVERVRLGSS	QYQNRVRDTH	720
	RLITQMQLSL	AESASLGN	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	780
	ETEDYSKQAL	SLVRKALHEG	VSGSGSGSPDG	AVVQGLVEKL	EKTKSLAQQL	TREATQAEIE	840
	ADRSYQHSRL	LLDSVSRLOG	VSDQSPQVEE	AKRIKQKADS	LSTLVTRHMD	EFKRTQKNLG	900
	NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRAQEAISM	GNATPYEVES	ILKNLREFDL	960
75	QVDNRKAEAB	EMKRLSYIS	QKVSASDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	1020
	IEQEIGSLNL	EANVTADGAL	AMEKGLASLK	SEMRVEGEL	ERKELEFDTN	MDAVQMITE	1080
	AQKVDTRAKN	AGVTIQDTLN	TLDGLLHMD	QPLSVDEEGL	VLEEQKLSRA	KTIQNSQLRP	1140
80	MMSELEERAR	QQRGHLHLE	TSIDGILADV	KNLENIRDNL	PPGCYNTQAL	EQ	1193

Seq ID NO: C322 Protein Sequence  
Protein Accession #: NP\_066924.1

1	11	21	31	41	51	
MANAGLQLLG	FILAPLGNIG	AIVSTALPQW	RIYSYAGDNI	VTAQAMYEG	WMSCVSQSTG	60

QIQCKVFDL LNLSTLQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120  
 IGGAILLAG LAIVATANY GNRIVQEFYD PMTFVNARYE FGQALFTGWA AASLCLLGA 180  
 LLCCSCPRKT TSYTPRPYP KPAPSSGKDY V 211

5 Seq ID NO: C323 Protein Sequence  
 Protein Accession #: AAM77876

10 1 11 21 31 41 51  
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFAVAKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQBAKSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVFNMYW DVGNLVSKHM 240  
 NETSHTQGS RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300  
 15 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTRGH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

20 Seq ID NO: C324 Protein Sequence  
 Protein Accession #: NP\_006171.1

25 1 11 21 31 41 51  
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFAVAKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQBAKSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVFNMYW DVGNLVSKHM 240  
 NETSHTQGS RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300  
 30 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTRGH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF ISNDDDSASP 480  
 LHHSNGSNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDITF QHIKRHNIVL 540  
 KRELGEAGFG KYFLAECYNL CPEQDKILVA VKTLKDASDN ARKDPFHREAS LLTNLQHEHI 600  
 35 VKFYGVCEG DPLIMVFEYM KHGDLNKLFLR AHGEDAVLMA EGNPFTLTQ SQMLHIAQOI 660  
 AAGMVLASQ HFVHRDLATR NCLVGENLLV KIGDPGMSRD VYSTDYRVG GHTMLPIRWM 720  
 PPESIMYRK TTESDVWSLG VVLWEIFTYG KQPHYQLSNN EVIECITQGR VLQRPRTCPQ 780  
 EYVELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG 822

40 Seq ID NO: C325 Protein Sequence  
 Protein Accession #: Bos sequence

45 1 11 21 31 41 51  
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFAVAKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQBAKSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVFNMYW DVGNLVSKHM 240  
 NETSHTQGS RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300  
 50 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTRGH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

55 Seq ID NO: C326 Protein Sequence  
 Protein Accession #: NP\_570843.1

60 1 11 21 31 41 51  
 MPLKHYLLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLOI 60  
 LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFNRL GSLRYLSLAN NKQLVLPGL 120  
 FQGLDSLES LLSSNQLLOI QPAHFSQCSN LKELQLHGNH LEYIPDGAFO HLVLTKLNL 180  
 GKNSLTHISF RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQO NQIGLLSPGL 240  
 FHNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRLEWL 300  
 YDNHISLDP NVFNNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGNV 360  
 65 FRMLANLQNT SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLKGLCELRL 420  
 YDNFWRCDS ILPLRNWLLL NQPRIGTDTV PFCFSPANVR GQSLIIINVN VAVPSVHVE 480  
 VPSYPETPMY PDPSPYDPTT SVSSTTELTS PVEDYDILT IQVTDERSVW GMTQAQSGLA 540  
 IAAIVIGIVA LACSLAACVG CCCCKRSQA VLMQNKAPNE C 581

70 Seq ID NO: C327 Protein Sequence  
 Protein Accession #: NP\_002649.1

75 1 11 21 31 41 51  
 MRALLARLLL CVLVVSDSKG SNELHQVPSN CDCINGGTCV SNKYFSNIHW CNCPKFGGQ 60  
 HCEIDKSKTC YBNGHFPYRG KASTDTMGRP CLPMNSATVL QQTYHAHRSD ALQLGLGKH 120  
 YCRNPDNRRR PWCYVQGLK PLVQECMVHD CADGKKPSSP PEELKFCQG KTLRPRFKII 180  
 GGEFTTIENQ PWFPAIYRRH RGSVTVYCG GSLISPCWVI SATRCFIDYP KKEDIYVYL 240  
 RSRLNSNTQS EMKPEVENLI LHKDYSADTL AHNDIALLK IRSKEGRCAQ PSRTIQTICL 300  
 80 PSMYNDPQFG TSCEITGFGK ENSTDLYYPE QLRMTVVKLI SHRECCQPHY YGSEVTTKML 360  
 CAADPQWKTD SQQDSSGGL VCSLQGRMTL TGIVSVGRGC ALKDKPGVYT RVSHFLPWIR 420  
 SHTKEENGLA L 431

Seq ID NO: C328 Protein Sequence  
 Protein Accession #: XP\_087254.1



1 11 21 31 41 51  
 5 MQPRECSING MKYQIEINGRL VPEGPTPDSS EGNLSYLSSL SHLNNLSHLT TSSSFRTSPE 60  
 NETELIKEHD LFPKAVSLCH TVQISNVQTD CTGDGPWQSN LAPSQLEYA SSPDEKALVE 120  
 AAARIGIVFI GNSSETMEVK TLGKLELYKL LHILEFDSOR RRMSVIVQAP SGEKLLFAKG 180  
 AESSILPKCI GGEIEKTRIH VDEPALKGLR TLCIAYRKFT SKEYBEIDKR IFEARTALQQ 240  
 REEKLAAPVQ FIEKDLILLG ATAVEDRLQD KVRTIEALR MAGIKVWVLT GDKHETAVSV 300  
 10 SLSCGHPHRT MNILELINQK SDSECAEQLR QLARRITEDH VIQHGLVVDG TSLSLALREH 360  
 EKLFMVCRN CSAVLCCRMA PLQKAKVIRL IKISPEKPIT LAVGDGANDV SMIQEAHVGI 420  
 GIMGKEGRQA ARNSDYAIAR PKPLSKLLFV HGHFYIIRIA TLVQYFFYKN VCFITPQFLY 480  
 QFYCLFSQQT LYDSVYLTLY NICFTSLPIL IYSLLEQHVD PHVLQNKPTL YRDISKNRLL 540  
 SIKTFLYWTI LGFSHAFIFP FGSYLLIGKD TSLLGNGQMP GNWTFGLTVP TVMVTITVTK 600  
 15 MALETHFWTW INHLVTWGS IIFYFVSLFY GGILWPLGGS QNMVFPFIQL LSSGSAWFAI 660  
 ILMVVTCLFL DIKKVFDRIH LHPTSTKCAQ LTETNAGIKC LDSMCCFPFG EAACASVGRM 720  
 LERVIGRCSP THISRSWSAS DFFYTNDRSI LTLSTMDSSST C 761

Seq ID NO: C329 Protein Sequence  
 Protein Accession #: XP\_087461.1

1 11 21 31 41 51  
 20 MLPLLAALLA AACPLPFVRG GAADAPGLLG VPSNASVNAS SAASPSPRGC NPPRRPPGPS 60  
 ARARRRRRR RRLCNISVQR QMLSSLLVRW GRPRGFQCDL LLFSTNAHGR APFAAFHERV 120  
 25 GPPLLIHHLG LAAGGAQDDL RLCVGCWVR GRRTGRLRPA AAPSAATAA GAPTALPAYP 180  
 AAEPPLGLWL QGEPLHFCCL DFSLEELQGE PGWRLNRKPI ESTLVACFMT LVIVVWSVAA 240  
 LIWPVPIIAG PLPNGMEQRR TTASTAATP AAVPAGTTAA AAAAAAATA AVTSQVATK 299

Seq ID NO: C330 Protein Sequence  
 Protein Accession #: XP\_051522.2

1 11 21 31 41 51  
 35 MDLHLFDYSE PGNFSDISWP CNSSDCIVVD TVMCPNMPNK SVLLYTLSPF YIFIFVIGMI 60  
 ANSVVWVNI QAKTTGYDTH CYILNLAID LWVLTIPVW VVSLVQHQQW PMGELTCKVT 120  
 HLIFSINLFG SIFFLTQMSV DRYLSITYFT NTPSSRRKMW RRVVCILVWL LAFCVSLPDT 180  
 YLKVTVTSAS NNETYCRSFP PEHSIKEWLI GMELVSVVLG FAVPFSIIAV FYPLLARAI 240  
 40 ASSDQEKHSS RKIIPSYVUV FLVCWLPYHV AVLLDIFSLI HYIPFTCRLE HALFTALHVT 300  
 QCLSLVHCCV NPLVYSFINR NYRYELMKAP IFKYSAKTGL TKLIDASRVS ETEYSALEQS 360  
 TK 362

Seq ID NO: C331 Protein Sequence  
 Protein Accession #: NP\_000341.1

1 11 21 31 41 51  
 45 MGFVRQIQLL LMKQWTLRKR QKIRFVVELV WPLSLFLVLI WLRNANPLYS HHECHFPNKA 60  
 MPSAGMLPWL QGIFCNVNNP CFQSPTPGES PGIVSNYNNIS ILARVYRDPQ KLLAGNAPESQ 120  
 50 HLGRITWELH ILSQPMOTLR THERIAGRG IRIRDILKDE ETTLTLFLIKN IGLSDSVVYL 180  
 LINSQVREPEQ FAFHGVLDAL KDIAACEALL ERFIIPSQRR GAKTVRYALC SLSQGTQLWI 240  
 EDTLYANVDF FRLEFVLPPTL LDRSQGINL RSWGGILSDM SPRIQEFIRH PSMQDLLWVT 300  
 RPLMQNGGPE TFKLMGILS DLLCGYPEGG GSRVLSFNWY EDNNYKAFGL IDSTRKDIPIY 360  
 55 SYDRRTTSFC NALIQSLEEN PLTKIANRAA KPLLMGKILY TPDSPAARRI LKNNANSTFEE 420  
 LEHVRLKVK AWEVGPQIWF FFDNSTQMNM IRDTLGNPTV KDFLNRLQGE EGITAEAILN 480  
 FLYKGPRESQ ADDMANFDWR DIPNITDRTL RLNVQYLECL VLDKFESYND ETQLTQRAIS 540  
 LLEENMFNAG VVFPDMYFWT SSLPFHVYK IRMDIDVVEK TNKIKDRYWD SGPRADPVED 600  
 FRYINGGPAY LQDMVEQGIT RSQVQAEAFV GIYLLQMPYP CFVDDSPMII LNRCPPIPMV 660  
 60 LAWIVSMT VKSIVLEKEL RLKETLKNQ VSNVWICTW FLDSPFSIMS SIFLLTIFIM 720  
 HGRILHSDP FIFLFLPLAF STATIMLCPL LSTFFSKASL AAACSGVIYF TLYLPHILCF 780  
 AWQDRMTAEL KAVSLLSPV AFGFGTEYLV RFEBOGLGLQ WSNIGNSPTE GDEFSPLLSM 840  
 QMMLLDAACT GLLAWYLDQV FPGDYGTPLP WYFLLQESYV LSGEGCSTRE ERALEKTEPL 900  
 TEETEDPEHP EGIHDSPPER EHPGWNVPVC VKNLVKIFEP CGRPAVDRLN ITFYENQITA 960  
 65 FLYHNGAGKT TTLSILTGLL PPTSGTVLVG GRDIETSLDA VRQSLGMCQ HNILFHLTV 1020  
 AEHMLFYAQL KGKSQBEAQL EMEAMLEDTG LHHKRNEEAQ DLSGGMQRKL SVAIAPVGA 1080  
 KVVILDEPTS GVDPSYRRSI WDLKLYRSG RTIIMPTRHM DEADHQGDRI AIIAQGRLYC 1140  
 SGTPLFLKNC FGTGLYTLV RKMKNIQSOR KGSEGTCSGS SKGFSTTCPA HVDDLTPQV 1200  
 LDGDVNEAMD VVLLHVPEAK LVEICIGQLI FLLPNKNFKH RAYASLPREL EBTLDLGLS 1260  
 70 SFGISDTPL EIFLKVTEDS DSGPLFAGGA QQKRENVNPR HPCLGPKEKA GQTPQDSNVC 1320  
 SPGAPAAHPE QGPPPEPECP GPOLATGTQL VLQHVQALLV KRFBORTIRSH KDFLAQIVLP 1380  
 ATFVFLALML SIVILPGEY PALTLPWNIY GQYTFFSMD EPGSEQFTVL ADVLLNKPFG 1440  
 GNRCLKEGWL PEYPCGNSTP WKTPSVSPNI TQLFQKQWT QVNPSPSCRC STREKLTMLP 1500  
 75 ECPGEGAGLF PPQRTQRSTE ILQDLTDNRN SDFLVKTYPA LIRSSLSKFP WNEQRYGGI 1560  
 SIGGKLVVPE ITGEALVGL SDLGRIIMVS GGPITREASK EIPDFLKHLE TEDNIKVWFN 1620  
 NKGHNAVLSF LAVAHNAIRL ASLPKDRSPE EYGITVISQP LNLTKQLSE ITVLTTSVDA 1680  
 VVAICVIFSM SFVPASFVLY LIQERVNKS HLQFISGVSP TTYWVTFNFW DIMNYSVSAG 1740  
 LUVGIFIGFQ KAYTSPENL PALVALLLY GWAVIPMYF ASFLFDVPST AYVALSCANL 1800  
 FIGINSSAIT FIELEPDMNR TLLRFNAVLR KLLIVFPHFC LGRGLLDLAL SQAQVTVYAR 1860  
 80 FGEHSANPP HDLIGQLF AMVVEGVVYF LLTLVORHF FLSQWIAEPT KEPIVDEDD 1920  
 VAERQRIT GGNKTDILRL HELTKIYLG SSPAVDRLCV GVRPGECFGL LGVNGAGKTT 1980  
 TFKMLTGDTT VTSGDATVAG KSILTNISEV HQNMGYCPQF DAIDELLTGR EHLVLYARLR 2040  
 GVPAESGKTV YASGKSLGL TVYADCLAGT YASGKRLS TAIALIGCPP LVLLDEPTTG 2100  
 MDQARRMLM NVIVSIIRKG RAVVLTSHSM BECEALCTRL AIMVKGAFCR MGTIQLHLSK 2160  
 FGDGIYVTK IKSPKDDLLP DLNPFVQFFQ GNFFGVSQRE RHYNMLQFQV SSSSLARIFQ 2220  
 LLLSHKDSLL IBEYSVTQYT LDQVFVNFAK QQTESHDLPL HPRAAGASRQ AQD 2273

Seq ID NO: C332 Protein Sequence  
Protein Accession #: NP\_006662.2

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5      1      11      21      31      41      51
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MVPHAILARG RDVCCRNGLL ILSVLSVIVG CLLGFFLRTR RLSPQEISYF QPPGELLMRM 60
LRMMILPLVV SSIMSGLASL DAKTSSRLGV LTVAYYLTWT FMAVIVGIFM VSIHFGSAA 120
QKETTEQSGK PIMSSADALL DLIRNMFAN LVEATPKQYR TKTPPVVKSP KVAPEEAPPR 180
10    RILYGVQOEB NGSHVQNFAL DLTPPEVVY KSEPGTSDGM NVLGIVFFSA TMGIMLGRMG 240
DSGAPLVSFC QCLNESVMKI VAVAVWYFPF GIVFLIAGKI LEMDDPRAVG KCLGFYSVTV 300
VCGLVLRHGLF ILPLLYFFIT KKNPIVFIRG ILQALLIALA TSSSSATLPI TFKCLLENH 360
IDRRIARFVL PVGATINMDG TALYEAVAAI FIAQVNNYEL DFGQIITISI TATAASIGAA 420
GIPQAGLVTM VIVLTSVGLP TDDITLIIAV DWALDRFRMT INVGLDALAA GIMAHICRKD 480
15    FARDTGTEKL LECETKPVSL QEIVAAQONG CVKSVABASE LTLGPTCPHH VPVQVERDEE 540
LPAASLHCT IQISELETNV

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Seq ID NO: C333 Protein Sequence  
Protein Accession #: NP\_005680.1

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20      1      11      21      31      41      51
|      |      |      |      |      |
MVTVGNCEA EGPVGPAMWQ DGLSPCFFFT LVPSTERMALG TLALVLALPC RRRERPAGAD 60
SLSWAGPRRI SPYVLQLLLA TLQALPLAG LAGRVGTARG APLPSYLLA SVLESAGAC 120
25    GLWLLVVERS QARQLAMGI WIKPRHSPGL LLLWTVAFAA ENLALVSWNS PQWWHARADL 180
GQQVQFSLWV LRYVVSGLF VLGLWAPGLR PQSYTLQVHE EDQDVERSQV RSAAQQTWR 240
DFGRKLRLLS GYLWPRGSPA LQLVVLICLG LMGLERALNV LVPIFYRNIV NLLTEKAPWN 300
SLAWTVTSYV FLKPLQGGGT GSTGFVSNLR TFLWIRVOQF TSBRELLIF SHLHELRLW 360
HLGRRATGEVL RIADRGTSV TGLLSYLVEN VIPTLADIII GIIFYSMFFN AWFGLIVFLC 420
30    MSLYLTITIV VTEWRTKFRR AMNTQENATR ARAVDSLINF ETVKYNAES YEVEERYEAI 480
IKYQGLEWKS SASVLLNQT QNLVIGLGLL AGSLLCAYFV TEQLKQVGDY VLFGTYYIQL 540
YMLNWFQTY YRMIOQTNFID MENMFLLKE ETEVKDLPGA GPLRFQKGR IEFENVHFSYA 600
DGRETLQDVS FTVMPGQTLA LVGPGSGAGS TILRLLEFPY DISSGCIRID QODISQVTOA 660
35    SLRSHIGVVP QDTVLFNQDI ADNIRYGRVT AGNDEVEAAA QAAGIHDAIM APPEGYRTQV 720
GERGLKSGG EKQRVAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTIV 780
VAHRLSTVNV AQILVIKDG CIVERGRHEA LLSRGVYAD MWQLQQQOEB TSEDTPKQTM 840
ER

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Seq ID NO: C334 Protein Sequence  
Protein Accession #: NP\_000667.1

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40      1      11      21      31      41      51
|      |      |      |      |      |
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVLFA 60
IFPATISLG FCTDFYGLF LACFVLVLTQ SSIFSLAVA VDRYLAICVP LRYKSLVTGT 120
RARGVIAVLW VLAFGIGLTP FLGWSKDSA TNNCTEPWDG TTNSCCLVK CLFENVVEMS 180
YMWYFNFGCC VLPPLIMLV IYIKIFLVAC RQLQRTLM D HSRITLQREI HAAKSLAMIV 240
GIFALCNLFP HAVNCVTLFQ PAQGNKPKN AMNMAILLSH ANSVVNPIVY AYRNDRFRTY 300
50    FHKIISRYLL CQADVSKNG QAGVQPALGV GL
332

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Seq ID NO: C335 Protein Sequence  
Protein Accession #: NP\_443164

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55      1      11      21      31      41      51
|      |      |      |      |      |
MGLGARGAWA ALLGLTLQVL ALLGAHESA AMAETLQHVP SDHTNETSNS TVKPPTSVAS 60
DSSNTTIVTM KPTAASNTIT PGWVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMVTHNS 120
SVTSAASSVT ITTMHSEAK KGSKFDGTSF VGGIVLTLGV LSLIYIGCM YYRRRGIRYR 180
60    TIDEHDAII
189

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Seq ID NO: C336 Protein Sequence  
Protein Accession #: NP\_004186.1

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65      1      11      21      31      41      51
|      |      |      |      |      |
MAQHGAMGAP RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTARCC RVHTTRCCRD 60
YPGECCSEW DCMCVQPEFH CGDPCCTTCR HHPCPPGQGV QSQGFSGFG QCIDCASGTF 120
SGGHEGHCCK WTDCTQFGFL TVPPGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL 180
70    TSAQLGLHIW QLSQCWWPR ETQLLLEVPP STEDARSCQF PEEERGERSA EEKRLGLDW 240
V
241

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Seq ID NO: C337 Protein Sequence  
Protein Accession #: BAC03767.1

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75      1      11      21      31      41      51
|      |      |      |      |      |
MGCDGRVSG LARNLQPTLT YWSVFFSFLG CIAFLGPTLL DLRCQTHSSL PQISWVFFSQ 60
QLCLLGSAL GGVFKRTLAQ SLWALETSSL AISLVFAVIP FCRDVKVLAS VMALAGLAMG 120
CIDTVANMQL VMYQKDSAV FLQVLRFPVG FGALLSPLIA DPLSEANCL PANSTANTTS 180
80    RGHLEFVSRV LGQEHVDAKP WSNQTPPGLT PKDGAGTRVS YAFWIMALID LPVPMAVIML 240
LSKERLLTCC PQRRPLLLSA DELALETQPP EKEDASSLPP KFQSHLGHEH LPSCCQRKRL 300
RGAPYSFPAI HITGALVLFM TDGLTGAYSA FVYSYAVEKP LSVGHRVAGY LPSLFWGFIT 360
LGRLLSIPIS SRMKPATMVF INUVGVVTF LVLLIPSYNV VFLFVGTASL GLFLSSTFPS 420
MLAYTEDSIQ YKGCATTVLV TGAGVGEMVL QMLVGSIFQA QGSYSFLVCG VIFGCLAFTF 480

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YILLFFHRM HPGLPSVPTQ DRSIGMENSE CYQR

514

Seq ID NO: C338 Protein Sequence  
Protein Accession #: NP\_002194.1

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1	11	21	31	41	51	
MGPERTGAAP	LPLLLVLALS	QGIILNCCLAY	NVGLPEAKIF	SGPSSEQFGY	AVQQFINPKG	60
NWLLVGSPWS	GFPENRMGDV	YKCPVDLSTA	TCEKLNQTS	TSIPNVTEMK	TNMSLGLILT	120
RNMGTGGFLT	CGPLMAQCGQ	NQYYTTGVC	DISPDFQLSA	SFSPATQPCP	SLIDVVVVCD	180
ESNSIYPWDA	VKNFLKFKVQ	GLDIGPTKTQ	VGLIQYANNP	RVVFNLTATK	TKEEMIVATS	240
QTSQYGGDLT	NTFGAIQYAR	KYAYSASGG	RRSATKVMV	VTDGESHGDS	MLKAVIDQCN	300
HDNILRFGIA	VLGYLNRNAL	DTKNLIKEIK	AIASIPTRY	FFNVSDAAL	LEKAGTLGEQ	360
IPSIETVQG	GDNFQMEMSQ	VGFSADYSSQ	NDILMLGAVG	AFGWSGTIVQ	KTSHGHLIPP	420
KQAFDQILQD	RNHSSYLGSY	VAAISTGEST	HFVAGAPRAN	YTGQIVLYSV	NENGNTIVIQ	480
AHRGDQIGSY	FGSVLCSDV	DKDTITDVL	VGAPMYMSDL	KKEGGRVYLF	TIKKGILGOH	540
QFLEGPEGIE	NTRFGSAIAA	LSDINMDGFN	DVIVGSPLEN	QNSGAVIYIN	GHQGTIRTKY	600
SQKILGSDGA	FRSHLQYFGR	SLDGYGDLNG	DSITDVSIGA	FGQVVQLWSQ	SIADVAIEAS	660
FTPEKITTIVN	KNAQIILKLC	PSAKFRPTKQ	NNQVAIVYNI	TLDADGFSSR	VTSRGLFKEN	720
NERCLQKNMV	VNQASQCEPH	IYIQEPESDV	VNSLDLRVDI	SLENPGTSPA	LEAYSETAKV	780
PSIPFHKDSY	EDGLCISDLV	LDVRQIPAAQ	EQPFIVSNQN	KRLTFSVTLK	NKRESAYNTG	840
IVVDFSENLF	FASPSLPVDG	TEVTQQAAS	QKSVACDVGY	PALKREQQVT	FTINFDFNLQ	900
NLQNASLSF	QALSESQEEEN	KADNLVNLKI	PLLYDAEHL	TRSTNINPYE	ISSDGNVPSI	960
VHSFEDVQFK	FIFSLKVVTTG	SVPVSMATVI	IHIPQYTKKE	NPLMYLTGVQ	TDKAGDISCN	1020
ADINPLKIQG	TSSSVSKFSE	NFRHTKELNC	RTASCNSUTC	WLKDVHMKEG	YFVNVTTRIW	1080
NGTFASSTFQ	TQVLTAAAEI	NTYNPEIYVI	EDNTVTIPLM	IMKPDKEAEV	PTGVIIGSII	1140
AGILLLLALV	AILWKLGGFF	KRYKMTKNP	DEIDETTELS	S		1181

Seq ID NO: C339 Protein Sequence  
Protein Accession #: NP\_113648.1

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1	11	21	31	41	51	
MYRPRARAAP	EGRVRGCAVP	STVLLLLLAYL	AYLALGTGVF	WTLEGRAAQD	SSRSFQDKW	60
ELLQNFCTLD	RPAALDSLIRD	VQQAAYKNGAS	LLSNNTSMGR	WELVGSFFFS	VSTITTIGYG	120
NLSPNTMAAR	LFCIFFALVG	IPLNLVVLNR	LGHLMQQGVN	HWASRLGGTW	QDPDKARWLA	180
GSGALLSGLL	LFLLPLPLLF	SHMEGWSYTE	GFYFAPITLS	TVGFGDYVIG	MNPSQRYPLW	240
YKNMVSILWL	FGMAWLALII	KLILSQLETP	GRVCSCHHS	SKEDFKSQSW	RQGFDPREPES	300
HSPQGGCYPE	GPMGIHQHLE	PSAHAAGCCK	DS			332

Seq ID NO: C340 Protein Sequence  
Protein Accession #: NP\_004145.1

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1	11	21	31	41	51	
MEWMDNGTQA	LGLPPTTCVY	RENFKQLLLP	PVYSAVLAAG	LPLNICVITQ	ICTSRRALTR	60
TAVYTLNLAL	ADLLYACSLP	LLIYNYAQGD	HWPFQDFACR	LVRFLFYANL	HGSILPLTCI	120
SPQRYLGLCH	PLAPNHRKRG	RRAAMLVCVA	VWLAVTTQCL	PTAIFATGI	QRNRTVCYDL	180
SPPALATHYM	PYGMALTIVG	FLLPFAALLA	CYCLLACRLC	RODGPAPFVA	QERRGKAARM	240
AVVVAAAFAR	SFLPFHITKT	AYLAVRSTPG	VPCTVLEAFA	AAYKGTTPPA	SANSVLDPII	300
PYPTQKFKFR	RPHELLQKLT	AKWQRQGR				328

Seq ID NO: C341 Protein Sequence  
Protein Accession #: NP\_009128.1

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65  
70  
75  
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1	11	21	31	41	51	
MQRPGRLWL	VLQVMGSCAA	ISSMDMERPG	DGKQPIEIP	MCKDIGYNTM	RMPNLMGHEN	60
QREAAIQLHE	FAPLVEYGCH	GHLRFFLCSL	YAPMCTEQVS	TIPIACRVMC	EQARLKCSPI	120
MEQFNFKWPD	SLDCRKLPNK	NDPNYLCMEA	PNNGSDEPTR	GSGLFPPFLR	PQRPHSAQEH	180
PLKDGPGRG	GCDNPGKFEH	VEKSASCAPL	CTPGVDVYWS	REDKRFAPVV	LAIWAVLCFF	240
SSAFTVLTFL	IDPARFRYPE	RPIIFLSMCY	CVYSVGYLIR	LPAGAESIAC	DRDSGQLYVI	300
QEGLESTGCT	LVFLVLYYPG	MASLLMWVVL	TLTWFLAAGK	KWGHEATEAN	SSYFHLAANA	360
IPAVKTIILIL	VMRRVAGDEL	TGVCYVGSMD	VNALTGFVLI	PLACYLVIGT	SFILSGFVAL	420
FHIRRMKTG	GENTDKLEKL	MVRIGLFSVL	YTVPATCVIA	CYFYERLAMD	YWKILAAQHK	480
CKNNQTKTL	DCLMAASIPA	VEIFMVKIFM	LLVVGITSGM	NIWTSKTLQS	WQQVCSRRLK	540
KKSRRPASV	ITSGGIYKKA	QHPQKTHGK	YEIPAQSPTC	V		581

Seq ID NO: C342 Protein Sequence  
Protein Accession #: NP\_005752.1

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75  
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1	11	21	31	41	51	
MEVSRRKAPP	RPPRPAAPLP	LLAYILLALAA	PGRGADEFVW	RSEQAIGAIA	ASQEDGVFVA	60
SGSCLDQLDY	SLEHSLRLY	RDQAGNCTEP	VSLAPPARPR	PGSSFSKLLL	PYREGAAGLG	120
GLLLTGWTFD	RGACEVRPLG	NLSRNSLRNG	TEVVSCHPQG	STAGVVYRAG	RNRNRVLAFA	180
ATYVLPEPET	ASRCNPAASD	HDTAIALKDT	EGRSLATQEL	GRKLCEGAG	SLHFVDAFLW	240
NGSIYFPYYP	YNYTSGAATG	WPSMARIAQS	TEVLFQGGAS	LDQGHGHPDG	RRLLSSSLV	300
EALDVWAGVF	SAAAGEGQER	RSPTTTALCL	FRMSEIQARA	KRVSWDFKTA	ESHCKEGDQP	360
ERVQPIASST	LHSDLTSTVY	GTVMNRTVL	FLGTGQGQLL	KVILGENLTS	NCPEVIYBIK	420
EETPVVYKLV	PDPVKNIYIY	LTAGKEVRRR	RVANCNKHS	CSECLTATFD	HCGWCHSLQR	480
CTFGQDCVHS	ENLENWLDIS	SGAKKCPKIQ	IIRSSKEKTT	VTMVGSFSPR	HSKOMVKNVD	540
SSRELQCNKS	QPNRTCTCSI	PTRATYKDV	VNVMPSPGS	WNLSDRFNFT	NCSSLKECPA	600
CVETGCWACK	SARRCIHPPT	ACDPSDYERN	QECCPVAVEK	TSGGGRPKEN	KGNRTNQALQ	660
VFYIKSIEPQ	KVSTLGKSNV	IVTGANPTRA	SNITMILKGT	STCDKDVIVQ	SHVLNTHMK	720

5 FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITMGRNFD 780  
 VIDNLIISHE LKGNINVSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLOQ 840  
 REDPRFTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LEHGENGLN CSFENITRNQ 900  
 DLTTILCKIK GIKTASTIAN SSKKVRVKLG NLELYVEQES VPSTWYFLIV LPVLLVIVIF 960  
 AAVGVTRHKS KELSRKQSQQ LELLESELRK EIRDGFALQ MDKLDVVDSE GTVPFLDYRH 1020  
 10 FALRTFFPES GGFTHIPTED MNRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNFS 1080  
 VKDRCLPASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKMLLRTE SVVEKLLTNW 1140  
 MSVCLSGFLR ETVGEPFYLL VTTLNQKINK GPVDVITCKA LYTLNEDNLL WQVPEFSTVA 1200  
 LNVVFEKPE NESADVCRNI SVNVLDCDTI GQAKEKIPQA PLSKNGSPYG LQLNEIGLEL 1260  
 QMGTRQKELL DIBSSSVILE DGITKLNTIG HYEISNGSTI KVPKCIANFT SDVEYSDDHC 1320  
 15 HLILPDSBAF QDVQGRHRG KHKFKVKEMY LTKLLSTKVA IHSVLEKLF R SWSLPNSRA 1380  
 PFAIKYFFDF LDAQENKKI TDDPVVHIWK TNSLPLRFWV NILKNPQFVP DIKKTPIHDG 1440  
 CLSVIAQAFM DAPSLTEQQL GKEAPTNNLL YAKDIPTYKE EVKSYKPAIR DLPLLSSEM 1500  
 EEPLTQESKK HENEFNEEVA LTEIYKIYVK YPDEILNKLE RERGLEEAQK QLLHVKVLFD 1560  
 EKKCKWM 1568

Seq ID NO: C343 Protein Sequence  
 Protein Accession #: NP\_002176.1

20 1 11 21 31 41 51  
 | | | | | |  
 MTILGTTFGM VPSLLQVVSQ ESGYAQNGDL EDABLDYSP SCYSQLEVNG SQHSLTCAFE 60  
 DPDVNTTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK 120  
 25 IDLTTIVKPE APFDLSVIYR EGANDFVVT NTSHLQKKYV KVLMDVAYR QEKDENKWT 180  
 VNLSTKLTL LQRKLQPAAM YEIKVRSIPD HYFKGFWSEW SPSYFRTPE INNSSGEMDP 240  
 ILLTISILSF FSVALLVILA CVLWKKRIKP IWPVSLPDHK KTLHLCKKP RKNLNVSPNP 300  
 ESPLDQIHR VDDIQARDEV EGFLQDTFPQ QLEESERQRL GGDVQSPNCP SEDVVTTPES 360  
 FGRDSSLTCL AGNVACDAP ILSSSRSLDC RESGKNGPHV YQDLLSLGT TNSTLPPPPFS 420  
 30 LQSGILTLPN VAQQPILTS LGSNQEEAYV TMSSFYQNG 459

Seq ID NO: C344 Protein Sequence  
 Protein Accession #: NP\_002713.1

35 1 11 21 31 41 51  
 | | | | | |  
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60  
 TRPRYGRHK EDTLAFSEWG SPAAVPREL SPLDL 95

Seq ID NO: C345 Protein Sequence  
 Protein Accession #: NP\_115934.1

40 1 11 21 31 41 51  
 | | | | | |  
 MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSHPGE 60  
 45 VTGSAEGWGP EEPLPYSRFA GEGASARPRC CRNGGTCVLG SPCVCPAHT GRYCEHDQRR 120  
 SECQALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAGP SAGGAPSLLL 180  
 LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRCGRPGLG HRL 223

Seq ID NO: C346 Protein Sequence  
 Protein Accession #: NP\_006524.1

50 1 11 21 31 41 51  
 | | | | | |  
 MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISTMAVA LDYMAPDCR 60  
 55 FLTIHRGQVV YVPSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120  
 VKTDKWDPYC Q 131

Seq ID NO: C347 Protein Sequence  
 Protein Accession #: Eos sequence

60 1 11 21 31 41 51  
 | | | | | |  
 MTQVTEKSTE HPEKITSTTE KTRTPPEKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60  
 65 TETIKAPVKS TENPEKTAHV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120  
 TSRTKLSSIT SEATGNESH YLNKDGSKQG IHAGQMGEND SPPAWAIVIV VLVAVILLV 180  
 FLGLIFLVSY MMRTRRTLQ NTQYNDABDE GGPNSYPVYL MEQQLNGMQ IPSR 235

Seq ID NO: C348 Protein Sequence  
 Protein Accession #: NP\_543146.1

70 1 11 21 31 41 51  
 | | | | | |  
 MTQVTEKSTE HPEKITSTTE KTRTPPEKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60  
 75 TETIKAPVKS TENPEKTAHV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120  
 TSRTKLSSIT SEATGNESH YLNKDGSKQG IHAGQMGEND SPPAWAIVIV VLVAVILLV 180  
 FLGLIFLVSY MMRTRRTLQ NTQYNDABDE GGPNSYPVYL MEQQLNGMQ IPSR 235

Seq ID NO: C349 Protein Sequence  
 Protein Accession #: FGENESH predicted

80 1 11 21 31 41 51  
 | | | | | |

	MWRLAFCCW	GLALVSGWAT	FQOMSPSRNF	SFRLFPETAP	GAPGSIPAPP	APGDEAAGSR	60
	VERLQAFRR	RVRLLRELSE	RLELVPLVDD	SSSVGEVNF	SELMFVRKLL	SDFPVVPTAT	120
	RVAIVTFSSK	NYVVPRVDYI	STRRARQHKC	ALLLQEIPI	SYRGGTYTK	GAPQQAQIL	180
5	LHARENSTKV	VFLITDGYSN	GGDPRPIAAS	LRDSGVEIFT	FGIWQGNIRE	LNDMASTPKE	240
	EHCYLLHSFE	EFELALARRAL	HEDLPSGSFI	QDDMVHCYSL	CDGKDCDDR	MGSCKCGTHT	300
	GHFECICEKG	YVGKGLQYEC	TACPSGTYPK	EGSPGGISSC	IPCDENHITS	PPGSTSPEDC	360
	VCREGYRASG	QTCCLVHCPA	LKPPENGYFI	QNTCNHFNFA	ACGVRCHPGF	DLVGSIIILC	420
	LFNGLWSGSE	SYCRVTRCPH	LRQPKHGHIS	CSTREMLYKT	TCLVACDEGY	RLEGSCKLTC	480
10	QGNQMDGPE	PRCVERHCST	FQMPKDVII	PRNCGQPAK	FGTICVSCR	QGFILSGVKE	540
	MLRCTTSGKW	NVGVQAACVK	DVEAPQINCP	KDIBAKTLEQ	QDSANVTWQI	PTAKDNGSEK	600
	VSVHVPAPT	PPYLFPIGDV	AIVYTATDLS	GNQASCIFI	KVIDAEPFVI	DWCRSPPPVQ	660
	VSEKVAASW	DEPQSDNSG	AELVITRSHT	QGDLPQOET	IVQYTATDPS	GNNRTCDIHI	720
	VIKGSPCEIP	FTPVNGDFIC	TPDNTGVNCT	LTCLEGYDFT	EGSTDKYICA	YEDGVWKEPT	780
15	TTWPDCAK	RFAHNGFKSF	EMFYKAARCD	DTDLMKKFSE	AFETTLGKMV	PSFCSDAEDI	840
	DCRLEENLTK	KYCLEYNVDY	ENGFAIGPGG	WGAANRLDYS	YDDFLDTVQE	TATSIGNAKS	900
	SRIKRSAPLS	YKIKLIFNI	TASVPLPDER	NDTLENENQ	RLIQTLETIT	NKLKRTLNKD	960
	PMYSFQLASE	ILIADSNLS	TKKASPPCRP	GSVLRGRMCV	NCLPGTYYNL	EHTFCESCR	1020
	GSYQDEGQL	ECKLCPSGMY	TEYIHSRNI	DCKAQCKQGT	YSYSGLETCE	SCPLGTYPK	1080
20	FGSRSCLCSP	ENTSTVIRGA	VNISACGVPC	PEGKFSRSL	MPCHPCPRDY	YQPNAGKAF	1140
	LACPFYGTTP	PAGSRSITEC	STSVLNTIF	GGFGHLELLN	CPSEVFHECF	FNPCHNSGTC	1200
	QQLGRGYVCL	CPLGYTGLKC	ETDIDECSP	PCLNNGVCKD	LVGEFICECP	SGYTQORCEE	1260
	NINECSSP	LKNGICVDGV	AGYRCTCVKG	FVGLHCETE	NEQSNPCLN	NAVCEDQVGG	1320
	FLCKCPGFL	GTRCGKNVDE	CLSQPCNGA	TCKDGANSFR	CLCAAGFTGS	HCELNINEQ	1380
25	SNPCRNQATC	VBELNSYKSC	CQPGFSGRKC	ETBQSTGFNL	DFEVSGIYGY	VMLDGLMPSL	1440
	HALTCTFMWK	SDDDMNYGTP	ISYAVDNGSD	NTLLLTIDYNG	WVLYVNGREK	ITNCPSVNDG	1500
	RWHHIAITWT	SANGINKVYI	DGKLSDDGAG	LSVGLPIPGG	GALVILQEQD	KKGEFSPAE	1560
	SFVGSISQLN	LWDYVLSPPQ	VKSLATSCPE	ELSKGNVLAW	PDFLSQIVGK	VKIDSKSIFC	1620
	SDCPRLGGSV	PHLRTASELD	KPGSKVNLFC	DPGFQLVGNP	VQYCLNQGW	TQPLPHCERI	1680
30	SGVPPPLEN	FHSHADDFYA	GSTVTYQCN	GYLLGDSDRM	FCTDNGSWNG	VSPCLDVE	1740
	CAVGSDCSEH	ASCLNVDGSS	ICSCVPPYTG	DGKNCAEPIK	CKAPGNPENG	HSSGEIYTVG	1800
	AGVTFSCQEG	YQLMGVTKIT	CLESGEWNHL	IPYCKAVSCG	KPAIPENGCI	EELAFTPGSK	1860
	VTYRCNQLN	LAGDKESSCL	ANSSWSHSP	VCEPVKCSSP	ENINNGKYL	SGLTYLSTAS	1920
	YSCDTGYSLQ	GPSIIECTAS	GINDRAPPAC	HLVFCGEPPA	IKDAVITGN	FTFRNTVTYT	1980
35	CKEGYTLA	DTIECLADGK	WSRSDQCLA	VSCDEPIVD	HASPETAHRL	PGDIAFYCS	2040
	DGYSLADNSQ	LLCNAQKQW	PPEGQDMPC	IAHFCEKPPS	VSYSILESVS	KAKFAAGSVV	2100
	SFKCMGFLV	NTSAKIECMR	GGQWNPSPMS	IQCIPIVRCGE	PPSIMNGYAS	GSNYSFGAMV	2160
	AYSQNKGYI	KGEKSTCEA	TGQWSSPIPT	CHPVSCGEP	KVENGFLHT	TGRIFSEVR	2220
	YQCNPGYKSV	GSPFVPCQAN	RHWHSSEPLM	CVPLDCGKPP	PIQNGFMKGE	NFEVGSKVQF	2280
40	FCNEGVELVG	DSSWTCQKSG	KWNKSNPKC	MPAKCPPEPL	LENQLVLKEL	TTEVGVTFS	2340
	CKEGHVLQGP	FVLKCLPSQ	WNSFPVCKI	VLCTPPLIS	FGVPPISSAL	HFGSTVKYSC	2400
	VGGFLRNGS	TTLQPDGTW	SSPLPECVPV	ECQPPEEIPN	GIIDVQGLAY	LSTALYTCKP	2460
	GFELVGNNT	LOGENGHWLG	GKPTCKAIEC	LKPKELNGK	FSYTDLHYGQ	TVTYSNCRGP	2520
	RLEGPSALTC	LETGDWDVDA	PSCNAIHCD	PQPIENGFE	GADYSYGAI	IYSCFPGFQV	2580
45	AGHAMQTC	SGWSSSIPTC	MPIDCGLPH	IDFGDCTKLK	DDQGYFEQED	DMMEVPYVTP	2640
	HPPYHLGAVA	KTWENTKESP	ATHSSNFLYG	TMVSYTCNPG	YELGNPVL	QJEDGTWNGS	2700
	APSCISIEDC	LPTAPENGFL	RFTETSMGSA	VQYSCKPGHI	LAGSDLRCL	ENRKWSGASP	2760
	RCEAISCKKP	NPMVNGSIKG	SNYTYLSTLY	YECDFGVVLN	GTERRTQDD	KWDEDEPIC	2820
	IPVDCSSPPV	SANGQVRGDE	YTFQKEIEYT	CNEGFLLEGA	RSRVCLANGS	WSGATPDCVP	2880
50	VRCATPPQLA	NGVTGGLDYG	FMKEVTFHCH	EGYILHGAPK	LTCQSDGNWD	ABIPLCKPVN	2940
	CGPPEDLAHG	PVNGPFSFIHG	GHIQYQCFPG	YKLHGNSSRR	CLNSGWSGSG	SPSCLPCRS	3000
	TPVIBYGTVN	GTFDFCGKAA	RIQCFKFGKL	LGLSEITCEA	DGQWSSGFP	CBHTSCGSLP	3060
	MIENAFISET	SSWKENVITY	SCRSGYVIQ	SSDLICTEKG	VNSQYPPVCE	PLSCGSPSP	3120
	ANAVATGEAH	TYESEVKLRC	LEGYTMDDT	DTFTQKQDGR	WPPERISCSP	KKCPLEMIT	3180
55	HILVHGDDFS	VNRQVSVSCA	EGYTFEGVNI	SVCQLDGTW	PPFSDSCSP	VSCGKPSPE	3240
	HGFPVGSXYT	FESTIYQCE	PGYELEGNRE	RVCQENRQWS	GGVAICKETR	CSTPLEPLNG	3300
	KADIENRTTG	PNVVYSCNRG	YSLEGPSEAH	CTENGTSNHP	VPLCKPNPCP	VFPVIPENAL	3360
	LSEKEFYVDQ	NVSIKCREGF	LLQHGHIITC	NPDETWTQTS	AKCEKISGCP	PAHVENAIAR	3420
	GVHYQYGDMI	TYSCYSYML	EGFLRSVCLB	NGTWTSPPIC	RAVCRFPQCN	GGICQRPAC	3480
60	SCPEGWGRGL	CEEPICILPC	LNGGRCVAPY	QCDCPPGWTG	SRCHTAVQCS	PCLNGKCVR	3540
	FNRCCLSSW	TGHNCSR					3557

Seq ID NO: C350 Protein Sequence  
Protein Accession #: FGENESH predicted

65	1	11	21	31	41	51	
	MRFSVSGMRT	DYPRSVLAPA	YVSVCLLLLC	PREVIAPAGS	EPWLCQAPAPR	CGDKIYNPLE	60
	QCCYNDAIVS	LSETRQCGPP	CTFWPCFELC	CLDSFGLTND	FVVLKLVQGV	NSQCHSSPIS	120
70	SKCERGRIC						129

Seq ID NO: C351 Protein Sequence  
Protein Accession #: AAH35671.1

75	1	11	21	31	41	51	
	MVPGARGGGA	IARAAGRGLL	ALLLAVSAPL	RLQABSLDGG	CGHLVYQDS	GTMTSKNYPG	60
	TYPNHTVCEK	TITVPKGRKL	ILRLGLDIE	SQTCASDYLL	FTSSSDQYGP	YCGSMTVPKE	120
	LLLNSTSEVT	REFSGSHISG	RGFLLTYASS	DHPDLITCLE	RASHYLKTEY	SKPCPAGCRD	180
80	VAGDISGNMV	DGYRDTSLC	KAAIHAGIIA	DELGGQISVL	QRKQISRYEG	ILANGVLSRD	240
	GSLSDKRFLP	TSNGCSRSL	FEPDQIRAS	SSWQSVNESG	DQVHWSFGQA	RLQDQGPSWA	300
	SGDSSNNHKK	REWLEIDLGE	KKKITGIRTT	GSTQSNFNFY	VKSFVMNFKN	NNSKWTKYKG	360
	IVNNEKRVFQ	GNSNFRDPVQ	NNFIPPIVAR	YVRVVPTWTH	QRALKVELI	CGQITQGNDS	420
	LVRKTSQST	SVSTKQEDET	ITRPIPSEET	STGINITTVA	IPLVLLVVLV	PAGMGIFAAF	480
	RKKKKKGSPP	GSAAEQKTD	WKQIKYPPAR	RQSAEPTISY	DNEKEMTQKL	DLITSMDAG	539

Seq ID NO: C352 Protein Sequence  
Protein Accession #: Eos sequence

5  
1 11 21 31 41 51  
| | | | | |  
MGFGAGQRLR FVPAPRSSAE EAARPGQLRL GIRRGEAELA KLAPSGVMVP GARGGGALAR 60  
AAGRGLLALL LAVSAPLRLQ AEELGDGCGH LVTYQDSGTM TSKNYPGTYP NHTVCEKTIT 120  
10 VPKGKLLIIR LGDLDIESQT CASDYLLFTS SSDQYGPYCG SMTVPKELLN NTSEVTVRFE 180  
SGSHISGRGF LLTYASSDHP DLITCLERAS HYLKTEYSEK CPAGCRDVAG DISGNMVDGY 240  
RDTSLCLKAA IHAGIIADEL GGQISVLQRK GISRYEGILA NGVLSRDGSL SDKRFLFTSN 300  
GCSRSLSEFP DGQIRASSSW QSVNESGDQV HWSPGQARLQ DQGPSWASGD SSNNHKPREW 360  
LEIDLGEKKK ITGIRTTGST QSNFNFYVKS FVMNFKNNNS KWKTYKGIVN NEEKVFQGN 420  
15 NFRDPVQNNF IPPIVARYVR VVPQTHQRI ALKVELIGCQ ITQGNDSLVM RKTQSSTSVS 480  
TKKDEETITR PIPSEETSTG INITTVAIPL VLLVVLVPAG MGIFAAPRRK KKGSPYGSA 540  
BAQKTDCKWQ IKYPPARHQK AEFTISYDNE KEMTQKLDLI TSDMAG 586

20 Seq ID NO: C353 Protein Sequence  
Protein Accession #: FGENSEH predicted

1 11 21 31 41 51  
| | | | | |  
MFQRQERFLD LSSAEVAAM ILHQHPDIIN KGDGCGHLVT YQDSGTMTSK NYPGTYPNHT 60  
25 VCKRTITVPK GKRLILRLGD LDIESQTCAS DYLLFTSSSD QYGMQKEEBT EVLCLSVAGA 120  
QRVDIPVQLL PSFLEGWKGH ADARGPYCGS MTVPKELLN TSEVTVRFES GSHISGRGFL 180  
LYASSDHPD LITCLERASH YLKTEYSKFC PAGCRDVAGD ISGNMVDGYR DTSLLCKAAI 240  
HAGIIADELG GGQISVLQRK ISRYEGILAN GVLSRDGSL SDRFLFTSN CSRSLSFEFD 300  
GQIRASSSWQ SVNESGDQVH WSPGQARLQD QGPSWASGDS SSNNHKPREW BIDLGEKKKI 360  
30 TGIRTTGSTQ SNFNFYVKSF VMNFKNNNSK WKTYKGIVNN BEKVFGQNSN PRDPVQNNFI 420  
PPIVARYVRV VPQTHQRIA LKVELIGCQI TQGNDSLVMR KTSQSTSVST KKEDEETITR 480  
IPSEETSTDA MPVQIVGDHT QMISQRENLG PDEGKIPFKG TAESMVRVVF AVVVNDLGLM 540  
FLAHTPEEDI DHYCNKQIKY PFARHQSAEF TISYDNEKEM TQKLDLITSD MARYQQPLMI 600  
35 GTGTVTRKGS TFRPMDTDAE EAGVSTDAAG HYDCPQRAGR HEYALPLAPP EPEYATPIVE 660  
RHVLRHATFS AQSGYRVPGP QPGHKHSLSS GGFSPVAVGV AQDGDYQRPB SAQPADRGYD 720  
RPAKVSALAT ESHGPDSDQKP PTHPGTSDSY SAPRDCLTPL NQTAMTALL 769

40 Seq ID NO: C354 Protein Sequence  
Protein Accession #: NP\_004607.1

1 11 21 31 41 51  
| | | | | |  
MAGVSACIKY SMFTFNFLFW LOGILILALA IWVRVSNDSD AIFGSEDVGS SSYVAVDILI 60  
45 AVGAIIMILG FLCCCGAIKE SRCMLLFFI GLLIILLQV ATGILGAVPK SKSDRIVNET 120  
LYENTKLLSA AQSGYRVPGP QPGHKHSLSS GGFSPVAVGV AQDGDYQRPB SAQPADRGYD 180  
CQSYNGKQVY KETCISFIKD FLAKNLIIVI GISPLAVIE ILGLVFSMVL YCQIGNK 237

50 Seq ID NO: C355 Protein Sequence  
Protein Accession #: NP\_004608.1

1 11 21 31 41 51  
| | | | | |  
MCTGGCARCL GGTLIPLAFF GFLANILLFF PGKVIDDND HLSQBIWFFG GILGSGVIMI 60  
55 FPALVFLGLK NNDCCGCCGN EGCGKRFAMP TSTIFAVVGF LGAGYSPIIS AISINKGPKC 120  
LMANSTWGPV PHDGYLNDL ALMNKCREPL NVVWNLTLP SILLVVGIGI MVLCAIQVNN 180  
GLLGTLGDC QCCGCCGDDG PV 202

60 Seq ID NO: C356 Protein Sequence  
Protein Accession #: NP\_002372.1

1 11 21 31 41 51  
| | | | | |  
MPRPAPARRL PGLLLLLLWPL LLLPSAAPDP VARPGFRRLE TRPGGSGSPR RPSPAAPDGA 60  
65 PASGTSEPGR ARGAGVCKSR PLDLVFIIDS SRSVRPLEFT KVKTFSVRII DTLDIGPADT 120  
RVAVVNYAST VKIEFQLQAY TDKQSLKQAV GRITPLSTGT MSGLAIQTAM DEAFTEAGA 180  
REPSSNIPKV AIIVTDGRQP DQVNEAARA QASGIELYAV GVDRADMASL KMMASEPLEE 240  
HVPYVETYG VIEKSSSRFQE TPCALDPCVL GTHQCQHVCI SDGEGKHCE CSQGYTLNAD 300  
KKTCSALDRC ALNTHGCEHI CVNDRSGSYH CECYEGYTLN EDRKTCQAQD KCALGTHGCO 360  
70 HICVNDRTGS HHCCEYEGYT LNADKKTCSV RDKCALGSHG CQHICVSDGA ASYHCDYPG 420  
YTLNEDKKT CATEEARRLV STEDACGCEA TLAQDKVSS YLQRLNTKLD DILEKIKINE 480  
YQYHR 486

75 Seq ID NO: C357 Protein Sequence  
Protein Accession #: NP\_057723.1

1 11 21 31 41 51  
| | | | | |  
MARGSLRRL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCARPH 60  
80 SDFCLGCAAA PPAPFRLNWP ILGGALSLTF VLGLLSGFLV WRCRRREKFP TPIESTGGE 120  
GCPAVALIQ 129

Seq ID NO: C358 Protein Sequence  
Protein Accession #: NP\_001810.1

1 11 21 31 41 51  
 5 MQPTLLLSLL GAVGLAAVNS MPVDNRNHNH GMVTRCIIEV LSNALSKSSA PPITPECRQV 60  
 LKTSRDOVD KETTENENTK FEVRLLRDPD DASEAHSSSS RGEAGAPGEE DIQGPTKADT 120  
 EKWAEGGGHS RERADPEQWS LYPDSQVSE EVKTRHSEKS QREDEEEEG ENYQKGERGE 180  
 DSSEKHLLEE PGETQNAFLN ERKQASAIKK EELVARSETH AAGHSQEKTH SREKSSQESG 240  
 SEAGSQENHP QESKGQPRSQ EESEEGEEDA TSEVDKRRTR PRHHHGRSRP DRSSQGSLLP 300  
 SEEKGHPQEE SEESNVSMAS LGKRDHHTST HYRASEEPE YGEEIKGYPG VQAPEDLEWE 360  
 10 RYRGRGSEY RAPRPQSEES WDEEDKRNYP SLELDKMAHG YGEESEEEERG LEPGKGRHHR 420  
 GRGGEPRAYF MSDTREKRF LGEGHHRVQE NQMDKARRHP QGAWKELDRN YLYNGEGGAP 480  
 GKWQQQDLDQ DTKENREEAR FQDKQYSSHH TAEKRKLGE LFNPHYDPLQ WKSHPFERED 540  
 NMNDNFLEGE EENELTLNEK NFFPEYNYDW WEKKPFSESV NWGYEKRNLA RVPKLDLKRQ 600  
 YDRVAQLDQL LHYRKSAEF PDFYDSEEPV STEQEAENEK DRADQTVLTE DEKKELENLA 660  
 15 AMDLELQKIA EKFSQRG 677

Seq ID NO: C359 Protein Sequence  
 Protein Accession #: XP\_093082.1

1 11 21 31 41 51  
 20 MKLLCEGLKQ PNCVLQTLRW YRCLISSASC GALAAVLSTS QWLTELEFSE TKLEASALKL 60  
 LYGGKDPNC KLQKLNLPFS LSVTAALKPV GMVNCSEFS GSLVQSHFGY CQDSSPKCDL 120  
 CKLLWPSTRV AAACCGSPK SFLSEGLNWA GRLEAVEEVL GLGLVLVQPD PASQGGGHC 180  
 25 NYGSFRDLVD LEVKAEPSEL KGMQLQRP LQVLLCKIF SLKLFLEIAL PNPQGVSVV 240  
 QVTIPDGFVN VTVGSNVLI CIYTTTVASR EQLSIQWSFF HKKEMEPISS PWEKGKWDV 300  
 BAVKGLDGG QAEQLIYFSQ GQQAIVAGQF KDRITGSNDP GNASITISHM QPADSGIYIC 360  
 DVNNPFDLQ NQGLILNVSV LVKPSKPLCS VQGRPETGHT ISLSCLSLG TSPFVYVWHK 420  
 LEGRDIVPVK ENFNPTTGIL VIGNLTNFEQ GYQCTAINR LGNSSCEIDL TSSHPVGGII 480  
 30 VGALIGSLVG AAIISVVCV ARNKAKAKAK ERNSKTIAEL EPMTKINPRG ESEAMPREDA 540  
 TQLEVTLPSS IHETGPDITQ EPDYEPKPTQ EPAPEPAPGS EPMAPVDLDI ELELEPETQS 600  
 ELEPEPEPEP ESEPGVVPEP LSEDEKGVVK A 631

Seq ID NO: C360 Protein Sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 35 MVFAFWKVPF ILSCLAGQVS VVQVTIPDGF VNVTVGSNVT LICIIYTTTVA SREQLSIQWS 60  
 FPHKKEMPI SSPWEEGKWP DVEAVKGTLD GQQAELQIYF SQGQAIVAGI QPKDRITGSN 120  
 40 DPGNASITIS HMQPADSGIY ICDVNNPDPF LGQNQGILNV SVLVKPSKPL CSVQGRPETG 180  
 HTISLSCLSA LGTPSPVYVY HKLEGRDIVP VKENFNPTTG ILVIGNLTNF EQGYQCTAI 240  
 NTLGNSSCEI DLTSSEPEVG IIVGALIGSL VGAIIISV CFARNKAKAK AKERNSTIA 300  
 ELEPMTKINP RGESEAMPRE DATQLEVTLP SSIHETGPDITQ EPDYEPKPTQ EPAPEPAP 360  
 45 GSEPMAPVDL DLELEPET QSELEPEPEP EPSEPGVVV EPLSEDEKGV VKA 413

Seq ID NO: C361 Protein Sequence  
 Protein Accession #: NP\_003011.1

1 11 21 31 41 51  
 50 MVSRMVSTML SGLLFWLASG WTPAFAYSPP TDRVSEADI QRLHGVMEQ LGIARPRVEY 60  
 PAHQAMNLVG PQSIEGGAHE GLQHLGPFGN IPNIVAEITG DNIPKDFSED QGYDPPNPPC 120  
 PVGKTDGCL ENTPDTAEFS REFQLHQHLE DPEHDYPLG KWNKLLLYEK MKGGERRKRR 180  
 55 SVNPLYQQR LDNVVAKKSV PHFSDKDP B 211

Seq ID NO: C362 Protein Sequence  
 Protein Accession #: NP\_076926.2

1 11 21 31 41 51  
 60 MTTMQGMEQA MPGAGPGVPQ LGNMAVIHSH LNKGLQEKFL KGEPKVLGVV QILTALMSLS 60  
 MGITMCMAS NTYGSNPISV YIGYTINGSV MFIISGSLSI AAGIRTTKGL VRGSLGMNIT 120  
 SSVLAASGIL INTFLAFYS FHHPYCNYG NSNNCHGTMS ILMGLDGMVL LLSVLEPCIA 180  
 65 VLSAFGCKV LCCTPGGVVL ILPSHSHMAE TASPTPLNEV 220

Seq ID NO: C363 Protein Sequence  
 Protein Accession #: NP\_002082.1

1 11 21 31 41 51  
 70 MRGSELFLVL LALVLCIAPR GRAVPLPAGG GTVLTIMYPR GNHWAVGHLM GKSTGESSS 60  
 VSERGLKQ LREYIRWEEA ARNLLGLIEA KENRNEQPPQ PKALGNQPS WDSSESSNFK 120  
 DVGSGKGVGR LSAPGSQREG RNPQLNQ 148

Seq ID NO: C364 Protein Sequence  
 Protein Accession #: NP\_036393.1

1 11 21 31 41 51  
 80 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60  
 EPAKFIVPY DWASNYVDL ITEQADIALT RGAEVKRCG HSQSELQVFW VDRAVALKML 120  
 FVKESHNMK GPEATWRLSK VQPVYDSSEK THFKDAVSAG KHTANSHLS ALVTPAGKSY 180  
 EQQAQQTISL ASSDPKIVT MILSAVHIQ FDIISDFVS BEHKCPVDER EQLEETPLPI 240  
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKMG 280

Seq ID NO: C365 Protein Sequence  
Protein Accession #: NP\_003217.1

5 1 11 21 31 41 51  
| | | | |  
MLGLVLALLS SSSAEYVGL SANQCAVPAK DRVDCGYPHV TPKECNNGRC CFDSRIPGVP 60  
WCFKPLTRKT ECTF 74

Seq ID NO: C366 Protein Sequence  
Protein Accession #: NP\_002984.1

10 1 11 21 31 41 51  
| | | | |  
MSLPSSRAAR VPGPSGSLCA LLALLLLLTG PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60  
KTIGKLQVFP AGPQCSKVEV VASLKNKGQV CLDPEAPFLK KVIQKILDSG NKKN 114

Seq ID NO: C367 Protein Sequence  
Protein Accession #: NP\_005233.2

20 1 11 21 31 41 51  
| | | | |  
MRSPSAWLL GAAILLAASL SCSGTIQGTN RSSKGRSLIG KVDGTSHTVG KGVTVETVFS 60  
VDEFSASVLT GKLTTFPLPI VYTIIVFVVL PSNGMALWVP LFRITGKHPA VIYMANLALA 120  
25 DLLSVIWFPL KIAYHIHANN WIYGEALQNV LIGFFYGNMY CSILFMTCLS VQRYWVIVNP 180  
MGHSRKQANI AIGISLAIWL LILLVTIPLY VVKQTIPIPA LNITTCHDVL PEQLLVGDMF 240  
NYFLSLAIGV FLFPALITAS AYVLMIRMLR SSAMDENSEK KRKRAIKLIV TVLAMYLICP 300  
TPENLLLVVR YFLIKSQQS HVYALYIVAL CLSTLNSCID PFVYFVSHD FRDHAKNALL 360  
30 CRSVRTVKQM QVSLTSKHS RKSSSYSSSS TTVKTSY 397

Seq ID NO: C368 Protein Sequence  
Protein Accession #: NP\_003460.1

35 1 11 21 31 41 51  
| | | | |  
MAEAKTHWLG AALSLIPLIF LISGAZAAAF QRNQLLQKEP DLRLNVQKP PSPEMIRALE 60  
YIENLRQAH KEESPDPYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120  
AENEPQSAK ENKPYALNSE KNPPMDMSDD YETQQWPERK LKHMQFPPMY EENSERNPFK 180  
40 RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EEQKLYTDE DDIYKANNIA 240  
YEDVVGEDW NVVEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQGLGI QEEDLRKESK 300  
DQLSDDVSKV IAYLRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIETSRNLQI 360  
PPEDLIEMLK TGEKFGNSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420  
RAGTEALFDG LSVEDIALLL GMSAANQKT SYFFNFYNQE KVLRLPYGA GRSRSNQLPK 480  
AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVFPG GSSEDDLQEE 540  
45 EQIBQAIKEH LNQGSSQETD KLAPVSKRFP VGPPKNDDTP NRQYWDDEL MKVLEYLNQE 600  
KAEKGRHIA KRAMENM 617

Seq ID NO: C369 Protein Sequence  
Protein Accession #: NP\_112217.1

50 1 11 21 31 41 51  
| | | | |  
MPCAQSWLA NLSVVAQLLN FGALCYGRQP QPGFVRFPDR RQEHFIKGLP EYHVVGPRV 60  
DASGFILSYG LHYPIITSSRR KRDLGSEEDW VYYRISHEEK DLFPNLTVMQ GFLSNSYIME 120  
55 KRYGNLSHVK MMASAPLCH LSGTVLQQT RVGTAALSAC HGLTGPFQLP HGDFPIEPVK 180  
KHPLVEGGYH PHIVYRRQKV PETKBPCTGL KDSVNIQKQ ELWREKNERH NLPBSLSR 240  
SISKERNVET LUVADTKMIE YHGSERVESY ILTIMNMVTG LFNHNSIGNA IHIVVRLIL 300  
LEEEQGLKI VHHAECTLSS PCKWQKSNP KSDLNPVHHD VAVLLTRKDI CAGFNRCST 360  
LGLSHLSGMC QPHRSCTNINE DSGPLAFTI AHELGHSPGI QHDGKENDCE FVGRHPYIMS 420  
60 RQLQYDTPFL TWKSCSEYI TRPLDRGWGF CLDDIPKKG LKSKVIAPGV IYDVHQCQL 480  
QYGNATFCQ EVENVQTLW CSVKGFCSRK LDAAADGTQC GEKKWCMAGK CITVGGKPE 540  
IPGGWGRWSP WSHCSRTCGA GVQSAERLCN NPBPFGQKY CTGERKRYRL CNVHPCRSEA 600  
PTFRMQCSE FDTVPYKNEH YHWFFIPNPA HPCELYCRPI DGQFSEKMLD AVIDGTPCFE 660  
GNSERNVCIN GICKMVGCDY EIDSNATEDR CGVCLDGGSS CQTVRKMFQK KEGSGYVDIG 720  
65 LIPKARDIR VMEIEGAGNF LAIRSEDPEK YYLNGGFIIQ WNGNYKLAGT VFQYDRKIDL 780  
EKLMATGPTN ESWIQLLPQ VTNPGIKYEY TIQKDGLEDND VEQMYFWQYG HWTECSVTG 840  
TGIRRTAHC IKKGRGMVKA TFCDPETQFN GRQKKCHEKA CPPRWAGWE EACSAATGPH 900  
GEKRTVLCI QTMVDEQAL PPTDQHLK PKTLLSCNRD ILCPSDWTVG NWSECSVSCG 960  
70 GGVIRSVTC AKNHDEFCDV TRKFNRLALC GLQCPSSRR VLKPNKGTIS NGKNPFTLKP 1020  
VPPPTSRPRM LTTPTGPESM STSTFAISSP SPTTASKEGD LGKQWQDSS TQPELSSRYL 1080  
ISTGSTSQPI LITSQSLIQ SEENVSSSDT GPTSEGLVA TTTSGSLSS SRNPITWPT 1140  
PFYNTLTKGP EMBTHSGSGE EREQPEDKE SNPVIWTKIR VPGNDAPVES TEMPLAPPLT 1200  
PDLRESWNP PFSTVMEGLL PSQRPTTSET GTPRVEGMVT EKPANTLLPL GGDHQPEPSG 1260  
75 KTANRNHLKL PNMNMQTKSS EPVLTEDAT SLITEGFLN ASNYQLTNG HGSAHWIVGN 1320  
WSECSTTCGL GAYWKRVECT TQMSDCAAI QRDPAPKRCR LRPCAGWKEV NWSKSRNCS 1380  
GGFKIREIQ VDSRDHRLR PFHQFLAGI PPPLSMSCNP EPCEAWQVEP WSQCSRSQCG 1440  
GVQERGVFCP GGLCDWTKRP TSTMSCNEL CCHWATGNWD LCSTSCGGF QKRIVQCVSP 1500  
80 BGNKTEDQD CLCDHKRFP EFKKCNQAC KKSADLLCTK DKLSASFQCT LKAMKKCSVP 1560  
TVRAECCFSC PQTHITHYQR QRRQLLQKS KEL 1593

Seq ID NO: C370 Protein Sequence  
Protein Accession #: NP\_001053.1

1 11 21 31 41 51



	1	11	21	31	41	51	
	MRQSHQLPLV	GLLLFSFIPS	QLCEICEVSE	ENYIRLKPLL	NTMIQSNYNR	GTSAVNVVLS	60
	LKLVGIQIQI	LMQKMIQIQI	YVVKSRSLSDV	SSGELALIL	ALGVCRNAEE	NLIYDYHLTD	120
5	KLENKFQASI	ENMEAHNGTP	LITNYQLSLD	VIALCLFNNG	YSTAEVNVHF	TPENKNYYPG	180
	SQFSVDTGAM	AVLALTCVKK	SLINGQIKAD	EGSLKNISYI	TKSLVEKILS	EKKENGLIGN	240
	TFSTGEAMQA	LFVSSDYNE	NDWNCQQTIN	TVLTEISQGA	FSNPNAAAQV	LPALMGKTFI	300
	DINKSSSCVS	ASGNFNISAD	EPITVTPPDS	QSYISVNVSV	RINETYFTNV	TVLNGSVFLS	360
	VMEKAQKMD	TIFGFTMEER	SWGPIYTCIQ	GLCANNNDRT	YWELLSGGEP	LSQGAGSYVV	420
10	RNGENLEVRW	SKY					433
	Seq ID NO: C371 Protein Sequence						
	Protein Accession #: NP_004582.1						
15	1	11	21	31	41	51	
	MCCTKSLLLA	ALMSVLLHL	CGESEAAANF	DCCLGYTDRI	LHPKFIVGFT	RQLANEGCDI	60
	NAIIFHTKKK	LSVCANPKQT	WVKYIVRLLS	KVKQNM			96
	Seq ID NO: C372 Protein Sequence						
	Protein Accession #: NP_037403.1						
20	1	11	21	31	41	51	
	MAGSPILLMP	RAGGVGLLVL	LLLGLFRPFP	ALCARPVKEP	RGLSAASPPL	AETGAPRRFR	60
25	RSVPRGEAAG	AVQELARALA	HLLAEERQER	ARAEAQEAED	QOARVLAQLL	RVWGAPRNSD	120
	PALGLDDDDP	APAAQLARAL	LRARLDPAAL	AAQLVPAPVP	AAALRPRFPV	YDDGPAQDA	180
	EEAGDETEDV	DELLRYLLG	RILAGSADSE	GVAAPRRRLR	AAEDHVGSEL	PPEGVLGALL	240
	RVKRLTFAP	QVPARRLLFP					260
30	Seq ID NO: C373 Protein Sequence						
	Protein Accession #: NP_002236.1						
35	1	11	21	31	41	51	
	MLQSLAGSSC	VRIVERHRS	WCFGLVLVGY	LLYLTVFGAVV	FSSVELPYED	LRLQELRKIK	60
	RRFLSEHECL	SEQQLLEQLG	RVLEASNYGV	SVLSNASGNW	NWDFTSALFF	ASTVLSTTGY	120
	GHTVPLSDGG	KAPCIISYVI	GIPFTLLFLT	AVVQRITVHV	TRRPVLYFHI	RWGFSGQVVA	180
	IVHAVLLGFV	TVSCFFFIPI	AVFSVLEDDW	NFLESFYPCF	ISLSTIGLGD	YVPGEYNQK	240
40	FRELKIGIT	CYLLGLLIAM	LVLLETFCFL	HELEKKFRMF	VYKDKDEQ	VHIEHDQLS	300
	FSSITDQAAG	MKEDQKQNEP	FVATQSSACV	DGPANH			336
	Seq ID NO: C374 Protein Sequence						
	Protein Accession #: NP_005463.1						
45	1	11	21	31	41	51	
	METTINGTETW	YESLHVLKA	LNATLHSNLL	CRPGPGLGPD	NQTEERRASL	PGRDDNSYMY	60
	ILFVMPLEFAV	TVGSLILGYT	RSRKVDKRS	PYHVYIKNRV	SMI		103
50	Seq ID NO: C375 Protein Sequence						
	Protein Accession #: NP_005236.1						
55	1	11	21	31	41	51	
	MGRHLALLLL	LLLLFQHFQD	SDGSQRLEQT	PLQFTHLEYN	VTQENSAAK	TYVGHFVKMG	60
	VYITHPAWEV	RYKIVSGDSE	NLFKAEEYIL	GDQCFRLIRT	KGNTAILNR	EVKDHYYTLIV	120
	KALEKNTVE	ARTKVRVQVL	DTNDRPLFS	PTSYSVSLPE	NTAIRTSIAR	VSATDADIGT	180
	NGEFFYYSFKD	RTDMFAIHPT	SGVIVLTGRL	DYLETKLYEM	EILAADRGMK	LYGSSGSISSM	240
60	AKLTVHIEQA	NECAPVITAV	TLSPELORD	PAYAITVDD	CDQANGDIA	SLSTVAGDLL	300
	QQFRTVRSFP	GSKEYVKAI	GDIDWDSEPP	GYNLTQAKD	KGTTPQFSSV	KVHVTSPPQ	360
	KAGFVKFEKD	VYRAEISEPA	PENTFVVMVK	AIPAYSHLRY	VFKRTFGKAK	FSLNNTYGLI	420
	SILEFVKRQK	AAHFELEVT	SDRKASTKVL	VKVLGANSNP	PEFTQTAYKA	AFDENVPIGT	480
	TIMSLSAVDF	DEGENGYVTY	SIANLNHVPP	AIDHFTGAVS	TSENLDYELM	PRVYTLRIRA	540
65	SDWGLPYRRE	VEVLATITLN	NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSAIDADELQ	600
	LVQYQIEAGN	ELDLFSLNPN	SGVLSIKRSL	MDGLGAKVSF	HSLRITATDG	ENFATPLYIN	660
	ITVAASHKLV	NLQCEETGVA	KMLAEKLLQA	NKLHNQGEVE	DIPFDSSHVN	AHIPQFRSTL	720
	PTGIQVKENQ	PVGSSVIFMN	STDLDTPGNG	KLVAVSGGN	EDSCFMIDME	TGMLKILSPL	780
	DRETTDKYTL	NITVYDLGIP	QKAAWRLLLEV	VVVDANDNPP	EPLQESYFVE	VSEDKEVHSE	840
70	IIQVEATDKD	LGPNHGVYTS	ILTDITDTSI	DSVTGVVNIA	RPLDRELQHE	HSLKIEARDQ	900
	AREEPQLFST	VVVKVSLSDV	NDNPPTFIPP	NVRVKVREDL	PEGTVIMWLE	AHDEPLGQSG	960
	QVRYSLLDHG	EGNFDVDKLS	GAVRIVQQLD	FEKKQVYNLT	VRAKDKGKPV	SLSTCYVEV	1020
	EVVDVNEENH	PPVFSSFVEK	GTVKEDAPVG	SLVMTVSAHD	EDAGRDGEIR	YSIRDGSGVG	1080
	VFKIGESTGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS	SFBIYIEVE	DVMDNAPQTS	1140
75	EPVYYPEIME	NSPKDVSVMQ	IEAFDPSDSS	NDKLMYKITS	GNPQGFPSIH	PKTGILTTTS	1200
	RKLDREQQDE	HLLEVTVTDN	GSPPKSTIAR	VIVKILDEND	NKPOPLQKPY	KIRLPEREKP	1260
	DRERNARREP	LYRVIAITDK	EGPNABISYS	IEDGNEHGKF	FIEPKTGVS	SKRPSAAGEY	1320
	DILSIKAVDN	GRAPQSSSTR	LHIEWISKPK	QSLEPISFEE	SPTFTVMES	DPVAHMIGVI	1380
80	SVEPPGIPLW	FDITGGNYDS	HFDVDKGTGT	IIVAKPLDAE	QKSNYNLTVE	ATDGTITILT	1440
	QVFIKVIDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VDQDEKNKLI	YTLQSSRDPL	1500
	SLKKFRILDP	TGSLYTSEKL	DHEAVSPAHL	TMVVRDQDVP	VKNRFARIVV	NVSDTNDHAP	1560
	WFTASSYKGR	VYESAAVGSV	VLQVTALDKD	KGRNAEVLVS	IESGNIGNIG	NSFMIDPVLG	1620
	SIKTAKELDR	SNQASYDLMV	KATDKGSPPM	SEITSVRIFF	TIADNASPKF	TSKEYSVELS	1680
	ETVSGISFVG	MYTAHSQSSV	VYEIKDGNIG	DAFDINPHSG	TIITQKALDF	ETLPIYTLII	1740
	QGTNAGLST	NTTVLVHLQD	ENDNAPVFMQ	AEYTGILISES	ASINSVVLTD	RNVPLVIRAA	1800

	DADKDSNALL	VYHIVEPSVH	TYFAIDSSTG	AIHTVLSLDY	EETSIFHFTV	QVHDMGTPRL	1860
	FAEYANVTV	HVIDINDCPF	VFAKPLYEAS	LLLPYTKGVK	VITVNATDAD	SSAFSOLIYS	1920
	ITEGNIGKEF	SMDYKTGALT	VQNTTQLRSR	YELTVRASDG	RFAGLTSVKI	NVKESKESHL	1980
5	KFTQDVYSAV	VKENSTEABT	LAVITAIGSP	INEPLFYHIL	NPDRRFKISR	TSGLVSTTGT	2040
	PFDRQQEAF	DVVVEVIEEH	KPSAVAHVVV	KVIVEDQNDN	APVFNLPYY	AVVKVDTEVG	2100
	HVIRYVTAVD	RDSGRNGEVH	YYLKEHHEHF	QIGPLGEISL	KKQFELDTLN	KEYLVTTVAK	2160
	DGGNPAPSAE	VIVPITVMNK	AMPVFEKPFY	SABIAESIQQ	HSPVVEVQAN	SPEGLKVPYS	2220
	ITDGPFSQF	TINFNTGVIN	VIAPLDPEAH	PAYKLSIRAT	DSLTGAHAEV	FVDIIVDDIN	2280
10	DNPPVFAQQS	YAVTLSEASV	IGTSVVQVRA	TDSSEPNRG	ISYQMFNGHS	KSHDFPHVDS	2340
	STGLISLLRT	LDYEQSRQHT	IFVRAVDGGM	PTLSSDVIPT	VDVTDLNGNP	PLFBEQQIYEA	2400
	RISHAPHGH	FVTCVKAYDA	DSSDIDKLQY	SILSGNDHKK	FVIDSATGII	TLNLHRHAL	2460
	KPFYSLNLSV	SDGVFRSSTQ	VHVTVIGGNL	HSPAFLQNEY	EVELAENAPL	HTLVMEVKT	2520
	DGDSGIYGHV	TYHIVNDPAK	DRFYINERGQ	IFPLEKLDRE	TPAEKVISVR	LMADAGGKV	2580
	AECTVNVILT	DDNDNAQFPR	ATKYEVNIGS	SAAKGTSVVK	SASDADEGSN	ADITYAIEAD	2640
15	SESIVENLEI	NKLSGVITTK	ESLIGLENEF	FTFFVRAVDN	GSPSKESVVL	VYVKILPEEM	2700
	QLPKFSEPFY	TFTVSEDVFP	GTEIDLIRAE	HSGTVLYSLV	KGNTPESNRD	ESPVDRQSG	2760
	RLKLEKSLDH	ETTKWYQFSI	LARCTQDDHE	MVASVDVSIQ	VKDANDNSPV	FESSPYEAFI	2820
	VENLPGGSRV	IQIRASDADS	GTNGQVMYSL	DQSQSVEVIE	SFAINMETGW	ITTLKELDHE	2880
	KRDNYQIKVV	ASDHGEKIQ	SSTAIVDVTV	TDVNDSPPRF	TABIYKGTVS	EDDPQGGVIA	2940
20	ILSTTDADSE	EINRQVITYPI	TGGDPLGQFA	VETIQNEWKV	VYVKPILDREK	RDNYLLTITA	3000
	TDGTFSSKAI	VEVKVLDAND	NSPVCSEKTY	SDTIPEDVLP	GKLIMQISAT	DADIRSNABE	3060
	TYTLLGSGAE	KFKLNPDTGE	LKTSTPLDRE	EQAVYHLLVR	ATDGGGRFCQ	ASIVVTLEDV	3120
	NDNAPEFSAD	PYAITVFENT	EPGTLTLTRVQ	ATDADAGLNR	KILYSLIDSA	DGQFSINELS	3180
25	GIQLEKPLD	DELQAVYTLS	LKAVDQGLPR	RLTATGTIVV	SVLDINDNPP	VFEYREYGAT	3240
	VSEDILVGE	VLQVYAASRD	IEANAEITYS	IISGNEHGKF	SIDSKTGAVP	IENLOYESS	3300
	HEYLYTVEAT	DGGTPSLSDV	ATVNVNVTDI	NDNTPVPSQD	TYTIVISEDA	VLEQSVITYM	3360
	ADDADGPNIS	KHYHGIIDGN	QGSSTPIDPV	RGEVKVTKLL	DRETISGYTL	TVQASDNGSP	3420
	PRVNTTNYNI	DVSDVNDNAP	VFSRGNYSVI	IQENKPVGFS	VLQLVVTDED	SSHNGPPFFF	3480
	TIVTGNDKA	FEVNPQGVLL	TSSAIKRKEK	DHYLLQVKVA	DNGKPOLSSL	TYIDIRVIEE	3540
30	SIYPPAILPL	EIFITSSGEE	YSGGVIGKIH	ATDQDVYDTL	TYSLDPQMDN	LFSVSTGGK	3600
	LTAHKKLDIG	QYLLNVSVTD	GKFTTVADIT	VHIRQVTQEM	LNHTIARFA	NLTPPEFVGD	3660
	YWRNQRALR	NILGVRNDI	QIVSLQSEEP	HPHLDVLLFV	EKPGSAQIST	QQLLHKINSS	3720
	VTDIEIIGV	RILNVFQKLC	AGLDCPWKFC	DEKVSVDSEV	MSTHSTARLS	FVTPRHHRRA	3780
35	VCLCKEGRCP	PVHGGCEDDP	CPGSGECVSD	PWEEKHTCVC	PSGRFGQCPG	SSSMILTGN	3840
	YVKYRLTENE	NKLEMKLTMR	LRTYSTHAVV	MYARGTDYSI	LEIHHGRLQY	KPDCGSGPGI	3900
	VSVQSIQVND	GQWHAVALEV	NGNYARLVLD	QVHTASGTAP	GTLLKTLNLDN	VYFPGGHIRQ	3960
	QGTRHGRSPQ	VGNRGFRGCM	SIYLNQLELP	LNSKPRSYAH	IESVDVSPG	CFLTATEDCA	4020
	SNPCQNGGVC	NPSAGGYC	KCSALYIGTH	CEISVNPCSS	NPCLYGGTCV	VDNNGGFVQC	4080
	RGLYTGQRQ	LSPYCKDEPC	KNGGTCFDSL	DGAVCQCDG	FRGERCQSDI	DECSGNPCLE	4140
40	GALCENTHGS	YHCNCSHEYR	GRHCEDAAPN	QYVSTPWNIG	LAEGIGIVVP	VAGIFLLVVV	4200
	FVLCKRMISR	KKKHQAEPKD	KHLGPATAPL	QRPFYDSKLN	KNIYSDIPPQ	VEVRPISYTP	4260
	SIPSDRNNL	DRNSFEGSAI	PEHPEFSTFN	PESVHGHRKA	VAVCSVAPNL	PPPPPSNPS	4320
	DSDSIQKPSW	DFDYDTKVVD	LDPCLSKKPL	BEKPSQPYSA	RESLSEVQSL	SSPQSESCDD	4380
	NGYHMDTSDW	MPSVPLPDII	EPFNVEVIDE	QTPLYSADPN	AIDTDYYPGG	YDIESDPFPP	4440
45	PEDFPAABEL	PFLPPEFSNQ	FESIHPPRDM	PAAGSLGSSS	RNRQRFNLN	YLPNFYPLDM	4500
	SEPQTKGTGE	NSTCREPHAP	YPGQYQRHFE	APAVESMPMS	VIASASCSD	VSACCEVESE	4560
	VMMSDYESGD	DGHFEETVTP	PLDSQQHTEV				4590

Seq ID NO: C376 Protein Sequence  
Protein Accession #: NP\_055035.1

	1	11	21	31	41	51	
55	MCYKGCARCI	GHSVLGLALL	CIAANILLYP	PNGETKYASE	NHLSRFVWFF	SGIVGGGLLM	60
	LLPAFVPIGL	BQDDCCGCGG	HENCGKRCAM	LSSVLAALIG	IAGSGYCVIV	AALGLAEGPL	120
	CLDSLQGMNY	TFASTBQYQL	LDTSTWSECT	EPKHIVEWNV	SLFSILLALG	GIEFILCLIQ	180
	VINGVLGGIC	GFCCSHQQQY	DC				202

Seq ID NO: C377 Protein Sequence  
Protein Accession #: NP\_003750.1

	1	11	21	31	41	51	
65	MSTENVEGKE	SNLGERGRAR	SSTFLRVVQP	MFNHSIFTSA	VSPAARIRP	ILGEEDDSFA	60
	PPQLFTELDE	LLAVDQGEHE	WKETARWIKP	EEKVEQGGER	WSKPHVATLS	LHSLFELRTC	120
	MEKGSIMLDR	EASSLPQLVE	MIVDHIQIETG	LLKPELKDKV	TYTLRLKRRH	QTKKSNLRLS	180
	ADIGKTVSSA	SRMPTNPONG	SPAMTHRNLT	SSSLNDISDK	PEKQDLKQNF	MKRLPRDAEA	240
	SNVLGSEVDF	LDTFFIAPVR	LQQAIVLGLAL	TEVPVPTREF	FILLGPKGKA	KSYHEIGRAI	300
70	ATLMSDEVFH	DIAYKAKDRH	DLIAGIDEFL	DEVIVLPPGE	WDPAIRIEPP	KSLPSSDKRK	360
	NMYSGGENVQ	MNGDTPHDGG	HGGGGHGDC	ELQRTGRFCG	GLIKDIKRAK	PPFASDFYDA	420
	LNIALSAIL	PIYLATVINA	ITPGGLLGD	TDMQGVLES	FLGTAVSGAI	FCLPAQPLT	480
	ILSSTGVLV	PERLLFNFSK	DNNFDYLEFR	LWIGLWSAPL	CLILVATDAS	FLVQYPTFT	540
	BEGFSSLSIF	IPYVDAPFKM	IKLADYYPIN	SNFKVGYNTL	PSCTCVPPDP	ANISISNDIT	600
75	LAPEYLPTMS	STDYHNTTF	DWAFLSKKEC	SKYGNLVGN	NCNFVEDITL	MSFILFLGT	660
	TSSMALKKFK	TSPPYPTTAR	KLISDPAIL	SILIFCVIDA	LVGVDTPKLI	VPSEFKPTSP	720
	NRGWEVPPFG	EPMWVCLAA	AIPALLVTIL	IFMDQQTAV	IVNRKESHLK	KGAGYHLDLF	780
	WYALLMWICS	LMALPWYVAA	TVISIAHIDS	LKMETETSAP	GEQPKFLGVR	EQRVGTGLVF	840
	ITGLSEVMA	PILKPIPMFV	LYGVPLYMGV	ASLNGVQFMD	RLKLLMLPLK	HQPDFIYLRH	900
80	VPLRRVHLFT	FLQVLCALL	WILKSTVAAI	IPFVMILALV	AVRKGMDYLF	SQHDLSFLDD	960
	VIPEKDKKKK	EDBKDKKKK	GSLDSNDSDS	DCPYSEKVP	IKIPMDIMEQ	OPFLSDSKPS	1020
	DRERSPTLE	RQDSTC					1035

Seq ID NO: C378 Protein Sequence  
Protein Accession #: NP\_000949.1

1 11 21 31 41 51  
 5 MSTPGVNSSA SLSPDRINSP VTIPAVMFIF GVVGNLVAIV VLCKSRKEQK ETTFTYTLVCG 60  
 LAVTDLLGTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL FFSLSGLSII CAMSVERYLA 120  
 INHAYFYSHY VDKRLAGLTL FAVYASNVLF CALPNMGLGS SRLQYPDWTC FIDWTTNVTA 180  
 HAAYSYMYAG FSSFLILATV LCNVLVCGAL LRMHRQPMRR TSLGTEQHHA AAAASVASRG 240  
 HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICISPLVV RVFVNQLYQP 300  
 10 SLEREVSXNP DLQAIRIASV NPILDPIYI LLRKTVLVSKA IEKIKCLPCR IGGSRRRERG 360  
 QHCSDSQRTS SAMSQHSRSF ISRELKEISS TSQTLPLDLS LPDLSENGLG GRNLLPGVPG 420  
 MGLAQEDTTS LRLTRISETS DSSQGGQSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET 480  
 LNLSEKCI 488

15 Seq ID NO: C379 Protein Sequence  
 Protein Accession #: NP\_002650.1

1 11 21 31 41 51  
 20 MGHPPLLPFL LLLHTCPVAS WGLRCMQCKT NGDCRVEECA LGQDLCRTTI VRLWEBGEEL 60  
 ELVERKSTHS EKTNRITLSYR TGLKITSLTE VVCGLDLNCQ GNSGRAVYTS RSYLEICISC 120  
 GSSDMSCEER RHQSQCQCRP EEQCLDVVTH WIEGEGEGRP KDRHRLRCGG YLPGCPGNSG 180  
 FHNNDTFHFL KECNTTKCNE GPILLELENLP QNGRCQYCK GNSTHGCSSE ETFLIDCRGP 240  
 MNQCLVATGT HEPKQSYMV RGCATASMCQ HAHLGDAFSM NHIDVSCCTK SGCNRPDLV 300  
 25 QYRSGAAPQP GPAHLSLTIT LLMTARLWGG TLLWT 335

Seq ID NO: C380 Protein Sequence  
 Protein Accession #: BAB55406.1

1 11 21 31 41 51  
 30 MDEFSGQVDP LASVILPFL LENLSPEDSV LVVRAQFTFF NKTGLFQDVG PQRKTLVSYV 60  
 MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAFWDLN KNKSFQGMNT SGCVAHRDSD 120  
 ASETVCLCNH FTFGVLMDL PRSASQLDAR NTKVLTFISY ICGISAIIPS AATLLTYVAF 180  
 35 EKLRDYPSPK ILMNLSTALL FLNLLFLLDG WITSPNVDGL CIAVAVLLHP PLLATFTWVG 240  
 LEAIDHMYIAL VKVFNTYIRR YILKFCIIGW GLPALVVSVV LASRNNNEVY GKESYKKEKG 300  
 DEFQIQDPV IFYVTCAGYV GVMFPLNIAM FIVVMVQICG RNGKRSNRTL REEVLNRLS 360  
 VVSLTFLLGM TWGFAFPFAG PLNIPFMYLF SIFNSLQGLE IFIFHCAMKE NVQKQWRRLH 420  
 CQGRFRLADN SDWSKTATNI IKKSSDNLKG SLSSSSIGSN STYLTSKSKS SSTTPYKRNS 480  
 40 HTDNVSYEHS FNKSGSLRQC FHGQVLVKTG PC 512

Seq ID NO: C381 Protein Sequence  
 Protein Accession #: NP\_000565.1

1 11 21 31 41 51  
 45 MTVARPSVPA ALPLLGLPR LLLVLLCLP AVWGDCGLPP DVPNAQPALE GRTSPPEDTV 60  
 IYTKCEESFP KIPGEKDSVI CLKGSQWSDI EBFQNRSCFV PTRLNSASLK QPYITQNYFP 120  
 VGTVVEYECR PGYRREPSLS PKLTCLQNLK WSTAVEFCKK KSCPMPGEIR NGQIDVPGGI 180  
 50 LFGATISFSC NTGYKLFST SSPCLISGSS VQWSDPLEC REIYCPAPPQ IDNGIIQGER 240  
 DHYGRQSVT YACNKGFTMI GEHSIYCTVN NDEGEWSGPP PEBCRGKSLTS KVPPTVQKPT 300  
 TVNVPTTEVS PTSQKTTTKT TTPNAQATRS TPVSRTRHP HETTPNKGSG TTSGITRLLS 360  
 GHTCFTLTGL LGTLVTMGLL T 381

55 Seq ID NO: C382 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 60 MDTSLRGVLL SLFVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120  
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCPSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLTLD 240  
 65 LNYNNLDEFP TAIRTLNLK ELHFDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEFPDL 300  
 TGTANLESLE LTGAQISSLP QTVCNQLFNL QVLDLSYNLL EDLPSPSVQK KLQKIDLRN 360  
 EIYEIKVDTE QQLSLRLSIN LAWNKIAIHH FNAFSTLPSL IKLDLSSNLL SFPFITGLHG 420  
 LTHLKLITGNH ALQSLISSEN FPELKVIEMP YAYQCCAFGV CENAYKISNQ WNKGDNSMD 480  
 DLHKGDAGMF QAQDERDLED PLLDFREDLK ALHVSQCSPS PGPFKPCERL LDGWLIRIGV 540  
 70 WTIAVLALTC NALVTSTVPR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDAPTFGSF 600  
 ARHGAWWENG VGCHVIGFLS IPASESSVFL LTLAALERG SVKYSKPFET KAPFSSLEKI 660  
 ILLCALLAT MAAPVLLGGS KYGASPLCLP LPFGEPESTMG YMVALLILMS LCPLAMTIAY 720  
 TKLYCNLDKG DLENWDCSM VKHIALLLFT NCILNCPVAF LSFSSLINLT PISPEVIRFI 780  
 LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840  
 75 TQALVTFTSS SITYDLPPSS VPSPAYFVTE SCHLSSVAEV PCL 883

Seq ID NO: C383 Protein Sequence  
 Protein Accession #: NP\_003658.1

1 11 21 31 41 51  
 80 MDTSLRGVLL SLFVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120  
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCPSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLTLD 240  
 LNYNNLDEFP TAIRTLNLK ELGPHSNIR SIPEKAPVGN PSLITIHFDY NPIQFVGRSA 300

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FQHLPELRTL TLNGASQITE FFDLTGTANL ESLTLTGAQI SSLPQTVQCN LPNLQVLDLS 360  
 VNLLLEDLPF SVQCQLKQID LRHNEIYEIK VDTFOQLLSL RSLNLAWNKI AIHPNAFST 420  
 LPSLIKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELKV IEMPAYQCC 480  
 AFGVCENAYK ISNQMNKGDN SSMDDLHKKD AGMFQAQDER DLDDFLDDFE EDLKALHSVQ 540  
 CSPSPGPFKP CEHLDDGLNI RIGVWTIAVL ALTGNALVTS TVFRSPLYIS PIKLLIGVIA 600  
 AVNMLTGVSS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLLTLAAL 660  
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEF 720  
 STMGYMVALI LLNSLCFLMM TIATYTKLYCN LDKGDLLENW DCSMVKHIAL LLFTNCILNC 780  
 PVAFLSPSSL INLTISPSEV IKFILLVVVP LPACLNPPLY ILFNPFKED LVSLRKQTYV 840  
 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PFSSVPSPAY PVTESCHLSS 900  
 VAFVPCF 907

Seq ID NO: C384 Protein Sequence  
 Protein Accession #: NP\_003497.1

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1 11 21 31 41 51  
 MEMFTLLTLC IFLPLLRGHS LFTCEPITVF RCMQAYNMT FFPNLMGHYD QSIAAVEMEH 60  
 FLPLANLECS FNLETFLCKA FVPTCIEQIH VVPPCRKLCE KVSDDCKLI DTFGIRNPFE 120  
 LECDRLLQYCD ETVPVTFDPH TEFLSPQKKT EQVQRDIGFW CPRHLKTSGG QGYKFLGIDQ 180  
 CAPPENMYF KSDLELFAKS FIGTVSIFCL CATLFTPLTF LIDVRRFRYP ERPIIYYSVC 240  
 YSIVSLMYFI GFLLGSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFMAGTVWW 300  
 VILITITWFLA AGRKWCBAI BQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCVFG 360  
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQSKL KKFMRIGVF 420  
 SGLYLVPLVT LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMKY 480  
 LMTLVIGISA VFVVGSKKTC TEWAGPFKRN RKRDPISER RVLQESCEFF LKHNSKVHKH 540  
 KKHYPSSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQBTLEIQ TSPETSMREV 600  
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660  
 TGLAQSNLQ VPSSESPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT 706

Seq ID NO: C385 Protein Sequence  
 Protein Accession #: NP\_000573

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1 11 21 31 41 51  
 MRIAIVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60  
 PSKSNESHSH MDDMDDDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDEDELVT 120  
 DFPDLPATE VFTPVVPTVD TYDGRGDSV YGLRSKSKKF RRPDIQYDA TDEDITSHME 180  
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240  
 NEHSDVDSQ ELSKVSRFF SHEFHSHEM LVVDPKSKEE DKHLKFRISH ELDSASSEVN 300

Seq ID NO: C386 Protein Sequence  
 Protein Accession #: NP\_002812

45  
50  
55  
60  
65

1 11 21 31 41 51  
 MGAARGSPAR PRRLPLLSVL LPLLLGGTQT AIVFIKQPS QDALQRRAL LRCEVEARGP 60  
 VHVYWLIDGA PVQDTERFPA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANAFN 120  
 IKWIEAGPVV LKHPASEAEI PQQTQVTLRC HIDGHPRPTY QWRDGTPLS DGQSNHTVSS 180  
 KERNLTLRPA GEHSGLYSC CAHSAPGQAC SSQNTLSIA DESPARVVLA PQDVVVARYE 240  
 EAMPHQPSA QPPSLQWLF EDETPTNRS RPFHLRRATV FANGSLLLTQ VRPRNAGIYR 300  
 CIGQGQGRGP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCPLPKGLP EPSVWWEHAG 360  
 VRLPTHGRVY IASDAGVYT CHAANLAGQR RQDVNITVAT PPSWLKPKQD 420  
 SQLBEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFV FKNGTLRINS VEYDGTWYR 480  
 CMSSTPAGSI EAQARVQVLE KLKFTFPPOP QQCMFEDKEA TVPCSATGRE KPTIKWERAD 540  
 GSSLFENVTD NAGTLHFAV TRDDAGNYTC IASNGPQQI RAHVQLTVAV PITFKVEPER 600  
 TTVYQGHIAL LQCEAQGDPK FLIQWKGKDR ILDPITKLGR MHIFQNGSLV IHDVAPEDSG 660  
 RYTCLAGNSC NTKHTEAPLY VVDKPVPEES EGPSPPPYK MIQITGLSVG AAVAYIIAVL 720  
 GLMPYCKKRC KAKRLQKPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780  
 KRHSTDMLN PPRSLQPIIT TLGKSBFGEV FLAKAQGLEE GVAETLVVVK SLQTKDEQQQ 840  
 LDFRRELEMP GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ 900  
 PLSTKQKVAL CTQVALGMEH LSNRPFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960  
 YHFRQAWVPL RWMSPFAILE GDPSTKSDVW APGVLMWEVP THGEMPHGGQ ADDEVLDLQ 1020  
 AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSPK 1070

Seq ID NO: C387 Protein Sequence  
 Protein Accession #: NP\_002300.1

70  
75

1 11 21 31 41 51  
 MKVLAAGVVP LLLVLHWHKG AGSPLPITPV MATCAIRHPC HNNLMNQIRS QLAQLNGSAN 60  
 ALFILIYYTA GEFPFNLDK LCGFNVTFPP PFHANGTEKA KLVELYRIVV YLGTSLGNIT 120  
 RDQKILNPJA LSLHSLNAT ADILRGLLEN VLCRLCSKYH VGHVDVTYGP DTSGKDVFPK 180  
 KKLGCQLLKG YKQIIAVLAQ AF 202

Seq ID NO: C388 Protein Sequence  
 Protein Accession #: XP\_097508

80

1 11 21 31 41 51  
 MGRPRLTLVC HVSIIISARD LSMNNLTELO PGLFHHLRFL EELRLSGNHL SHIPQAFPSG 60  
 LYSKILMLQ NNQLGGIPAE ALWELPSLQS LRLDANLISL VPERSEFGLS SLRHLWLDN 120  
 ALTEIPVRAL NNLPALQAMT LALNRISHIP DYAFQNLTSV VVLHLHNNRI QHLGTHSPFG 180  
 LHNLETLDELN YNKLEQFPVA IRTLGRQLSL GFHNNNIKAI PEKAFMGNPL LQTIHFYDNP 240

5  
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15

IQFVGRSAFQ YLPKLHTLSL NGAMDIQEPF DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP 300  
RLRVLELSHN QIEELPSLHR CQKLEEEIGLQ HNRIWEIGAD TFSQLSSLOA LDLSWNAIRS 360  
IHPEAFSTLH SLVKLDLTDN QLTTLPLAGL GGLMHLKLG NLALSQAFSK DSFPKLRILE 420  
VPYAYQCCPY GMCASFYKAS QWEAEADLHL DDEESSKRPL GLLARQAENH YDQDLDELQL 480  
EMEDSKPHPS VQCSPTPGPF KPCYEYLPESW GIRLAVMAIV LLSVLCNGLV LLTVFAGGPV 540  
PLPPVKFVVG AIAGANTLTG ISCGLLASVD ALTFQGFSEY GARWETGLGC RATGFLAVLG 600  
SEASVLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG 660  
ASPLCLPYAP PEGQPAALGF TVALVMNSF CFLVVAGAYI KLYCDLPRGD FEAVWDCAMV 720  
RHVAMLIFAD GLLYCPVAPL SFASMLGLFP VTPEAVKSVL LVVLPPLACL NPLLYLLFNP 780  
HFRDDLRLRL FRAGDSGSLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE 840  
TYGFFSVTLI SCQPGAPRL EGSCHVEPEG NHFGNPQPSM DGEILLRAEG STPAGGGLSG 900  
GGGFQPSGLA FASHV 915

Seq ID NO: C389 Protein Sequence  
Protein Accession #: NP\_570901

20  
25  
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1 11 21 31 41 51  
MASLVSELG LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLLNT LADRVHCTNG 60  
PCGKCLSVED ALGLGEPEGS GLPPGPVLEA RYVARLSAAA VLYLSNPEGT CEDTRAGLWA 120  
SHADHLLALL ESPKALTPGL SWLLQRMQAR AAGQTPKTAC VDIPQLLEA VGAGAPGSAG 180  
GVLAALLDHV RSGSCFHALP SPQYFVDFVF QHSSEVPMT LAELSALMQR LGVGREAHSD 240  
HSRHRGASS RDPVPLISSS NSSSVMDTVC LSARDVMAAY GLSEQAGVTP BAWAQLSPAL 300  
LQQQLSGACT SQSRPPVODQ LSQSERYLYG SLATLLICLC AVFGLLLTTC TGCRCVHAHY 360  
LQTFLSLAVG ALTGDAVLHL TPKVLGLHHT SEEGLSPOPT WRLLAMLAGL YAFFLFENLF 420  
NLLLPDPED LEDGPCGHSS HSHGGHSHGV SLQLAPSELK QPKPPHEGSR ADLVAEESPE 480  
LLNPEPRRLS PELRLPYMI TLGDAVHNFA DGLAVGAAPA SSWKTGLATS LAVFCHELPH 540  
ELGDFAAALH AGLSVRQALL LNLASALTAF AGLYVALAVG VSESEAWIL AVATGLFLYV 600  
ALCDMLPAML KVRDPRPWL FLLHNVGLLG GWTVLLLLSL YRDDITF 648

Seq ID NO: C390 Protein Sequence  
Protein Accession #: NP\_061844

35  
40

1 11 21 31 41 51  
MANASEPGGS GGGEAAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPIYLLLDL 60  
CLADGLRALA CLPAVMLAAR RAAAAAGAPP GAGCKLLAF LAALFCFHAA FLLLGVGVT 120  
YLATAHRFY AERLAGWPCA AMLVCAAWAL ALAAAFPPVL DGGGDEEDAP CALEQRPDGA 180  
PGALGFLLLL AVVVGATHLV YLRLLFFIHD RRRMRPARLV FAVSHDWTFF GPFGATGAAA 240  
NWTAGFVRIS TFPALVGRIR AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LLLFLLWGPY 300  
VVASYLRVLV RGAVPQAYL TASVWLTFQA AGINPVVCFE FNRELRDCFR AQFPCCQSPR 360  
TTQATHPCDL KGIGL 375

Seq ID NO: C391 Protein Sequence  
Protein Accession #: NP\_005622

45  
50  
55  
60

1 11 21 31 41 51  
MAAARPARGP ELPELLGLLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP 60  
LSHCGRAPC EPLRYNCLG SVLPYGATST LLAGDSDSQE EAHGKLVLS GLRNAPRCWA 120  
VIQPLLCAVY MPKCENDRVE LPSRTLQCAT RGPCAIVERE RGWDFLRCCT PDRFPPEGCTN 180  
EVQNKFNSS GQCEVPLVRT DNPKNWYEDV ECGGIQCCNP LFTBAEQDM HSYIAAPGAV 240  
TGLCTLFTLA TFVADWRNSN RYPAVILFYV NACPFVGSIG WLAQFMDGAR REIVCRADGT 300  
MRLGEPSTNE TLSCVIIFVI VYALMAGVV WFVVLTYAWH TSFKALGTTY QPLSGKTSYF 360  
HLLTWSLEFF LTVALLAVAL VDGDVSIGIC FVGKYNRYR AGFVLAPIGL VLIUGGYFLI 420  
RGVMTLFSIK SNIKPGLLSEK AASKINETML RLIGIFGLAF GFVLITFSCH FYDFFNQAEW 480  
ERSFRDYVLC QANVTIGLEPT KQPIPDCEIK NRPSLLVEKI NLFAMFGTGI AMSTVWVTKA 540  
TLIIWRRTNS RLGTQSDDEP KRIKSKMIA KAFSKREHLL QNPQGLSEFS MHTVSHDGPV 600  
AGLAFDLNEP SADVSSAWAQ HVTQMVARRG AILPQDISVT PVATPVPPPE QANLWLVAE 660  
ISPELQKRLG RKIGRRKRAK EVCPLAPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG 720  
AGDSCRQAW TLVSNPFCEP PSPPQDPFLP SAPAPVAWAH GRRQGLGPIH SRTNLMDEL 780  
MDADSD 788

Seq ID NO: C392 Protein Sequence  
Protein Accession #: BAC04382

65  
70  
75  
80

1 11 21 31 41 51  
MGARSARGA LLLALLLCWD FRLSQAGRKR SGEVLPSDFP SAPAEPLPYF LQEPQDAYIV 60  
KNKPVELRCR AFPATQIYFR CMGEWVSQND HVTQEGLEDA TLGARGGLRV REVQIEVSRQ 120  
QVEELFGLSD YWQCQVAWSS AGTTKSRAY VRIAYLRKNF DQEPKGKEVP LDBEVLLQCR 180  
PPEGVPVAVV EWLKNEDVID PTQDTNFLT IDENLIIRQA RLSDTANYTC VAKNIVAKRR 240  
STTATVIVV NGWSSWAEN SPCSNRCGRG WQKTRTCTN PAFPLNGAFC EGQAQKRTAC 300  
TTICPVDGAW TEWSKWSACS TECAHWSRE CMAPPNGG RDCSGTLDS KNCTDGLCMQ 360  
NKKTLSDFNS HLEASGDAA LYAGLVVAIF VVVAILMAVG VVVYRRNCRD FDTDITDSSA 420  
ALTGGFHPVN FKTARPSNPQ LLHPSVFPDL TASAGIYRGP VYALQDSTDK IPMTNSPLLD 480  
PLPSLKVEVY SSSTTSGSGP LADGADLGV LPPGTYPSPF ARDTHFLHL SASLGSQQLL 540  
GLPRDPGSSV SGTFGCLGGR LSIPGTGVS LVPNGAIPQG KFYENYLLIN KAESTLPLSE 600  
GTQTVLSPSV TCGPTGLLLC RPVILTMFHC AEVSARDWIF QKTKQAHQGH WEEVVTLEE 660  
TLATPCYCQL EPRACHILL QLGTVVTPE SYRSARKRL QLAVFAPALC TSLEYSRLRV 720  
CLEDTVPALK EYELERTLG GYLVEEPKPL MFKDSYHNL LSLHDLPHAH WRSKLLAKYQ 780  
EIPFYHIWGS SQKALHCTFT LERHSLASTE LTCKICVRQV EGGQIFQLH TTLAETPAGS 840  
LDTLCSAPGS TTTQLGPYA FKIPLSIRQK ICNSLDAPNS RGNDRWMLAQ KLSMDRYLNY 900  
FATKASPTGV ILDLWEALQQ DGDGLNSLAS ALEEMGKSEM LVAVATDGDG 950

Seq ID NO: C393 Protein Sequence  
Protein Accession #: NP\_004616

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MNRKARRCLG HLFSLSGMVY LRIGGFSSVV ALGASTICNK IPGLAPRQRA ICQSRPDAIL 60
VIGEGSQMGL DEQCFQFRNG RWNCSALGER TVFGKELKVG SREAAPTYAI IAAGVAHAIT 120
AACTQGNLSD CGCDKEKQGG YHRDEGWKMG GCSADIRYGI GFAKVFVDAR EIKQNARTLM 180
10    NLHNNAGRKK ILEENMKLEC KCHGVSGSCT TKTCTWTLPO FRELGTVLKO KYNEAVHVEP 240
VRASNRKPT FLKIKKPLSY RKPMDTDLVY IEKSPNYCEE DFTVGSVGTQ GRACNKTAPO 300
ASGCDLMCCG RGYNTHQYAR VWQCNCCKFH CCYVKCNTCS ERTEMYTCK 349

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Seq ID NO: C394 Protein Sequence  
Protein Accession #: NP\_003777

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15      1      11      21      31      41      51
      |      |      |      |      |      |
MDALCGSGEL GSKFWDNLS VHTENPDLT CPONSLLAUV PCIVLWVALP CYLLYLRRHHC 60
20    RGYIILSHLS KLMVGLVLL WCVSWADLFY SFHGLVHGRA PAPVFFVTPV VGVVITMLLAT 120
      LLTIQYERLQG VQSSGVLIIF WFLCVCAIV PFRSKILLAK AEGEISDPFR FTTFYIHFAI 180
      VLSALILACF REKPPFSAK NVDPNPYPET SAGFLSRLFP WFTKMAIYG YRHPLEEKDL 240
      WSLKEEDRSQ MVVQQLLEAW RKQEKQTARH KASAAPGKNA SGEDEVLLGA RPRPRKPSFL 300
      KALLATFGSS FLISACFKLI QDLLSFINPO LLSILIRFIS NFMAPSWMGF LVAGLMFLCS 360
25    MMQSLILQHY YHYIFVTGVK FRTGIMGVII RKALVITNSV KRASTVGEIV NLMSSVDAQRF 420
      MDLAPFLNLL WSAPLQIILA IYFLNQNLGP SVLAGVAFMV LLIPLNGAVA VKMRAFQVKQ 480
      MKLKDSRIKL MSBILNIGIKV LKLYAWEPSP LKQVEGIRQG ELQLLRTAAY LHITTTFTWM 540
      CSFPLVTLIT LWVYVVDPN NVLDAAEKAFV SVSLFNILRL PLNMLPQLIS NLTAQASVSLK 600
      RIQQLSQEE LDPSQVERKT ISPGYAITIH SGTFTWAQDL PPTLHSLDIQ VPKGALVAVV 660
30    GPVGCCKSSL VSALLGEMEK LEGKVHMKGS VAYVPPQAWI QNCTLQENVL PGKALNPTRY 720
      QQTLEACALL ADLEMLPGGD QTEIGERGIN LSGGQRQVRS LARAVYSADAD IFLLDDPLSA 780
      VDSHVAKHIF DHVIGPEGVL AGKTRVLVTH GISFLPQTDI IIVLADGGVS EMGPYPALLQ 840
      RNGSFANFLC NYADEDEQGH LEDSWTALEG AEDKEALLIE DTLSNHTDIT DNDPVTYVVO 900
      KQFMRQLSAL SSDGEGQGRP VPRRHLPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW 960
35    DYAKAVGLCT TLAICLLYVG QSAAGANV WLSAWTNDAM ADSRQNTSL RLGVYALGI 1020
      LQGLVNLMLA MAMAAGGIAQ ARVLHQAALL NKIRSPQSF DTTPSGRILN CFSKDIYVVD 1080
      EVLAPVILML NSFFNAIST LVVIMASTPL FTVVILPLAV LYTIVQRFYA ATSRQLKRLE 1140
      SVSRSPYISH FSETVTGASV IRAYNRSRDF EIISDTKVDA NQRSCYPYII SNRWLSIGVE 1200
      FVGNVCVFLA ALFAVIGRSS LNPGLVLGSV SYSLQVTFAL NWMIRMMSDL ESNIVAVERV 1260
40    KEYSKTETEA PWVVEGSRPP EGWPPRGEVE PRNYSVRYRP GLDLVLRDLS LHVHGGEKVG 1320
      IVGRGTGAGKS SMTLCLFRIL EAAKGEIRID GLNVADIGLH DLRSQLTIIIP QDPILFSGTL 1380
      RMNLDPFGSV SEEDIWALE LSHLETFSVS QPAGLDFQCS EGGENLSVGO RQLVCLARAL 1440
      LRKSRILVLD BATAAIDLET DNLQIATIRT QFDTCTVLTII AHRNTIMDY TRVLVLDKGV 1500
45    VAEPDSPANL IAARGIFYGM ARDAGLA 1527

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Seq ID NO: C395 Protein Sequence  
Protein Accession #: NP\_004617

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50      1      11      21      31      41      51
      |      |      |      |      |      |
MRARPQVCEA LLFALALQTG VCYGIKWLAL SKTPSALALN QTOHCKOLEG LVSAQVQLCR 60
      SNLELMHTVV HAAREVMKAC RRAFPDMRWV CSSIELAPNY LLDLERGTRE SAPVYALSAA 120
      AISHAIARAC TSGDLPGCSC GPVPGEPGP GNRWGGCADN LSYGLLMGAK FSDAPMKVVK 180
55    TGSQANKLMR LENSVEGRQA LRASLEMKCK CHGVSGSCSI RTCWKGLEL QDVAADLKTR 240
      YLSATKVVHR PMGTRKHLVP KDLDIRPVKD SELVYLQSSP DFCMKNEKVG SHGTQDRQCN 300
      KTSNGSDSCD LMCCGRGYNP YTDVVVERCH CKYHWCYVY CRRCERTVER YVCK 354

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Seq ID NO: C396 Protein Sequence  
Protein Accession #: NP\_114072

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60      1      11      21      31      41      51
      |      |      |      |      |      |
MEWGYLLEVT SLLAALALI QSSGAAAAASA KELACQETV PLCKGIGYNY TYMPNQFNHD 60
      TQDEAGLEVH QFWPLVEIQ SPDLKFFLCS MYTPICLEDY KKPLPPCRSV CERAKAGCAP 120
65    LMRQYGFAMP DRMRCDRLPE QGNPDTLQMD YNRTDLTTAA PSEPRRLPPP PFGEQPPSGS 180
      GHGRPPGARF PHRGGGRGGG GGDAAAAPPAR GGGGGGKARP PGCGAAPCEP GCQCRAPMVS 240
      VSSEHPLYN RVKTGQIANC ALPCHNPFPS QDERAFTVFW IGLMSVLCFV STFATVSTPL 300
      IDMERFKYPE RPIIFLSACY LFVSVGYLVR LVAGHEKVAC SGGAFGAGGA GGAGGAAAGA 360
70    GAAGAGAGGP GGRGEYELG AVEQHVRVET TGPALCTVVF LLVYFFGMAS SIWWVILSLT 420
      WFLAAGMKMG NEAIGAGSYQ FHAAWLVPV VKSIIVLALS SVDGDPVAGI CVGNQSLDN 480
      LRGFVLAPLV IYLFITGMFL LAGFVSLFRI RSVIKQDQGP TKTHLEKILM IRLGLFTVLY 540
      TVPAVAVVAC LFYEQHNRRP WEATHNCPCL RDLQPDQARR PDYAVFMLKY FMCLVVGITS 600
      GVVWSGKTLR ESWSLCTRC CWASKGAAGV GGAGATAAGG GGGPGGGGGG GPGGGGGPGG 660
75    GGGSLYSDVS TGLTWRSCTA SSVSYPKQMP LSQV 694

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Seq ID NO: C397 Protein Sequence  
Protein Accession #: XP\_050625

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80      1      11      21      31      41      51
      |      |      |      |      |      |
MLQPGSLLL LFLASHCCLG SARGFLFLGQ PDFSYKRSNC KPIPANLQLC HGIEYQNMRL 60
      PNLLGHETMK EVLEQAGAWI PLVMKQCHPD TKKFLCSLEA FVCLDDDET IQPCHSLCVQ 120
      VKDRCAPVMS AFGFPFWDML ECDRPPQDND LCIFLASSDH LLPATEAPK VCEACKNKND 180
      DDNDIMETLC RNDPALKIKV KBITYINRDT KIILETKSKT IYKLVGVSER DLKKSVLWLK 240

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DSLQCTCEEM NDINAPYLVH GQKQGSELVI TSVKRWQKGQ REFKRISRSI RKLQC 295

Seq ID NO: C398 Protein Sequence  
Protein Accession #: NP\_001297.1

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1      11      21      31      41      51
|      |      |      |      |      |
MSMGLBITGT ALAVLGLWGT IVCCALPMWR VSAFIGSNII TSQNIWEGWL MNCVVQSTGQ 60
MQCKVYDSSL ALPQDLQAAR ALIVVAILLA AFGLLVALVG AQCTNCVQDD TARAKITIVA 120
GVLFLLAALL TLVPVWSAN TIIRDFYNPV VPEAQKREMG AGLYVGWAAA ALQLLGGALL 180
CCSCPPEKK YTATKVYSA PRSTGPGASL GTGYDRKDYY 220

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Seq ID NO: C399 Protein Sequence  
Protein Accession #: NP\_036581.1

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1      11      21      31      41      51
|      |      |      |      |      |
MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR FVLLHLHQTA HADEFDCPSE 60
LQHTQELFPQ WHLPKIAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM 120
VSITLLALVY LFGVIAAIVQ LKNGTKYKCP PHWLDKMLT RKQFGLLSFF PAVLHAIYSL 180
SYPMRSYRY KLLNWAYQOV QONKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
VSDSLTWREF HYIQSKLGIV SLLLGTIHAL IFAWNKWIDI KQFVWYTPPT FMIAVELPIV 300
VLIPKSLPL PCLRRKILKI RHGWEDVTKI NKTEICSQL 339

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Seq ID NO: C400 Protein Sequence  
Protein Accession #: NP\_001766.1

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1      11      21      31      41      51
|      |      |      |      |      |
MANCEFSPVS GDKPCCLSR RAQLCLGVSI LVLILVVVLA VVPRWRQTN SGPGETTKRFP 60
ETVLARCVKY TEIHPMRHV DQSVMDAFK GAPISKHPCN ITEEDYQPLM KLGTQIVPCN 120
KILLWSRIKD LAHQPTQVQR DMFTLEDTL GYLADDLTWC GEFNTSKINY QSCPDWRKDC 180
SNMPVSVFWK TVSRFPABAA CDVVHVMLNG SRSKIFDKNS TFGSVEVHNL QPEKVQTLA 240
WVIHGREDSS RDLQDPTIK ELESIIISKRN IQFSCKNIYR PDKFLQCVKN PEDSSCTSEI 300

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Seq ID NO: C401 Protein Sequence  
Protein Accession #: XP\_120513.2

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1      11      21      31      41      51
|      |      |      |      |      |
MVSCFSPGSL RETNENVKCF YALRAFMRM SSEAAMLGES RTPKPKHRA TTRAKIFKRF 60
PSEGESNSR LVEELAVIHT YSDDPAPTTS PSSVQPREFG VMQAPARAF GSRTPPAAAE 120
ASSPHLGIGE AACQSGARAA APRAGARRCQ PORQAAAAA TAQHTLPHA RTRADPAGRR 180
RRHPRSPAPG GEGTCEGPA PRRRMEEMQ PAEGGPSVPK IYKQSPYSV LKTFPSKRPA 240
LAKRYERPTL VELPHGLHRT PAQPPFPASPA ASSSSSFAAV VRLGAPPRPP RRGFRARGTI 300
PPLLPAQVGA GTLLPPPTSS SPSPRPRPW BAAAPRGTS HTHMWSQST LPGSDTMVSV 360
FGLMAQRRLQ HRLSLQFEWG ILGSWGTWPC QDWLEKEGQ VAVLLPRSEG NTAPKKSRLMI 420
LDAFAQQCSR VLSLNCGGK LLDNHSQSM ISCVKQEGSS YNERQEHCHI GKGVHSQSD 480
NVDIEMQYMQ RKQQTSAFLR VFTDSLQNYL LSGSFPTPNP SSASEYGHIA DVDPLSTSPV 540
HTLENISLDS TASLCKSRHL SREPPVKSDP FNPLQALAG GASRPFSGAQ GSIAIRVNSE 600
LEDGIRSVVP LSCALEMDL TSLGSKQLLN NYPVYITSQ WDEAVNSSKK DGRRLRYLI 660
RPVFTDELK YSCGLGKRKR SVQSGETGPE RRLDPVKVT CLRGTASFRS VSPSVISFHR 720
IGCGSPRTSV QPSVF 735

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Seq ID NO: C402 Protein Sequence  
Protein Accession #: BAA92562.1

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1      11      21      31      41      51
|      |      |      |      |      |
METTVLSGIN FEYKGMTGWE VAGDHIYTAA GASDNDFMIL TLVVPGRFP QSMADTENK 60
EVARITFVPE TLCSVNCELY FMVGVSRTN TPVETWKGSK GKQSYTYIE ENTITSPTWA 120
PQRTTFHEAS RYLTNDVAKI YSINVTVNMN GVASYCRPCA LEASDVGSSC TSCPAGYYID 180
RDSGTCTSCP PNTILKAHQF YGVQACVPCG PGTGNKNIHS LCYNDCTFSR NTPTRTFNYN 240
FSALANTVTL AGGPSFTSKG LKYFRHFTLS LCGNQGRKMS VCTDNVTDLR IPEGESGFSK 300
SITAYVCQAV IIPPEVTGYK AGVSSQFVSL ADRLIGVTTD MTLDGITSPA ELPHLESIGI 360
PDVIFFYRSN DVTQSCSSGR STTIRVRCSP QKTVPGSLLL PGTCSGTCG GCFHFLWES 420
AAACPLCSVA DYHAIVSSCV AGIQKTTYVW REPKLCSGGI SLPEQRVTIC KTIDFWLKVG 480
ISAGTCTAIL TLVLTCTYFWK KNQKLEYKYS KLVNMATLKD COLPAADSCA IMEGEDVEDD 540
LIFTSKSLF GKIKSPTSQ PAPVTISLSE DS 572

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Seq ID NO: C403 Protein Sequence  
Protein Accession #: NP\_055139.1

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1      11      21      31      41      51
|      |      |      |      |      |
MALQGISVVE LSGLAPGRXC AMVLADFGAR VVRVDRPGSR YDVSRLGRGK RSLVLDLKQP 60
REPRAAASVQ AVGCAAGALP PRCHGETPAG PRDAAAGKSK AYLCQAEWIN PVQSFPCRLA 120
GHDINYFLAS GVLISKIGRSG ENPYAPLNLV ADFAGGGLMC ALGIIMALPD RTRTDKGQVI 180
DAMVEGTAY LSSFLNKTQK SSLWEAPRGQ NMLDGGAPFY TTYRTADGEP MAVGAIEPQF 240
YELLKGLGL KSDLEPNQMS TDDWPEMKKK PADVFAKTK AEWQIPIGT DACVTPLTF 300
EEVVHHDHMK ERGSFITSEE QDVSPRLAPL LLNTPAIPSS KGDPPFIGHT EEILEEFGPS 360
REEIYQLNSD KIIESNKVKA SL 382

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Seq ID NO: C404 Protein Sequence

Protein Accession #: XP\_091332.1

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1      11      21      31      41      51
5  MQRWTLWAAA FTLHSAQAF PQTDISISPA LPELPLPSLC PLFWMEFKGH CYRFFPLNKT 60
   WAEADLYCSE FSVGRKSAKL ASIHSEENV FVYDLVNSCV PGIPADVWTG LHDHRQEGQF 120
   EWTDGSSYDY SYWDGSPQDD GVHADPEEED CVQIWRPPTS EQLQAPPEQL PLISSEATDV 180
   YLPEDFPAEP KLMDQSWVSR KSLKPSKSHL MEPPTPVAKH QKAKTRHRSI RGVWVPSGKA 240
10 GSWKERMNAD YGRRKRSAPR QEGRLRCRER RLRAASGQGR PEGQRKQRQ ERQERGWEEL 300
   GGVSPFMRGA AQHGLGAGS QRGAAPCEGE NHQAPELGST WRGRLQPQT AALCHFALEK 360
   LFGNAHGLAA AFVQPALQVQ EEKNNRTRFS GAYFTMSDPT CDQDSKEQSL RRGREAEKD 420
   GPYRLVKKKR GPVACPSSFE LQSGGEVCLD PPVELRAGTW IAREPP 466

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Seq ID NO: C405 Protein Sequence  
Protein Accession #: XP\_054869.2

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1      11      21      31      41      51
20 MHTCCPPVTL EQDLHRKMHS WMLQTLAFV TSLVLSAET IDYYGEICDN ACPCEEKDG 60
   LTVSCENRGI ISLSEISPPR FPIYHLLLSG NLLNRLYPNE FVNYTGASIL HLGSNVIQDI 120
   ETGAFFGLRG LRRHLHLNNK LELLRDDTFL GLENLEYLQV DYNYSVIEP NAFGKLHLLQ 180
   VLILADNLLS SLFNNLFRFV PLTHLDLRGN RLKLLPYVGL LQHMDKVVEL QLEENPWNC 240
   CELISLKDML DSISYSALVG DVVCETPFR L HGRDLDEVSQ QELCPRLIS DYEMRPQTPL 300
25 STTGVLHTTP ASVNSVATSS SAVYKFPPLK PKGTRQPNKP RVRPTSRQPS KDLGYSNYGP 360
   SIAYQTKSPV PLECPACSC NLQISDLGLN VNCQERKIES IAELOPKPYN PKMYLTENY 420
   IAVVRTDFL EATGLDLLHL GNNRISMIQD RAFGDLNLR RLYLNGNRI RLSPELFYGL 480
   QSLQYLFLQY NLIREIQSGT FDPVFNQLLL FLNNLLQAM PSGVPSGLTL LRLNLRNHF 540
   TSLPVSGVLD QLSLIQIDL HDNPDWCTCD IVGMKLWVEQ LKVGVLVDEV ICKAPKKFAE 600
   TDMRSIKSEL LCPDYSVVV STPTPSIQV PARTSAVTPA VRLNSTGAPA SLGAGGGASS 660
30 VPLSVLILSL LLVFMVSFV AAGLFVLVMK RRKNQSDHT STNNSDVSSF NMQYSVYGGG 720
   GGTGGHPAH VHRHGPALPK VKTPAGHVYE YIPHLGHMC KNPIYRSRG NSVEDYKDLH 780
   ELKVITYSSNH HLQQQQPPF PPQQPQQPPF PQLQLQPGEE ERRESHLRS PAYSVSTIEP 840
   REDLLSPVQD ADRFYRGILE PDKHCSTTPA GNSLPEYKPF PCSPAAYTFS PNYDLRRPHQ 900
35 YLHPGAGDSR LREPVLYSPP SAVFVEPNRN EYLELAKLN VEPDYLEVLE KQTTFSQF 958

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Seq ID NO: C406 Protein Sequence  
Protein Accession #: NP\_000784.2

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1      11      21      31      41      51
40 MGILSVDLLI TLQILPVFFS NCLFLALYDS VILLKHVLL LSRKSTRGE WRRMLTSEGL 60
   RCVWKSFLLD AYQVKLGED APNSSVVHVS STEGGDNSGN GTQEKIAEGA TCHLLDFASP 120
   ERPLVVNFGS ATUPPFTSQL PAFRKLVEEF SSVADFLVY IDEAHPSDGN AIPGDSLSL 180
45 EVKKHQQED RCAAQQLLE RFSLPQCRV VADRMNNAN IAYGVAPERV CIVQRQKIAY 240
   LGKGKPFYSN LQEVHRWLEK RFSKRUKTR LAG 273

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Seq ID NO: C407 Protein Sequence  
Protein Accession #: NP\_006540.2

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1      11      21      31      41      51
50 MSSCVSSQSS SNRAAPQDEL GGRGSSSSSES QKPCEALRGL SLSIHLGME SFIVVTECEP 60
   GCAVDLGLAR DRPLEADGQE VPLDSSGSQA RPHLSGRKLS LQERSQGGLA AGGSLDMNGR 120
55 CICPSLPYSP VSSPQSSPRL PRRTVESHH VSITGMQDCV QLNQYTLKDE IGKGSYGWVK 180
   LAYNENDNTY YAMKVLKSKK LIRQAGFPRR PPRGTRPAP GGCIQPRGPI EQVYQETAIL 240
   KKLIDHPNVVK LVEVLDDPNE DHLVMVFELV NQGPVMEVPT LKPLSEDOAR FYFQDLIKGI 300
   EYLHYQKIIH RDIKPSNLLV GEDGHKIAD FGVSENEFKGS DALLSNTVGT PAFMAPESLS 360
   ETRAKIPSGA LDVWAMGVTL YCFVFGQCPP MDERIMCLHS KIKSQALEPP DQPDIAEDLK 420
60 DLITRMLDIN PESRIVVPEI KLHPVVTREG AEPLPSEDEN CTLVEVTEEE VENSVKHIPS 480
   LATVILVKTM IRKRSFGNPF EGSRREERSL SAPGNLLTKK PTRECELSLS LKEARQRHQ 540
   PGRHPAPRG GGSALVRGSP CVESCWAPAP GSPARMHPLR PEEAMEPE 588

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Seq ID NO: C408 Protein Sequence  
Protein Accession #: NP\_061116.2

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1      11      21      31      41      51
65 MGLSLPKKKG LILCLWSKFC RWFQRRSWA QSRDEQNLIQ QKRIWESPLL LAAKNDVQA 60
   LNKLLKYEDC KVHQRGAMGE TALHIAALYD NLEAAMVME AAPVLVFEPM TSELYEGQTA 120
70 LHIAVNVQNM NLVRALLARE ASVSARATGT AFRRSPCNLI YFGEHPLSFA ACVNSEIIVR 180
   LLIEHGADIR AQDSLGNLVL HILILQPNKT FACQMYNLLI SYDRHGHLQ PLDLVFNHGG 240
   LTPPKLAGVE GVTVMFQHLM QKRKHTQWY GPLTSTLYDL TEIDSSGDEQ SLELEIITTK 300
   KREARQILDQ TPVKELVSLK WKRYGRPYFC MLGAIYLLYI ICTMCCIYR PLKPRTNNTT 360
75 SPRDNTLLQ KLGQAYMTP KDDIRLVGEL VTVIGAIIL LVEVPDIFRM GVTRPFGQTI 420
   LGGPFVLI IYAFMVLVTM VMRLISASGE VVPMSPALVL GWCNMVYFAR GFQMLGPPTI 480
   MIQKMIQGD LMRFCWMAVV ILGFASAPYI IFQTEDPREL GHFYDYPMAL FSTFELPLTI 540
   IDGPANYND LPFMYISITYA APAIIATLLM LNLIIAMMGD THWRVAHERD ELWRAQIVAT 600
   TVMLERKLPR CLWPRSGICG REYGLGDRWF LRVEDRQDLN RQRIQRYAQA FHTRGSEDLD 660
80 KDSVEKLELG CFPSPHLSLP MPSVSRSTSR SSANWERLRQ GTLRRLRGI INRGLEDGES 720
   WEYQI 725

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Seq ID NO: C409 Protein Sequence  
Protein Accession #: NP\_068710.1



1 11 21 31 41 51  
 1 MQKVTILGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW 60  
 5 RSGGEGAGRG WGSPPPLTTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS 113

Seq ID NO: C410 Protein Sequence  
 Protein Accession #: NP\_005962.1

1 11 21 31 41 51  
 10 1 MQKVTILGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK 60  
 CKCKFGQKSG HHPGETPPLI TPGSAQS 87

Seq ID NO: C411 Protein Sequence  
 Protein Accession #: NP\_004952.1

1 11 21 31 41 51  
 20 1 MLSKVLPLVL GILLILQSRV RGPQTBSKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60  
 TGSRVGKLPE ASRIILNTLS NYDHKLRLPGI GEKPTVVTV E IAVNSLGPLS ILDMYETIDI 120  
 IFSQTYWDER LCYNDTFESL VLNQNVVSQ L WIPDTFFRNS KRTHEHEITM PNQMVRIYKD 180  
 GKVLTYTIRMT IDAGCSLHML RPFMDSHSCP LSFSSFSYPE NEMIVKWENF KLEINEKNSW 240  
 25 KLFQDFDTGV SNKTEIITTP VGDFMVMTIF FNVSRFPYGV AFQNYVPSSV TMLSWVSWF 300  
 IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIACFPV CPCALLEFAV 360  
 LNFLIYNQTK AHASEKLEHP RINSRAHART RARSACARQ HQEAPVQIV TTEGSDGEER 420  
 PSCSAQQPPS PGSPGPRSL CSKLACCCEWC KRFFKYFCMV PCEGSTWQQ GRLCIHVYRL 480  
 DNYSRVVPFV TFFFFNVLYW LVCLNL 506

Seq ID NO: C412 Protein Sequence  
 Protein Accession #: NP\_068819.1

1 11 21 31 41 51  
 35 1 MEYTIIDIFS QTWYDERLCY NDTFESLVN GNVVSQLWIP DTFPRNSKRT HEHEITMPNQ 60  
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120  
 INEKNWSKLF QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180  
 LSWVSFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFPVFCFC 240  
 ALLEPAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE APVQIVTTE 300  
 40 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCCEWCKRF KKYFCMVPCD EGSTWQQARL 360  
 CIHVRLDNY SRVVPVPTFF FPNVLYWLVC LNL 393

Seq ID NO: C413 Protein Sequence  
 Protein Accession #: NP\_068822.1

1 11 21 31 41 51  
 45 1 MEYTIIDIFS QTWNSKRTHE HEITMPNQMV RIYKDGKVLY TIRMTIDAGC SLHMLRFPMD 60  
 SHSCPLSFSS FSYPENEMIY KWENFKLEIN EKNWSKLFQF DFTGVSNKTE IITTPVGDPM 120  
 50 VMTIFFNVSR RFGYVAFQNY VPSSVTMLS WVSFWIKTES APARTSLGIT SVLMTTLGT 180  
 FSRKNFPRVS YITALDFYIA ICFVFCFAL LEPAVLNFI LYNQTKAHAS KLRHPRINSR 240  
 AHARTRARS ACARQHQRAF VCQIVTTEGS DGEERPSCSA QQPPSPGSPE GPRSLCSKLA 300  
 CCEWCKRFK YFCMVPCDCEG STWQQGRLCI HVYRLDNYSR VVPVPTFFFF NVLYWLVCIA 360  
 L 361

Seq ID NO: C414 Protein Sequence  
 Protein Accession #: NP\_068830.1

1 11 21 31 41 51  
 60 1 MEYTIIDIFS QTWYDERLCY NDTFESLVN GNVVSQLWIP DTFPRNSKRT HEHEITMPNQ 60  
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120  
 INEKNWSKLF QDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180  
 LSWVSFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFPVFCFC 240  
 65 ALLEPAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE APVQIVTTE 300  
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCCEWCKRF KKYFCMVPCD EGSTWQQGRL 360  
 CIHVRLDNY SRVVPVPTFF FPNVLYWLVC LNL 393

Seq ID NO: C415 Protein Sequence  
 Protein Accession #: NP\_068591.1

1 11 21 31 41 51  
 70 1 MPAVSGPGPL FCLLLLLLDP HSPBTGCPPL RRFYKLSFK GPRALPGAG IPFWSHHGDA 60  
 ILGLEEVRLT PSMNRNSGAV WSRASVPFSA WEVEVQMRVT GLGRRGAGM AVWYTRGRGH 120  
 75 VGSVLGGLAS WDGIGIFFDS PAEDTQDSPA IRVLASDGH I PSEQPGDGAS QGLGSCHWDF 180  
 RNRPHPRFRAR ITYNQRLRM SLNSGLTFS D PGEFCVDVGP LLLVPGGFFG VSAATGTIAD 240  
 DHDVLSPLTF SLSEPSPEVP PQPFLEMQLL RLARQLEGLW ARLGLGTRED VTPKSDSEAG 300  
 GEGERLFDLE ETLGRHRRIL QALRGLSKQL AQAERQWKQ LGPPGQARPD GGWALDASCQ 360  
 80 IPSTPGRGGH LSMSLNKD SA KVGALLHGQW TLLQALQEMR DAAVRMAAEA QVSYLPVIGIE 420  
 HHFLELDHIL GLLQELRGP AKAAAKAPRP PQQPPRASSC LQPGIFLFYL LIQTVGFFGY 480  
 VHFQELNKS LQECSTGSL PLGPAPHTPR ALGILRRQPL PASMPA 526

Seq ID NO: C416 Protein Sequence  
 Protein Accession #: XP\_117036.1

5	1	11	21	31	41	51	
	MERRTRGALG	SRPPPPPLPA	LRHLCTGLQA	AGMAWPGTLW	RHTCQGRAXA	AEGPWGLFRP	60
	HRCFPREAGQA	PVGSPETQG	VAHVCSRARV	SVDREPGGG	AYAMHVTPRW	KGCHRHSGRT	120
	VRGSVSWKRP	EQAAPETGRG	PAVARGSGDG	NECGWG			156
	Seq ID NO: C417 Protein Sequence						
	Protein Accession #: XP_167803.2						
10	1	11	21	31	41	51	
	MPGKGQRKTA	TNKPGLPGA	PGVGIGGHCL	YVLECKCFIK	NKTKTHHHKK	KNFAAKRNEE	60
15	KLKKKKQEK	KNHTKPFHHT	YPLSQDPLP	AKSYFCGNP	CPLWQGLF		108
	Seq ID NO: C418 Protein Sequence						
	Protein Accession #: NP_079056.1						
20	1	11	21	31	41	51	
	MFRIVERIEM	PRHEVYVLLI	RNIFLKISII	GILCYWLNT	VALSGEECWE	TLIGQDIYRL	60
	LLMDVFVSLV	NSFLGEFLRR	IIGMQLITSL	GLQEFDIARN	VLELIYAQTL	VWIGIFFCPL	120
	LPPIQMIMLF	IMFYSKNISL	MMNFQPPSKA	WRASQMMTFP	IFLLFPSPST	GVLCTLAITI	180
25	WRLKPSADCG	PFRGLPLFIH	SIYSWIDTSL	TRPGYLVVVV	IYRNIGSVH	FFILTILIVL	240
	ITITLYNQIT	EGRKIMIRLL	HEQIINEGKD	KMFLIEKLIK	LQDMEKKANP	SSLVLERREV	300
	EQQGFHLGGE	HDGSLDLRSR	RSVQEGNPRA				330
	Seq ID NO: C419 Protein Sequence						
	Protein Accession #: Eos sequence						
30	1	11	21	31	41	51	
	MLSDDHVNEI	IIQVENVSSG	VQSHPPSSNQI	FQEKVLLDSS	INMVLISIDI	DVIDSQTVSK	60
	RNDQKGNQVL	RFSTSLNESM	SQTLHSLECM	GIDTPGSSHE	TVQGGKLIAS	LIPMTSRDRI	120
35	KAIRNQPRMT	EKKRNLKIV	DKEKSKQTHR	ILQLNCCIQC	LNSISRAYRR	SKNSLSEILN	180
	SISLWQKTLK	IIGGKFGTSV	LSYFNFLRWL	LKFNIPSPIL	NFSFIIIPQF	TVAKKNTLQF	240
	TGLEFFTGVG	YPRDTVMYYG	FYTNSTIQHG	NSGASYNMQL	AYIPTIGACL	TTCFFSLLFS	300
	MAKYFRNNFI	NPHIYSGGIT	KLIPCWDFTV	THEKAVKLKQ	KNLSTEIREN	LSELRQENSK	360
	LTPNQLLTRF	SAYMVAVVVS	TGVAIACCAA	VYLAENLE	FLKTHSNPGA	VLLLPFVWSC	420
40	INLAVPCIYS	MFRIVERIEM	PRHEVYVLLI	RNIFLKISII	GILCYWLNT	VALSGEECWE	480
	TLIGQDIYRL	LLMDVFVSLV	NSFLGEFLRR	IIGMQLITSL	GLQEFDIARN	VLELIYAQTL	540
	VWIGIFFCPL	LPPIQMIMLF	IMFYSKNISL	MMNFQPPSKA	WRASQMMTFP	IFLLFPSPST	600
	GVLCTLAITI	WRLKPSADCG	PFRGLPLFIH	SIYSWIDTSL	TRPGYLVVVV	IYRNIGSVH	660
45	FFILTILIVL	ITITLYNQIT	EGRKIMIRLL	HEQIINEGKD	KMFLIEKLIK	LQDMEKKANP	720
	SSLVLERREV	EQQGFHLGGE	HDGSLDLRSR	RSVQEGNPRA			760
	Seq ID NO: C420 Protein Sequence						
	Protein Accession #: NP_002241.1						
50	1	11	21	31	41	51	
	MGGDLVLGLG	ALRRKRRLLE	QEKSLAGWAL	VLAGTGIGLM	VLHAEMWFG	GCSWALYLF	60
	VKCTISISTP	LLLCLIVAFH	AKEVQLFMTD	NGLEDWRVAL	TGRQAAQIVL	ELVVCGLHPA	120
	PVRGPPPCVD	LGAPLTSPOQ	WPGFLGQGEA	LLSLAMLLRL	YLVPRAVLLR	SGVLLNASYR	180
55	SIGALNQVRP	RHWFAVKLYM	NTHPGRLLLG	LTGLGLWLT	WVLSVAERQA	VNATGHLSDT	240
	LWLIPITFLT	IGYGDVVPQT	MWGKIVCLCT	GVMGVCTAL	LVAVVARKLE	FNKAERHVEN	300
	FMDIQYTKK	MEBSAARVLQ	EAMMFYKHTR	RKESHAARRH	QRKLAAAINA	FRQVRLKHRK	360
	LREQVNSMVD	ISKMMILYD	LQQLSSSRH	ALEKQIDTLA	GKLDALTELL	STALGPRQLP	420
60	EPSQQSK						427
	Seq ID NO: C421 Protein Sequence						
	Protein Accession #: NP_079533.1						
65	1	11	21	31	41	51	
	MGGKQRDEDD	EAYGKPVKYD	PSFRGPIKNR	SCTDVICCVL	FLLFILGYIV	VGIVAWLYGD	60
	PRQVLYPRNS	TGAYCGMGEN	KDKPYLLYFN	IFSCILSSNI	ISVAENGLQC	PTPQVCVSSC	120
	PEDPWTGVGN	EPSTVGEVF	YTKNRNFCLE	GVPWNMTVIT	SLQELCPSF	LLPSAPALGR	180
	CPFWTNITPP	ALPGITNDTT	IQQGISGLID	SINARDISVK	IFEDFAQSWY	WILVALGVAL	240
70	VLSLLFILLL	RLVAGPLVLV	LILGVLGVLA	YGIYYCWEY	RVLADKQASI	SQLGFTTNLS	300
	AYQSQVETWL	AALIVLAVLE	AILLVLVIFL	RQRIRIAIAL	LKEASKAVGQ	MMSTMIFYPLV	360
	TFVLLLICIA	YWMATLYPL	PTQPATLGYV	LWASNISSPG	CEKVPINTSC	NPTAHLVNSS	420
	CPGLMCVPOG	YSSKGLIQRS	VFNLIQYGV	GLFWTLNWL	ALGQCVLAGA	PASFYWAFHK	480
	PQDITPTPLI	SAFIRTLRYH	TGSLAFGALI	LTLVQIARVI	LEYIDHKLRG	VQNPVARCIM	540
75	CCFKCCLWCL	EKFIKFLNRN	AYIMIAIYK	NPCVSAKNAP	MLLMRNIVRV	VVLDDKVTDL	600
	LFFGKLLVVG	GVGVLSFFFP	SGRIPGLGKD	FKSPHLYYTW	LPINTSILGA	YVIASGFFSV	660
	FGMCVDTLFL	CFLIEDLRNN	GSLDRPYYS	KSLKLILGKK	NEAPPDNKKR	KK	712
	Seq ID NO: C422 Protein Sequence						
	Protein Accession #: NP_057264.1						
80	1	11	21	31	41	51	
	MGSNSGQAGR	HIYKSLADDG	PFDSVEPPKR	PTSLRLIMHSM	AMFGREFCYA	VEAAYVTPVL	60

5 LSVGLPSSLY SIVWFLSPIL GFLLPVVGS ASDHCRSRWG RRRPYILTIG VMMLVGMALY 120  
 LMGATVVAAL IANPRKRLVM AISVTMIGVV LDFDAADFID GPIKAYLFDV CSHQDKEKGL 180  
 HYHALFTGFG GALGYLLGAI DWAHLELGRLL LGTEFQVMFF FSALVLTLCF TVHLCSISEA 240  
 PLTEVAKGIP PQQTPODPPL SSDGMVEYGS IREKVKNGYVN PELAMQGAKN KNEAEQTRRA 300  
 MTLKSLRLAL VNMPPHYRYL CISHLIGWTA FLSNMLFFTD PMGQIVYRGD PYSAHNSTEF 360  
 LIYERGVEVG CWGFCINSVF SSLYSYFQKV LVSYIGLKLGL YFTGYLLFGL GTGPIGLFPN 420  
 VYSTLVLCSL FGVMSSTLYT VPFNLITEYH REEEKERQQA PGGDFFDSVR KGKMDCATLT 480  
 CMVQLAQILV GGLGLFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD 530

10 Seq ID NO: C423 Protein Sequence  
 Protein Accession #: NP\_003264.1

15 1 11 21 31 41 51  
 | | | | |  
 MEGFGGVGGR GTRGFAAKGV WRGRAEEDGPV LGAAERGFMV STGSRRRVFE GPGGGGLRWT 60  
 PGKGTGRQRG AWGPRADGV RRRTLGMPRG SRRDVRAPCG PAGSWGARGG RRRDGPSSRR 120  
 RGSATAAARH HVPPAPGGPF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT 180  
 AGAQAGAPAR GRSGESEWA RRGKGRPGPY QSPGPAVAE GQELKDKSRL RYPINGPQAL 240  
 20 VLTALLVGLG MSAGLPLGAL PEMLLPLAFV ATLTAIFISL FLYMKAQVAP VSALAPGGNS 300  
 GNPIYDFPLG REINPRICPF DFKYFCELRP GLIGWVLINL ALLMKEARL GSPSLAMWLV 360  
 NGPQLLYVGD ALWHEEAVLT TMDITHDGF FMLAFGDMAW VPFTYSLQAQ FLLEHPQPLG 420  
 LPMASVICLI NATGYIIFRG ANSQNTFRK NPSDPRVAGL ETISTATGRK LLVSGWGMV 480  
 RHPNYLGLDI MALAWSLPCG VSHLLPYFYL LYPTALLVHR EARDERSACR STAWPGRSTA 540  
 25 GHVPTHPPAH PGPAGSTHLG LKGLHPTQP 589

Seq ID NO: C424 Protein Sequence  
 Protein Accession #: NP\_056535.1

30 1 11 21 31 41 51  
 | | | | |  
 MGRLLRAARL PPLLSPLLLL LVGGAFGLGAC VAGSDEPGPE GLTSTSLDL LPTGLEPLD 60  
 SEEPSETMGL GAGLGAPGSG FPSENEESR ILQPPQYFWE EEEELNDSSL DLGPTADYVF 120  
 PDLTEKAGSI EDTSQAEQLP NLPSPLPKMN LVEPPWHMPP REEEKEEVEE EEREKEVEK 180  
 35 QEEEEEEELL PVNGSQEEAK PQVRDFSLTS SSQTPGATKS RHEDSGDQAS SGVEVESSMG 240  
 PSLLLPSTVF TTVTPGQDS TSQEAETVL PAAGLGVEFE APQEAASEAT AGAAGLSGQH 300  
 EEPVLPSPFP QTTAPSGAEH PDEDPLGSRT SASSPLAPGD MELTPSSATL QGEDLNQQLL 360  
 EGQAEEAQR IPWDSQVIC KDWSNLGKN YIILNMTENI DCEVFRQHRG PQLLALVEEV 420  
 LPRHGSQHG AWHISLSKPS EKEQHLLMTL VGEQGVVPTQ DVLSMLGDIR RSLREIGIQN 480  
 40 YSTSSQCAR ASQVRSYGT LFPVVLVIGA ICIIIIALGL LYNCWQRRLP KLKHVSHGEE 540  
 LRFVENGCHD NPTLDVASDS QSEMQEKHPS LNGGGALNGP GSWGALMGK RDPEDSDVPE 600  
 EDTHL 605

Seq ID NO: C425 Protein Sequence  
 Protein Accession #: NP\_001188.1

45 1 11 21 31 41 51  
 | | | | |  
 MSEVRPLSRD ILMETLLYEQ LLEPPTMEVL GMTDSEEDLD PMEDFDSLEC MEGSDALALR 60  
 LACIGDEMVD SLRAPRLAQL SEVAMHSLGL APIYDQTEDI RDVLSRFMDG FTTILKENIMR 120  
 50 FWRSPFNGSW VSCQVLLAL LLLLALLLPL LSGGLHLLK 160

Seq ID NO: C426 Protein Sequence  
 Protein Accession #: AAF76225.1

55 1 11 21 31 41 51  
 | | | | |  
 MATPLPPSP RHLRLRLRL SGLVLGAALR GAAAGHPDVA ACPGSLDCAL KRRARCPFGA 60  
 HACGCLQPF QEDQQLCVP RMRRPPGGGR PQPRLEDEID FLAQELARKE SGQSTPPLPK 120  
 60 DRQRLPEPAT LGFSARGQGL ELGLPSTPTG PTPPTHTSLG SPVSSDPVEM SPLEPRGGQG 180  
 DGLALVLILA FCVAGAAALS VASLCWCRLQ REIRLTQKAD YATAKAPGSP AAPRISPGDQ 240  
 RLAQSAEMYH YQHQQQMLC LERHKEPPKE LDTASSDEEN EDGDFTVYEC PGLAPTGE 300  
 VRNPLFDHAA LSAPLPAPSS PPALP 325

65 Seq ID NO: C427 Protein Sequence  
 Protein Accession #: NP\_004436.1

70 1 11 21 31 41 51  
 | | | | |  
 MVCSLWVLLL VSSVLALIEV LLDITGETSE IGWLTYPGG WDEVSVLDDQ RRLTRTFEAC 60  
 HVAGAPPGTG QDNWLQTHFV ERRGAQRAHI RLHFSVRACS SLGVSGGTCR ETFTLYYRQA 120  
 EEPDSDSVS SWHLKRWTKV DTIAADESP SSSSSSSSS SAAMAVGPHG AGORAGLQLN 180  
 VKERSFGPLT QRGFYVAFQD TGACIALVAV RLFSYTCPAV LRSFASFPET QASGAGGASL 240  
 75 VAAVGTCTVAH AEPEEDGVGG QAGGSPFRLH CNBEGKMWVA VGGCQCQPGY QPARGDKACQ 300  
 ACPRGLYKSS AQNAPCSPCP ARSHAPNPA PVPCLBGFY RASDPPBPAP CTGPPSAPBP 360  
 LWFVQGSAL MWRRLPREL GGRGDLLENV VCKEGRQES PASGGGTCR RCRDEVHFD 420  
 RQRGLTESV LVGGLRAHVP YILEVQAVNG VSELSPDPQ AAANVSTSH EVPSAVPVVH 480  
 QVSRASNSIT VSWPQPDQTN GNILDYQLRY YDQAEDESHS FTLTSETNTA TVTQLSPGHI 540  
 YGFQVRARTA AAGHPYGGKV YFQTLPGQEL SSQLEPRLSL VIGSILGALA FLLLAITVL 600  
 80 AVVFQKRKRG TGYTEQLQY SSPGLGVXY IDPSTYEDPC QAIRELAREV DPAYIKIEEV 660  
 IGTGSPGEVR QGRQLPRGR EYTVAIQALW AGGAESLQMT FLGRAAVLQG FOHFNILRLE 720  
 GVVTKSRLPM VLTEFMEELP LDSFLRQREG QPSSQLQVAM QRGVAAAMQY LSSFAVHRS 780  
 LSAHSLVNS HLVCCKVARLG HSPQGPSCLL RWAAPVIAH GKHTSSDVW SPGILMWEV 840  
 SYGERPYNDM SEQEVNABE QEFRLPPPPG CPPLGLHLLM DTWQKDRARR PHFDQLVAAP 900  
 DKMIRKFDTL QAGDGPGERP SQALLTPVAL DFPCLDSPQA WLSAIGLECY QDNFSEKPLC 960

TFSDVAQLSL EDLPALGITL AGHQKLLHH IQLLQHLRQ QGSVEV

1006

Seq ID NO: C428 Protein Sequence  
Protein Accession #: XP\_043340.2

1	11	21	31	41	51	
MPDFRRFDI	YRKVPKDLTQ	PTYTGAIISI	CCCLFILFLF	LSELTGFITT	EVVNELYVDD	60
PDKDSGGKID	VSLNISLPLN	HCELVGLDIQ	DEMGRHEVGH	IDNSMKIPLN	NGAGCRFEGQ	120
FSINKVPGNF	HVSTHSATAQ	PQNPDMTHVI	HKLSFGDTLQ	VQNIHGAFNA	LGGADRLTSN	180
PLASHDYILK	IVPTVYEDKS	GKQRYSYQYT	VANKEYVAYS	HTGRIIPAIW	FRYDLSPITV	240
KYTERRQPLY	RFITTICAI	GGTFTVAGIL	DSCIPTASEA	WKIKQLGKMH		290

Seq ID NO: C429 Protein Sequence  
Protein Accession #: NP\_002142.1

1	11	21	31	41	51	
MAQKEGGRTV	PCCSRPKVAA	LTAGTLLLLT	AIGAASWAIV	AVLLRSDQEP	LYPVQVSSAD	60
ARLMVFDKTE	GTWRLLCSSR	SNARVAGLSC	EEMGFRLALT	HSELDVRTAG	ANGTSGFFCV	120
DEGRLPHTQR	LLEVISVDCD	PRGRFLAAIC	QDCGRRKLPV	DRIVGGRTDS	LGRWPWQVSL	180
RYDGAHLCCG	SLLSGDWILT	AAHCFPERNR	VLSRWRFVAG	AVAQASPHGL	QLGVQAVVYH	240
GGYLPFRDPN	SEENSNDIAL	VHLSSPLPLT	EYIQPVCLPA	AGQALVDGKI	CTVTGWGNTQ	300
YYGQAGVLQ	EARVPIISND	VCGADFYGN	QIKPKMPCAG	YPEGGIDACQ	GDSSGPFVCE	360
DSISRTPRNR	LCGIVSWGTS	CALAQKPGVY	TKVSDFREWI	FQAIKTHSEA	SGMVTQL	417

Seq ID NO: C430 Protein Sequence  
Protein Accession #: BAA92562.1

1	11	21	31	41	51	
METTIVLSGIN	FEYKGMTGWE	VAGDHIYTAA	GASDNDFMIL	TLVVPGFRRP	QSVMA DTENK	60
EVARITVFVE	TLCVSNCELY	FMVGVNSRTN	TPVETWKGSK	GKQSYTYIIE	ENTTTSFTWA	120
FORTTFHEAS	RKYTNDVAKI	YSINVTNVNM	GVASVCRPCA	LEASDVGSSC	TSCPAGYYID	180
RDSGTCHSCP	PNTILKAHQ	YGVQACVPCG	PGTKNNKIHS	LCYNDCTFSR	NTPTRTFNYN	240
FSALANTVTL	AGGPSFTSKG	LKYPHHFTLS	LCGNQGRKMS	VCIDNVTDLR	IPEGESGFSK	300
SITAYVCQAV	IIPPEVTGYK	AGVSSQPVSL	ADRLIGVTID	MTLDGTTSPA	ELPHLESGLI	360
PDVIFFYRSN	DVTQSCSSGR	STTIRVRCSP	QKTVPGLLL	PGTCSGDTGC	GCNFHFLWES	420
AAACPLCSVA	DYHAIVSSCV	AGIQKTTYVW	REPCLCSGGI	SLPEQRVTIC	KTIDFWLKVG	480
ISAGTCTAIL	LTVLTCYFWK	KNQKLEYKYS	KLVMNATLKD	CDLPAADSCA	IMGEDVEDD	540
LIFTSKSLF	GKIKSFTSKQ	PAPVTISLSE	DS			572

Seq ID NO: C431 Protein Sequence  
Protein Accession #: NP\_004855.1

1	11	21	31	41	51	
MPGQELRTVN	GSQMLLVLLV	LSWLPHGGAL	SLAEASRAS	PGPSELHSED	SRFRELKRY	60
EDLLTRLRAN	QSWEDSNTDL	VPAPAVRIIT	FEVRLGSGGH	LHLRISRAAL	PEGLPEASRL	120
HRALFRLSPT	ASRSWDVTRP	LRRQLSLARP	QAPALHLRLS	PPPSQSDQLL	AESSSARPQL	180
ELHLRQQAAR	GRRRARARNG	DDCPLGPGRC	CLRLTVRASL	EDLGWADWVL	SPREVQVTMC	240
IGACPSQFRA	ANMHAQIKTS	LHRLKPDTEP	APCCVPASYN	FMVLIQKTD	GVSLQTYDDL	300
LAKDCHCI						308

Seq ID NO: C433 Protein Sequence  
Protein Accession #: NP\_443090.1

1	11	21	31	41	51	
MEDPSGAREP	RARPRERDFG	RRPHPDQGR	HDRPRDRPGD	PRRKRSSDGN	RRRDGDRDPK	60
RDQERDGNRD	RNRDRERERE	RERDPDRGPR	RDTRDAGPR	AGEHGVWEKP	RQSRTRDGAR	120
GLTWDAAPFP	GPAPWEAPEP	POPQRKQDPG	RRRPESEKPS	ERYLPSTPRP	GREVEVEYQS	180
BAEGLLECHK	KYKLTGRAC	CQMLEVLLNL	LILACSSVS	SSTGGYTGIT	SLGGIYYYP	240
GGAYSGFDGA	DGEKAQQLDV	QFYQLKLPV	TVAMACSGAL	TALCCLFVAM	GVLRVPHWCP	300
LLLVTGELL	MLIAGGYIPA	LYPYFHYLSA	AYGSPVCKER	QALYQSKGYS	GFGCSFHGAD	360
IGAGIFALG	IVVFALGAVL	AIKGYRKVRK	LKEKPAEMFE	P		401

Seq ID NO: C435 Protein Sequence  
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGAAGRQDFL	FKAMLTISWL	TLTCFPGATS	TVAAGCPDQS	PELQPNWPGH	DQDHHVHIGQ	60
GKTLILTSSA	TVYSIHISBG	GKLVKIDHDE	PIVLTRTHIL	IDNGGELHAG	SALCPFGGNF	120
TIIILGRADE	GIQDPYPYGL	KYIGVGKGA	LELHGQKLS	WTFLNKTLHP	GGMAEGGYFF	180
ERSWGHGRVI	VHVIDPKSGT	VIHSDRFDTY	RSKKESERLV	QVLNAVDPGR	ILSVAVNDEG	240
SRNLDDMARK	AMTKLGSKHF	LHLGFRHPWS	FLTVKGNPSS	SVEDHIEYHG	HRGSAARVP	300
KLPTHEGEY	FNVSLSEWV	QDVETWEPD	HDKVSQTKGG	EKISDLWKAH	PGKICNRPID	360
IQATTMDGVN	LSTEVVYKKG	QDYRFACYDR	GRACRSYRVR	FLCGKPVRPK	LTVTIDTNVN	420
STILNLEDNV	QSNWPKGDTLV	IATDYSMYQ	AEEFQVLPCR	SCAPNQVKVA	GKPMYHLIGE	480
EIDGVDMAE	VGLLSRNIIV	MGEMEDKCYP	YRNHICNFPD	PDTFGGHIKF	ALGFKAHLE	540
GTELKRMGQ	LVGYPIRHP	LAGDVDERGG	YDPPTYIRDL	SIHRTFSRCV	TVHGSNGLLI	600
KDVVGYNL	HCFTEDGPE	ERNFTDHCLG	LLVKSQTLLP	SDRDSKMCQM	ITEDSYPGYI	660
PKPRQDCNAV	STFWMANPNN	NLINCAAAGS	EBTGFWFIFH	HVPTGPSVGM	YSPGYSEHIP	720

LGKFYNNRAH	SNYRAGMIID	NGVKITEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFIAYKNQ	DHGAWLRGGD	VWLDSCHFRG	EAQEGFLLTG	MKAGGILLGG	DEAASGMAQG	840
FSPPCRCLLK	LVTGSPFAH	VSLAHS				866

5

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein  
5 incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1           1.     A method for determining the presence or absence of a pathological cell in a  
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%  
3 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient,  
4 thereby determining the presence or absence of said pathological cell.

1           2.     The method of Claim 1, wherein:  
2           a) said pathology is described in Table 1, including a cancer; and/or  
3           b) said biological sample comprises isolated nucleic acids.

1           3.     The method of Claim 1, wherein said biological sample is tissue from an organ  
2 which is affected by said pathology of Table 1, including a cancer.

1           4.     The method of Claim 2, wherein said nucleic acids are mRNA

1           5.     The method of Claim 2:  
2           a) further comprising a step of amplifying nucleic acids before said step of detecting  
3           said nucleic acid; or  
4           b) where said detecting is of a protein encoded by said nucleic acid.

1           6.     The method of Claim 1, wherein said nucleic acid comprises a sequence as  
2 described in Tables 2A-80.

1           7.     The method of Claim 2, wherein:  
2           a) said detecting step is carried out by:  
3           i) using a labeled nucleic acid probe;  
4           ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence  
5           as described in Tables 2A-80; or  
6           iii) detecting a polypeptide encoded by said nucleic acid; or  
7           b) said patient is:  
8           i) undergoing a therapeutic regimen to treat said pathology of Table 1; or  
9           ii) is suspected of having said pathology or cancer.

1           8.     An isolated nucleic acid molecule comprising a sequence as described in  
2 Tables 2A-80.

- 1           9.     The nucleic acid molecule of Claim 8, which is labeled.
- 1           10.    An expression vector comprising the nucleic acid of Claim 8.
- 1           11.    A host cell comprising the expression vector of Claim 10.
- 1           12.    An isolated polypeptide which is encoded by a nucleic acid molecule  
2 comprising a sequence as described in Tables 2A-80.
- 1           13.    An antibody that specifically binds a polypeptide of Claim 12.
- 1           14.    The antibody of Claim 13:  
2 a) conjugated to an effector component;  
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a  
4 cytotoxic chemical;  
5 c) which is an antibody fragment; or  
6 d) which is a humanized antibody.
- 1           15.    A method for specifically targeting a compound to a pathological cell in a  
2 patient, said method comprising administering to said patient an antibody of Claim 13,  
3 thereby providing said targetting.
- 1           16.    A method for determining the presence or absence of a pathological cell in a  
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1           17.    The method of Claim 16, wherein:  
2 a) said antibody is conjugated to:  
3 i) an effector component; or  
4 ii) a fluorescent label; or  
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1           18.    A method for identifying a compound that modulates a pathology-associated  
2 polypeptide, said method comprising the steps of:



- 3 a) contacting said compound with a pathology-associated polypeptide, said  
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence  
5 at least 80% identical to a sequence as described in Tables 2A-80; and  
6 b) determining the functional effect of said compound upon said polypeptide.

1 19. A drug screening assay comprising the steps of:

- 2 a) administering a test compound to a mammal having a pathology of Table 1 or a  
3 cell isolated therefrom; and  
4 b) comparing the level of gene expression of a polynucleotide that selectively  
5 hybridizes to a sequence at least 80% identical to a sequence as described in  
6 Tables 2A-80 in a treated cell or mammal with the level of gene expression of said  
7 polynucleotide in a control cell or mammal, wherein a test compound that  
8 modulates said level of expression of the polynucleotide is a candidate for the  
9 treatment of said pathology.  
10